PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6:		NDER THE PATENT COOPERATION TREATY (PCT)		
	42	(11) International Publication Number: WO 98/4543		
C12N 15/12, C07K 14/47, A61K 38/17, C12N 5/10, C12Q 1/68	A2	(43) International Publication Date: 15 October 1998 (15.10.98		
(21) International Application Number: PCT/US9	(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO paten (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian paten (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European paten (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT			
(22) International Filing Date: 10 April 1998 (10				
(30) Priority Data: 08/837,312 10 April 1997 (10,04.97)				
(71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 8 bridgePark Drive, Cambridge, MA 02140 (US).	s/ Can	LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI CM, GA, GN, ML, MR, NE, SN, TD, TG).		
(72) Inventors: JACOBS, Kenneth; 151 Beaumont Avenut ton, MA 02160 (US). MCCOY, John, M.; 56 Street, Reading, MA 01867 (US). LAVALLIE, I R.; 113 Ann Lee Road, Harvard, MA 01451 (US). Lisa, A.; 124 School Street, Acton, MA 01720 (US) BERG, David; 2 Orchard Drive, Acton, MA 0172 TREACY, Maurice; 93 Walcott Road, Chestnut H 02167 (US). SPAULDING, Vikki; 11 Meadowbanl Billerica, MA 01821 (US). AGOSTINO, Michael Wolcott Avenue, Andover, MA 01810 (US).	Howar Edward RACII MER O (US) IIII, MA k Road	Published Without international search report and to be republished upon receipt of that report.		
74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, 1 CambridgePark Drive, Cambridge, MA 02140 (US).	Inc., 8			
54) Title: SECRETED EXPRESSED SEQUENCE TAGS	(aDST)			
57) Abstract	(2023)			
Secreted expressed sequence tags (sESTs) isolated from	m a va	ety of human tissue sources are provided.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
ΑT	Austria	FR	France	LU	Luxembourg	SN	Senegal
ΑU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
ΑZ	Azerbaijan	GB	United Kingdom	MC	Monaco .	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	ТĴ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav	TM	Turkmenistan
BF	Burkina Faso	GR	Greece		Republic of Macedonia	TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	ΙE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	zw	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's	NZ	New Zealand		
CM	Cameroon		Republic of Korea	PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

SECRETED EXPRESSED SEQUENCE TAGS (SESTS)

FIELD OF THE INVENTION

5

25

30

The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

BACKGROUND OF THE INVENTION

Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of target organisms which are not actually expressed wastes substantial effort on areas not likely to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they were transcribed.

Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect. Since the EST approach theoretically identifies all expressed proteins, it produces an EST library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators searching for secreted proteins because they must separate the secreted "wheat" from the non-secreted "chaff", wasting effort and resources in the process.

Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted

5

10

15

20

25

30

proteins, namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

SUMMARY OF THE INVENTION

The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEO ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEO ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEO ID NO:87, SEO ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEO ID NO:101, SEO ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEO ID NO:106, SEO ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEO ID NO:110, SEO ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEO ID NO:115, SEO ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEO ID NO:119, SEO ID NO:120, SEO ID NO:121, SEO ID NO:122, SEO ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,

5

10

15

20

25

30

SEO ID NO:128, SEO ID NO:129, SEO ID NO:130, SEO ID NO:131, SEO ID NO:132, SEO ID NO:133, SEO ID NO:134, SEO ID NO:135, SEO ID NO:136. SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEO ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145. SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEO ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154. SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163. SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEO ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEO ID NO:191, SEO ID NO:192, SEO ID NO:193, SEO ID NO:194, SEO ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEO ID NO:205, SEO ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEO ID NO:218, SEO ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEO ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEO ID NO:236, SEO ID NO:237, SEO ID NO:238, SEO ID NO:239, SEO ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEO ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280,

5

10

15

20

25

30

SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEO ID NO:313, SEO ID NO:314, SEO ID NO:315, SEO ID NO:316. SEO ID NO:317, SEO ID NO:318, SEO ID NO:319, SEO ID NO:320, SEO ID NO:321, SEO ID NO:322, SEO ID NO:323, SEO ID NO:324, SEO ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEO ID NO:367, SEO ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEO ID NO:385, SEO ID NO:386, SEO ID NO:387, SEO ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433,

5

10

15

20

25

30

SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442. SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEO ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451. SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEO ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460. SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEO ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469. SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487. SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496. SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505. SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586,

5

10

15

20

25

30

SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEO ID NO:595. SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604. SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEO ID NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEO ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEO ID NO:631. SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649. SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEO ID NO:658. SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685. SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703. SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739,

5

10

15

20

25

30

SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748. SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEO ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757. SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEO ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEO ID NO:772, SEO ID NO:773, SEO ID NO:774, SEO ID NO:775. SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784. SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID NO:789, SEO ID NO:790, SEO ID NO:791, SEO ID NO:792, SEO ID NO:793. SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829, SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874, SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEQ ID NO:884, SEO ID NO:885, SEO ID NO:886, SEO ID NO:887, SEQ ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892,

5

10

15

20

25

30

SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEO ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910. SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEO ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEO ID NO:919. SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEO ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928. SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEO ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937. SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946. SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955. SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEO ID NO:961, SEO ID NO:962, SEO ID NO:963, SEO ID NO:964. SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID

```
NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID
           NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID
           NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEO ID
           NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID
 5
           NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID
           NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID
           NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID
           NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID
           NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID
10
           NO:1077, SEQ ID NO:1078, SEQ ID NO:1079. SEQ ID NO:1080, SEQ ID
           NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID
           NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID
           NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID
           NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID
15
           NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID
           NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID
           NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID
           NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID
           NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID
20
           NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID
           NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID
           NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID
           NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID
           NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID
           NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID
25
           NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID
           NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID
           NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID
           NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID
           NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID
30
           NO:1161, SEO ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID
           NO:1165, SEO ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID
           NO:1169, SEO ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID
           NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID
```

```
NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID
           NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID
           NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID
           NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID
           NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID
 5
           NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID
           NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID
           NO:1205, SEO ID NO:1206, SEO ID NO:1207, SEO ID NO:1208, SEO ID
           NO:1209, SEO ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID
           NO:1213, SEO ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID
10
           NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID
           NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID
           NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID
           NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID
           NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID
15
           NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID
           NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID
           NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID
           NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID
20
           NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID
           NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID
           NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID
           NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID
           NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID
25
           NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID
           NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID
           NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID
           NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID
           NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID
           NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID
30
           NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID
           NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID
           NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID
           NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID
```

```
NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID
           NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID
           NO:1321, SEQ ID NO:1322, SEQ ID NO:1323. SEQ ID NO:1324, SEQ ID
           NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID
           NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID
 5
           NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID
           NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID
           NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID
           NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID
           NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID
10
           NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID
           NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID
           NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID
           NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID
15
           NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID
           NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID
           NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID
           NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID
           NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID
20
           NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID
           NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID
           NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID
           NO:1401, SEO ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID
           NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID
           NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID
25
           NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID
           NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID
           NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID
           NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID
           NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ ID
30
           NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ ID
           NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID
           NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID
           NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID
```

en en 1900 Lineare de la companya de la companya Lineare de la companya de la companya

NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID 5 NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID 10 NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, SEQ ID NO:1500, SEQ ID NO:1501, SEQ ID NO:1502, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID NO:1505, SEQ ID NO:1506, SEQ ID NO:1507, SEQ ID NO:1508, SEQ ID 15 NO:1509, SEQ ID NO:1510, SEQ ID NO:1511, SEQ ID NO:1512, SEQ ID NO:1513, SEQ ID NO:1514, SEQ ID NO:1515, SEQ ID NO:1516, SEQ ID NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;

or a complement of said sequence.

20

25

30

In other embodiments, the present invention provides an isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:41, SEQ ID NO:47, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:6

5

10

15

20

25

30

ID NO:66, SEO ID NO:67, SEO ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEO ID NO:72, SEO ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEO ID NO:77, SEO ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEO ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEO ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEO ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEO ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEO ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

5

10

15

20

25

30

NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEO ID NO:245, SEO ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEO ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEO ID NO:272, SEO ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEO ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEO ID NO:299, SEO ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEO ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEO ID NO:313, SEO ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEO ID NO:331, SEO ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEO ID NO:335, SEO ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEO ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEO ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEO ID NO:371, SEO ID NO:372, SEO ID NO:373, SEO ID NO:374, SEO ID

5

10

15

20

25

30

NO:375, SEO ID NO:376, SEO ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEO ID NO:380, SEO ID NO:381, SEO ID NO:382, SEO ID NO:383, SEO ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEO ID NO:389, SEO ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406. SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEO ID NO:416, SEO ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEO ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEO ID NO:425, SEO ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEO ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEO ID NO:461, SEO ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEO ID NO:475, SEO ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEO ID NO:479, SEO ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEO ID NO:493, SEO ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEO ID NO:497, SEO ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEO ID NO:502, SEO ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEO ID NO:506, SEO ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEO ID NO:515, SEO ID NO:516, SEO ID NO:517, SEQ ID NO:518, SEQ ID NO:519. SEO ID NO:520, SEO ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID

5

10

15

20

25

30

NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEO ID NO:532. SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEO ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEO ID NO:541. SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEO ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEO ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559. SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEO ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568. SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577. SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586. SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEO ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEO ID NO:595. SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599. SEO ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID

5

10

15

20

25

30

NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEO ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEO ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEO ID NO:700, SEO ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEO ID NO:704, SEO ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEO ID NO:708, SEO ID NO:709, SEO ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEO ID NO:718, SEO ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEO ID NO:722, SEO ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEO ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEO ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEO ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEO ID NO:772, SEO ID NO:773, SEQ ID NO:774, SEQ ID NO:775, SEO ID NO:776, SEO ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784, SEO ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEO ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807. SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEO ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEO ID NO:821, SEO ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEO ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829, SEO ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID

anda Taragaran Majaran Sasar Taragaran Sasar 5

10

15

20

25

30

NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEO ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEO ID NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEO ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874, SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEO ID NO:884, SEO ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892, SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901, SEO ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEO ID NO:911, SEO ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEO ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEO ID NO:929, SEO ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937, SEO ID NO:938, SEO ID NO:939, SEO ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEO ID NO:947, SEO ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID

5

10

15

20

25

30

NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEO ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEO ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID NO:1057, SEO ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID NO:1065, SEO ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1069. SEO ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID NO:1081. SEO ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID

```
NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID
          NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID
           NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID
           NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID
           NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID
 5
           NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID
          NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID
           NO:1153, SEO ID NO:1154, SEO ID NO:1155, SEO ID NO:1156, SEO ID
           NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID
           NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID
10
           NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID
           NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID
           NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID
           NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID
           NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID
15
           NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID
           NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID
           NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID
           NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID
           NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID
20
           NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID .
           NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID
           NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID
           NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID
           NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID
25
           NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID
           NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID
           NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID
           NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID
30
           NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID
           NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID
           NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID
           NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID
           NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID
```

```
NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID
           NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID
           NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID
           NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID
 5
           NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID
           NO:1281, SEO ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEO ID
           NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID
           NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEO ID
           NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID
10
           NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID
           NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID
           NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID
           NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID
           NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID
           NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID
15
           NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID
           NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID
           NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID
           NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID
20
           NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID
           NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID
           NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID
           NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID
           NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID
           NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID
25
           NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID
           NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID
           NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID
           NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID
30
           NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID
           NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID
           NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID
           NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID
           NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID
```

```
NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID
           NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEO ID
           NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID
           NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID
 5
           NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID
           NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID
           NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID
           NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID
           NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEO ID
10
           NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEO ID
           NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID
           NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID
           NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID
           NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID
15
           NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID
           NO:1457, SEO ID NO:1458, SEO ID NO:1459, SEO ID NO:1460, SEO ID
           NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID
           NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID
           NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID
           NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID
20
           NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID
           NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID
           NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID
           NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID
25
           NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID
           NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, SEQ ID NO:1500, SEQ ID
           NO:1501, SEQ ID NO:1502, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID
           NO:1505, SEQ ID NO:1506, SEQ ID NO:1507, SEQ ID NO:1508, SEQ ID
           NO:1509, SEQ ID NO:1510, SEQ ID NO:1511, SEQ ID NO:1512, SEQ ID
30
           NO:1513, SEQ ID NO:1514, SEQ ID NO:1515, SEQ ID NO:1516, SEQ ID
           NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;
```

or a complement of said sequence.

In further embodiments, the present invention provides an isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

5

10

15

20

25

30

SEO ID NO:1, SEO ID NO:2, SEO ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEO ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEO ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEO ID NO:22, SEO ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEO ID NO:27, SEO ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEO ID NO:32, SEO ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEO ID NO:37, SEO ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEO ID NO:101, SEO ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEO ID NO:119, SEO ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEO ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEO ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEO ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159. SEO ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

5

10

15

20

25

30

SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172. SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222. SEO ID NO:223, SEO ID NO:224, SEQ ID NO:225, SEO ID NO:226, SEO ID NO:227, SEO ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEO ID NO:241, SEO ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEO ID NO:250, SEO ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEO ID NO:254, SEO ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316,

5

10

15

20

25

30

SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEO ID NO:376, SEO ID NO:377, SEO ID NO:378, SEO ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEO ID NO:403, SEO ID NO:404, SEO ID NO:405, SEO ID NO:406, SEO ID NO:407, SEO ID NO:408, SEO ID NO:409, SEO ID NO:410, SEO ID NO:411, SEO ID NO:412, SEO ID NO:413, SEO ID NO:414, SEO ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469,

5

10

15

20

25

30

SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEO ID NO:515, SEO ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEO ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEO ID NO:556, SEO ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEO ID NO:587. SEO ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEO ID NO:592, SEO ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEO ID NO:601, SEO ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEO ID NO:610, SEO ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEO ID NO:619, SEO ID NO:620, SEQ ID NO:621, SEQ ID NO:622,

5

10

15

20

25

30

SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEO ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEO ID NO:731, SEO ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775,

5

10

15

20

25

30

SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784, SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEO ID NO:821, SEO ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829, SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEO ID NO:835, SEO ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEO ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEO ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874, SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEO ID NO:884, SEO ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, SEO ID NO:889, SEO ID NO:890, SEQ ID NO:891, SEQ ID NO:892, SEO ID NO:893, SEO ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEO ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEO ID NO:911, SEO ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEO ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928,

5

10

15

20

25

30

SEO ID NO:929, SEO ID NO:930, SEO ID NO:931, SEO ID NO:932, SEO ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937, SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946. SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955. SEO ID NO:956, SEO ID NO:957, SEO ID NO:958, SEO ID NO:959, SEO ID NO:960, SEO ID NO:961, SEO ID NO:962, SEQ ID NO:963, SEO ID NO:964. SEO ID NO:965, SEO ID NO:966, SEO ID NO:967, SEO ID NO:968, SEO ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEO ID NO:974, SEO ID NO:975, SEO ID NO:976, SEO ID NO:977, SEO ID NO:978, SEO ID NO:979, SEO ID NO:980, SEO ID NO:981, SEO ID NO:982, SEO ID NO:983, SEO ID NO:984, SEO ID NO:985, SEO ID NO:986, SEO ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEO ID NO:992, SEO ID NO:993, SEO ID NO:994, SEO ID NO:995, SEO ID NO:996, SEO ID NO:997, SEO ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID

5

10

15

20

25

```
NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEO ID
NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID
NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID
NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID
NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID
NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID
NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEO ID
NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID
NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEO ID
NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID
NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID
NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID
NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID
NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID
NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID
NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID
NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID
NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID
NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID
NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID
NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID
NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID
NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID
NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID
NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID
NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID
NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID
NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID
NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID
NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID
NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID
NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID
NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID
NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID
```

```
NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID
           NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID
           NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID
           NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID
           NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID
 5
           NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID
           NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID
           NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID
           NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID
           NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID
10
           NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID
           NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID
           NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID
           NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID
           NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID
15
           NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID
           NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID
           NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID
           NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID
           NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID
20
           NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID
           NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID
           NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID
           NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID
           NO:1305, SEO ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID
25
           NO:1309, SEO ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID
           NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID
           NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID
           NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID
           NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID
30
           NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID
           NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID
           NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID
           NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID
```

```
NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEO ID
           NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID
           NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEO ID
           NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEO ID
           NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEO ID
 5
           NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEO ID
           NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEO ID
           NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID
           NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID
           NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID
10
           NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEO ID
           NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID
           NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID
           NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID
15
           NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEO ID
           NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID
           NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID
           NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID
           NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID
20
           NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID
           NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID
           NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ ID
           NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ ID
           NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID
25
           NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID
           NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID
           NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID
           NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID
           NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID
30
           NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID
           NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID
           NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID
           NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID
           NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID
```

NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, SEQ ID NO:1500, SEQ ID NO:1501, SEQ ID NO:1502, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID NO:1505, SEQ ID NO:1506, SEQ ID NO:1507, SEQ ID NO:1508, SEQ ID NO:1509, SEQ ID NO:1510, SEQ ID NO:1511, SEQ ID NO:1512, SEQ ID NO:1513, SEQ ID NO:1514, SEQ ID NO:1515, SEQ ID NO:1516, SEQ ID NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;

or a complement of said sequence.

5

10 -

15

20

25

30

In yet other embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100,

5

10

15

20

25

30

SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEO ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109. SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEO ID NO:127. SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136. SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEO ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154. SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEO ID NO:163. SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172. SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181. SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEO ID NO:205, SEO ID NO:206, SEO ID NO:207, SEO ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253,

5

10

15

20

25

30

SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEO ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280. SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289. SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEO ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307. SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316. SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEO ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406,

5

10

15

20

25

30

SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424. SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433. SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451. SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEO ID NO:470, SEO ID NO:471, SEO ID NO:472, SEO ID NO:473, SEO ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEO ID NO:484, SEO ID NO:485, SEO ID NO:486, SEO ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559,

5

10

15

20

25

30

SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568. SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEO ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577. SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEO ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEO ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEO ID NO:595. SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEO ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613. SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEO ID NO:619, SEO ID NO:620, SEO ID NO:621, SEO ID NO:622. SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEO ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEO ID NO:632, SEO ID NO:633, SEO ID NO:634, SEO ID NO:635, SEO ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEO ID NO:641, SEO ID NO:642, SEO ID NO:643, SEO ID NO:644, SEO ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712,

5

10

15

20

25

30

SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEO ID NO:718, SEO ID NO:719, SEQ ID NO:720, SEQ ID NO:721. SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEO ID NO:731, SEO ID NO:732, SEO ID NO:733, SEO ID NO:734, SEO ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748. SEQ ID NO:749, SEO ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEO ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775, SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784, SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEO ID NO:826, SEO ID NO:827, SEO ID NO:828, SEO ID NO:829, SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEO ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEO ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEO ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865,

5

10

15

20

25

30

SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEO ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874. SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEO ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEO ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892. SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901. SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910. SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEO ID NO:919. SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937. SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEO ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID

```
NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEO ID
           NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEO ID
           NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEO ID
           NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID
           NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID
 5
           NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID
           NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEO ID
           NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEO ID
           NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEO ID
10
           NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID
           NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID
           NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEO ID
           NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID
           NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID
15
           NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID
           NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID
           NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID
           NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID
           NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID
20
           NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID
           NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID
           NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID
           NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID
           NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID
25
           NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID
           NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID
           NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID
           NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID
           NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID
30
           NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID
           NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID
           NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID
           NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID
           NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID
```

en de la companya de la co

```
NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEO ID
           NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID
           NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID
           NO:1165, SEQ ID NO:1166, SEQ ID NO:1167; SEQ ID NO:1168, SEQ ID
 5
           NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID
           NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID
           NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID
           NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID
           NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID
10
           NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID
           NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID
           NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID
           NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEO ID
           NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID
15
           NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID
           NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID
           NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID
           NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID
           NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID
20
           NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID
           NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID
           NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID
           NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID
           NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID
           NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID
25
           NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID
           NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID
           NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID
           NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID
30
           NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID
           NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID
           NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID
           NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID
           NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID
```

```
NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID
           NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEO ID
           NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEO ID
           NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID
 5
           NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID
           NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID
           NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID
           NO:1317, SEO ID NO:1318, SEO ID NO:1319, SEO ID NO:1320, SEO ID
           NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID
10
           NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEO ID
           NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID
           NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID
           NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID
           NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID
           NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID
15
           NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID
           NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID
           NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID
           NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID
           NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID
20
           NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID
           NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID
           NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID
           NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID
           NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID
25
           NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID
           NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID
           NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID
           NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID
30
           NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID
           NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID
           NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID
           NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID
           NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID
```

in 12 The green of the second second The second second second

```
NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID
           NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEO ID
           NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ ID
           NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID
 5
           NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID
           NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID
           NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEO ID
           NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEO ID
           NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEO ID
10
           NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID
           NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID
           NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEO ID
           NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID
           NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID
           NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID
15
           NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID
           NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID
           NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID
           NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, SEQ ID NO:1500, SEQ ID
20
           NO:1501, SEQ ID NO:1502, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID
           NO:1505, SEQ ID NO:1506, SEQ ID NO:1507, SEQ ID NO:1508, SEQ ID
           NO:1509, SEQ ID NO:1510, SEQ ID NO:1511, SEQ ID NO:1512, SEQ ID
           NO:1513, SEQ ID NO:1514, SEQ ID NO:1515, SEQ ID NO:1516, SEQ ID
           NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;
```

or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described polynucleotides.

DETAILED DESCRIPTION

The nucleotide sequences of the sESTs of the present invention are reported in the Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each SEQ ID NO: in the Sequence Listing.

Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

		101101124 07 111	- 0.0	12 110. 10. 0=0.	»-que	(e.g., 211, 2		•
	1	BK8	32		62	DY307	93	DY611
5	2	BV216	DW10	01	63	DY643	94	EC259
	3	BV274	33	DW831	64	DY656	95	DY711
	4	BV48	34	DW859	65	DY675	96	EC248
	5	DN351	35	DW875	66	DY988	97	EC32
	6	DN381	36	DW888	67	DY992	98	DO703
10	7	DN405	37	DW901	68	DY225	99	DO713
	8	DU651	38	DW902	69	DY236	100	DR294
	9	DU660	39	DW904	70	DY242	101	DY1
	10	DU675	40	DW905	71	DY254	102	DY10
	11	DU684	41	DW906	72	DY914	103	DY106
15	12	DD364	42	DW929	73	DY946	104	DY117
	13	DD379	43	DW981	74	DY955	105	DY148
	14	DD389	44	DX191	75	DY959	106	DY167
	15	DD401	45	DX219	76	DY961	107	DY17
	16	DD413	46	DX245	77	DY981	108	DY174
20	17	DD426	47	DX256	78	DY357	109	DY175
	18	DD428	48	DX267	79	DY358	110	DY178
	19	DN293	49	DX66	80	DY381	111	DY23
	20	DD454	50	DX81	81	DY413	112	DY27
	21	DD472	51	DY780	82	DY414	113	DY41
25	22	DD475	52	DY803	83	DY415	114	DY42
	23	DT306	53	DY809	84	DY431	115	DY8
	24	DW282	54	DY814	85	DY433	116	DY93
	25	DW300	55	DY261	86	DY436	117	EB107
	26	DW303	56	DY264	87	DY543	118	EB113
30	27	DW323	57	DY266	88	DY565	119	EB163
	28	DT258	58	DY271	89	DY585	120	EB25
	29	DW246	59	DY287	90	DY331	121	EB77
	30	DW324	60	DY297	91	DY586	122	EC172
	31	DW333	61	DY306	92	DY696	123	EC302

	124	EC317	158	EJ90	192	EJ224	226	EP378
	125	EC328	159	EM270	193	EJ240	227	EP38
	126	EC341	160	EM278	194	EJ254	228	EO109
	127	EC349	161	EN186	195	EJ258	229	EO120
5	128	ED105	162	EN215	196	EJ265	230	EQ166
	129	ED21	163	EN217	197	EJ280	231	EQ187
	130	ED23	164	EN234	198	EJ285	232	EQ188
	131	ED30	165	EN239	199	EJ307	233	EQ190
	132	ED43	166	EN256	200	EJ38	234	EQ194
10	133	ED54	167	EN260	201	DO235	235	EQ207
	134	EE177	168	EN264	202	DO238	236	EQ208
	135	EE65	169	EN266	203	DO263	237	EQ214
	136	DQ365	170	EN271	204	DO319	238	EQ215
	137	DK393	171	EN274	205	EJ324	239	EQ218
15	138	DK399	172	EN287	206	EN470	240	EQ219
	139	DO1128	173	EN310	207	EN477	241	EQ220
	140	DO1150	174	EN342	208	EN539	242	EQ221
	141	DZ34	175	EN363	209	EP451	243	EQ226
	142	DZ42	176	EN423	210	EO10	244	EQ229
20	143	EE116	177	EH106	211	EO14	245	EQ230
	144	EE93	178	EH145	212	EO48	246	EQ231
	145	DJ387	179	EH166	213	EO58	247	EQ233
	146	DJ402	180	EH167	214	EO60	248	EQ237
	147	DN551	181	EH178	215	EO62	249	EQ261
25	148	DN559	182	EH180	216	EO68	250	EQ272
	149	DN603	183	EH186	217	EO89	251	ER104
	150	DN629	184	EH188	218	EO90	252	ER106
	151	DN631	185	EH189	219	EO92	253	ER128
	152	DO11	186	EH190	220	EO97	254	ER134
30	153	DO118	187	EH203	221	EP108	255	ER174
	154	DO15	188	EH206	222	EP165	256	ER201
	155	DO157	189	EH95	223	EP219	257	ER77
	156	DO19	190	EJ148	224	EP234	258	ER80
	157	EJ53	191	EJ179	225	EP277	259	ER97

	260	ES136	294	ER399	328	FB264	362	FG208
	261	ES306	295	ER408	329	FB38	363	FG265
	262	ES35	296	ER418	330	FB71	364	FG274
	263	ES37	297	ER430	331	FB78	365	FG278
5	264	ES206	298	ER471	332	FC12	366	FG281
	265	ET13	299	ER476	333	FB349	367	FG291
	266	ET22	300	ER493	334	FC136	368	FG294
	267	ET39	301	ER496	335	FC170	369	FG340
	268	ET84	302	ER498	336	FD152	370	FG363
10	269	EF121	303	ER524	337	FE141	371	FG372
	270	EF129	304	EW13	338	FE5	372	FG380
	271	EF45	305	EX25	339	FD131	373	FG401
	272	EF48	306	EX53	340	EC425	374	FG99
	273	EF5	307	EY165	341	EC428	375	FI203
15	274	EF88	308	EY29	342	ED204	376	FE311
	275	EG194	309	EZ35	343	ED205	377	FE315
	276	EG251	310	EZ4	344	ED210	378	FE322
	277	EH12	311	EZ88	345	ED223	379	FE329
	278	EH213	312	EZ93	346	DI301	380	FE341
20	279	EH22	313	FA8	347	DI303	381	FE366
	280	EH221	314	EV234	348	DI310	382	FE375
	281	EH248	315	EW101	349	DI39	383	FE412
	282	EH29	316	EW109	350	DJ90	384	FE415
	283	EH61	317	EW150	351	DM290	385	FE442
25	284	EH68	318	EY197	352	DM304	386	FE472
	285	EH78	319	EY206	353	DN618	387	FE557
	286	EH80	320	EY215	354	DN896	388	FE568
	287	ER311	321	EZ209	355	DN904	389	FE619
	288	ER329	322	FA139	356	FG119	390	FE676
30	289	ER343	323	FA171	357	FG126	391	FE682
	290	ER366	324	FA252	358	FG140	392	FF150
	291	ER369	325	FA28	359	FG193	393	FF153
	292	ER381	326	FA316	360	FG197	394	FF168
	293	ER395	327	FA95	361	FG198	395	FF175

	396	FF181	430	FH17	464	FN203	498	FO201
	397	FF46	431	FH170	465	FN228	499	FO209
	398	FF49	432	FH24	466	FN229	500	FO211
	399	FF97	433	FH3	467	FN251	501	FO215
5	400	FG41	434	FH39	468	FN254	502	FO253
	401	FG437	435	FH56	469	FP134	503	FO254
	402	FG441	436	FH6	470	FP14	504	FO261
	403	FG448	437	FH66	471	FP163	505	FO267
	404	FG45	438	FM109	472	FP172	506	FO275
10	405	FG492	439	FM13	473	FP71	507	FO290
	406	FG504	440	FM15	474	F P87	508	FO292
	407	FG565	441	FM150	475	EI118	509	FO316
	408	FG567	442	FM170	476	EI16	510	FO324
	409	FG57	443	FM28	477	EI187	511	FO327
15	410	FG577	444	FM3	478	EI203	512	FO348
	411	FG615	445	FM32	479	E1228	513	FO36
	412	FG625	446	FM36	480	EI231	514	FO38
	413	FG630	447	FM60	481	E1236	515	FO40
	414	FG659	448	FM86	482	EI239	516	FO66
20	415	FG708	449	FM95	483	EI243	517	FO75
	416	FG91	450	FM98	484	EI250	518	FP185
	417	FG884	451	FM99	485	EI255	519	FP193
	418	FG891	452	FN172	486	EI264	520	FP233
	419	FG909	453	FN19	487	EI273	521	FP239
25	420	FG912	454	FN29	488	FO11	522	FP246
	421	FG949	455	FN53	489	FO125	523	FP262
	422	FG952	456	FK199	490	FO128	524	FP268
	423	FG965	457	FK217	491	FO133	525	FP271
	424	FH10	458	FK23	492	FO135	526	FP273
30	425	FH116	459	FK32	493	FO147	527	FQ505
	426	FH123	460	FK59	494	FO152	528	DN647
	427	FH13	461	FK78	495	FO160	529	DN650
	428	FH136	462	FN189	496	FO173	530	DN676
	429	FH149	463	FN191	497	FO182	531	DO94

	532	FR292	566	DN827	600	FY201	634	DU4
	533	FR436	567	DN833	601	FY202	635	DU75
	534	FR451	568	DN834	602	FY243	636	FY386
	535	FR473	569	DN850	603	FY265	637	FY388
5	536	FS10	570	DO913	604	FY316	638	FY398
	537	FS106	571	DO923	605	FY318	639	FY414
	538	FS107	572	DO935	606	FY321	640	GA48
	539	FS143	573	DO938	607	FY354	641	GA63
	540	FS173	574	DO944	608	FY356	642	GA64
10	541	FS28	575	DO949	609	FY421	643	DT382
	542	FS31	576	DO952	610	FY430	644	DT385
	543	FS40	577	DQ12	611	FY455	645	DT388
	544	FV35	578	DT2	612	FY484	646	DT464
	545	FV49	579	DT44	613	FY524	647	DT470
15	546	FV68	580	DT53	614	FY530	648	DT478
	547	FW13	581	DT8	615	FY628	649	DT482
	548	FW64	582	FQ661	616	DQ242	650	DU114
	549	FY127	583	FQ672	617	DQ262	651	DU118
	550	FY136	584	FQ696	618	DQ276	652	DU123
20	551	FY60	585	FR1087	619	DQ285	653	DU133
	552	FY65	586	FR927	620	DQ304	654	DU156
	553	FY72	587	FR938	621	DQ313	655	DU157
	554	DN1112	588	FR980	622	DQ51	656	FZ5
	555	DN1118	589	FV122	623	DQ54	657	FZ87
25	556	DN1122	590	FV131	624	DR628	658	DW181
	557	DN782	591	FV132	625	GU215	659	DW309
	558	DN793	592	FV84	626	FM481	660	DX1
	559	DN795	593	FV85	627	DT117	661	DX15
	560	DN806	594	FV95	628	DT133	662	DX19
30	561	DN809	595	FX115	629	DT139	663	DX22
	562	DN810	596	FX127	630	DT164	664	DX29
	563	DN814	597	FX154	631	DU160	665	DX3
	564	DN815	598	FY187	632	DU164	666	DX4
	565	DN823	599	FY199	633	DU166	667	FZ428

	668	FZ163	702	FZ209	736	GE89	770	GF151
	669	DY474	703	FZ254	737	DY516	771	GF179
	670	FZ139	704	FZ346	738	DY529	772	GF99
	671	FX76	705	GA82	739	DY530	773	GB261
5	672	FX65	706	GA85	740	DY538	774	GC499
	673	FX55	707	GA91	741	DY830	775	GD177
	674	DU536	708	DX299	742	DY857	776	GD7
	675	FZ534	709	DX304	743	EA17	777	GE300
	676	DU515	710	DX309	744	EA36	778	DX179
10	677	DU475	711	DX316	745	GG73	779	DY757
	678	DU462	712	DX328	746	DU544	780	EC392
•	679	DU353	713	DX336	747	DU560	781	EE15
	680	DU341	714	DX354	748	DZ109	782	DU408
	681	DU306	715	DX357	749	EA105	783	DU410
15	682	DU278	716	DX359	750	EA106	784	DU416
	683	DU244	717	DX363	751	EA110	785	DU447
	684	DU238	718	DX364	752	EA123	786	DXIII
	685	DU236	719 `	DY478	753	EA46	787	DX112
	686	DU231	720	DY497	754	EA58	788	DX123
20	687	FZ639	721	DY508	755	EA7	789	DX138
	688	GC456	722	EA89	756	EA82	790	DX146
	689	GG126	723	EA9	757	GE361	791	DX153
	690	GG129	724	EA90	758	FZ510	792	DX157
	691	GG152	725	GC52	759	GE387	793	EE4
25	692	GG170	726	GC57	760	GE410	794	FZ676
	693	GG182	727	GC585	761	GE463	795	FZ683
	694	GG217	728	GC74	762	GE466	796	GD309
	695	GG440	729	GE28	763	GE468	797	GD358
	696	GG619	730	GE41	764	GE471	798	GG543
30	697	DX279	731	GE51	765	GE524	799	FX516
	698	DX288	732	GE60	766	GE539	800	FX536
	699	DX290	733	GE68	767	GE548	801	FZ1032
	700	DX295	734	GE80	768	GE549	802	FZ1041
	701	DX298	735	GE82	769	GE99	803	FZ1072

	804	FZ781	838	DD12	872	GP304	906	EM40
	805	GA147	839	DD127	873	GP329	907	EM42
	806	GA284	840	DD177	874	GP338	908	EM58
	807	DY723	841	DD204	875	GP340	909	GF185
5	808	DY737	842	DD207	876	GQ13	910	GF187
	809	DY739	843	DD211	877	GQ18	911	GF196
	810	EC399	844	DD217	878	GQ22	912	GF197
	811	EM254	845	DD504	879	GQ38	913	GF207
	812	FX194	846	DD509	880	GQ40	914	GF209
10	813	FX234	847	DD518	881	GQ56	915	GF212
	814	FX281	848	DD537	882	GQ6	916	GF218
	815	FX317	849	DD541	883	DD312	917	GF221
	816	FX353	850	DD71	884	DD352	918	GF222
	817	FX395	851	DH941	885	EK145	919	GF250
15	818	GA293	852	DQ194	886	EK208	920	GF255
	819	GA321	853	DQ204	887	EK223	921	GF256
	820	GA327	854	DQ215	888	EK234	922	GI28
	821	GB160	855	DQ216	889	EK480	923	GI3
	822	GA132	856	EK423	890	EK491	924	G130
20	823	GA135	857	EK424	891	EK499	925	GI51
	824	GA205	858	EK450	892	EK571	926	GI63
	825	GB814	859	EL15	893	EK578	927	GI7
	826	GF87	860	DD285	894	EK581	928	GI74
	827	GG687	861	EK598	895	EK591	929	G188
25	828	GG692	862	EK622	896	DD215	930	G19
	829	GG694	863	EK626	897	EK634	931	DY874
	830	GG702	864	EK649	898	EL358	932	DY886
	831	GG705	865	GO653	899	EL360	933	DY900
	832	GP23	866	GP107	900	EL387	934	EM358
30	833	GP56	867	GP123	901	EL391	935	EM381
	834	GP61	868	GP168	902	EM111	936	EM386
	835	GP65	869	GP232	903	EM112	937	EM388
	836	DD115	870	GP274	904	EM12	938	EM396
	837	DD119	871	GP297	905	EM125	939	EM397

	940	EM401	974	GT43	1008	HU212	1042	EY290
	941	EM406	975	GT6	1009	HU141	1043	EY304
	942	EM408	976	HR712	1010	HS555	1044	EY313
	943	EM409	977	HR704	1011	HR95	1045	FK295
5	944	EM423	978	HR693	1012	HR906	1046	FK301
	945	EM424	979	HR628	1013	HR76	1047	FK317
	946	FE196	980	HR605	1014	HR753	1048	FK328
	947	FE204	981	EK341	1015	HR731	1049	FK349
	948	FE205	982	EK390	1016	EN116	1050	FK350
10	949	FE207	983	EN108	1017	EM341	1051	FK354
	950	FE215	984	FK235	1018	FJ283	1052	FK365
	951	FE222	985	GK428	1019	FJ307	1053	FQ105
	952	FE227	986	GT56	1020	FJ70	1054	FQ239
	953	,FE228	987	FQ562	1021	FM176	1055	FQ360
15	954	FE248	988	FQ605	1022	FM197	1056	FQ45
	955	FE263	989	FQ608	1023	FM205	1057	GU353
	956	FE271	990	FQ609	1024	FM208	1058	GX167
	957	GF296	991	FQ612	1025	FM229	1059	GX183
	958	GN38	992	FS49	1026	FQ419	1060	GX208
20	959	GN45	993	FS87	1027	GX48	1061	GX210
	960	GN60	994	GM101	1028	GX5	1062	FM369
	961	GN68	995	GM103	1029	GX92	1063	FM375
	962	GN82	996	GM114	1030	· FM289	1064	FM389
	963	GR286	997	GM129	1031	FM290	1065	FM432
25	964	EN10	998	GM153	1032	FM296	1066	FM459
	965	EN37	999	GM158	1033	FM300	1067	FM462
	966	FK127	1000	GM196	1034	FM312	1068	FM479
	967	FK151	1001	GM243	1035	GU512	1069	GX301
	968	GS26	1002	GM259	1036	GU534	1070	GX336
30	969	GS4	1003	GM266	1037	GU608	1071	GX354
	970 -	EV391	1004	HV38	1038	GX159	1072	GX361
	971	FG535	1005	HV23	1039	GX97	1073	GX403
	972	FG852	1006	HV199	1040	EW304	1074	GX408
	973	GT28	1007	HV181	1041	EY281	1075	GX418

	1076	GU830	1110	GG3	1144	GN97	1178	HE91
	1077	GU925	1111	HA510	1145	HB443	1179	HF289
	1078	GU940	1112	HA422	1146	HC324	1180	HG444
	1079	GX1031	1113	HA382	1147	HC327	1181	HF137
5	1080	GX496	1114	HA360	1148	HC505	1182	HD706
	1081	GX504	1115	HA249	1149	HC724	1183	HG710
	1082	GX509	1116	HA199	1150	HA1054	1184	HG733
	1083	GX536	1117	HA192	1151	HB1041	1185	HG775
	1084	GX540	1118	GZ568	1152	HB746	1186	HI222
10	1085	GX645	1119	GY520	1153	HB752	1187	HI39
	1086	GX700	1120	GY515	1154	HB975	1188	HH215
	1087	GX730	1121	GY330	1155	HC705	1189	HH357
	1088	GX750	1122	GY307	1156	HA791	1190	HH372
	1089	GX753	1123	HA81	1157	HC1002	1191	HH378
15	1090	GX760	1124	HA73	1158	HC1071	1192	HH390
	1091	GX814	1125	HA29	1159	HC1089	1193	HH396
	1092	GX851	1126	HA24	1160	HC831	1194	HH404
	1093	GX909	1127	HA18	1161	HC986	1195	HH433
	1094	GY102	1128	GZ78	1162	GY72	1196	HI2
20	1095	GY105	1129	GZ70	1163	HG159	1197	HH544
	1096	GY138	1130	GZ7	1164	HG620	1198	HH608
	1097	GY211	1131	GZ496	1165	HD161	1199	HH612
	1098	GX1082	1132	GZ495	1166	HD353	1200	HH625
	1099	GX1108	1133	GZ485	1167	HD378	1201	НН640
25	1100	GX1140	1134	GZ436	1168	HD417	1202	HH648
	1101	GX1165	1135	GZ420	1169	HD427	1203	HH691
	1102	GX576	1136	GZ378	1170	HD434	1204	HJ120
	1103	GX595	1137	GZ37	1171	HD499	1205	НЈ140
	1104	GX606	1138	GY558	1172	HD569	1206	HJ181
30	1105	GX619	1139	GG894	1173	HD627	1207	HJ184
	1106	G G87 4	1140	GG907	1174	HD648	1208	HJ22
	1107	GG858	1141	GN114	1175	HE111	1209	HJ253
	1108	GG836	1142	GN115	1176	HE142	1210	HJ265
	1109	GG8	1143	GN145	1177	HE178	1211	HJ362

		1212	HJ395	1246	HM372	1280	HO722	1314	HT166
		1213	HJ411	1247	HM380	1281	HO799	1315	HT176
		1214	HJ444	1248	HM422	1282	HO801	1316	HT193
		1215	HJ65	1249	HM444	1283	HO817	1317	HT43
	5	1216	HJ674	1250	HM497	1284	HO82	1318	HT81
		1217	НJ705	1251	HM544	1285	HK719	1319	HW149
		1218	HJ81	1252	HM643	1286	HO1077	1320	HW152
		1219	HJ862	1253	HN72	1287	HO1080	1321	HW190
		1220	НЈ949	1254	HN78	1288	HO1087	1322	HW204
1	10	1221	HK10	1255	HO107	1289	HO1143	1323	HW221
		1222	HK26	1256	HO237	1290	HO1176	1324	HW243
		1223	HK60	1257	HO266	1291	HO1183	1325	HW261
		1224	HJ1037	1258	HO277	1292	HO1216	1326	HW368
		1225	HJ968	1259	HO283	1293	HO1271	1327	HW74
1	15	1226	HJ981	1260	HO292	1294	HO1329	1328	HX10
		1227	HJ994	1261	HO294	1295	HO1434	1329	HX102
		1228	HJ995	1262	HO305	1296	HO1441	1330	HX110
		1229	HK189	1263	HO315	1297	HO1453	1331	HX113
		1230	HK234	1264	HO332	1298	HO854	1332	HX155
2	20	1231	HK650	1265	HO358	1299	HO868	1333	HX188
		1232	HK658	1266	HO476	1300	HP262	1334	HX29
		1233	HK669	1267	HO48 ₁ 1	1301	HQ36	1335	HX50
		1234	HK713	1268	HO502	1302	HQ72	1336	HY13
		1235	HK899	1269	HO54	1303	GM16	1337	HY3
2	25	1236	HE187	1270	HO60	1304	GM286	1338	HY55
		1237	HK162	1271	HO600	1305	GM295	1339	HY57
		1238	HL25	1272	HO617	1306	GM335	1340	HZ15
		1239	HL380	1273	HO640	1307	GM365	1341	HZ8
		1240	HL73	1274	HO663	1308	HR397	1342	IAl
3	3 0	1241	HM50	1275	HO688	1309	HR560	1343	IA21
		1242	HM54	1276	HO692	1310	HR593	1344	IA32
		1243	HM91	1277	HO693	1311	HR598	1345	IA36
		1244	HM236	1278	HO703	1312	HT13	1346	IB2
		1245	HM280	1279	HO717	1313	HT137	1347	IC2

	1348	IC9	1382	IA167	1413	HW786	1447	IE362
	1349	HY229	1383	1A183	1414	HW810	1448	IH32
	1350	HY244	1384	IA188	1415	HW846	1449	II113
	1351	HY344	1385	IA200	1416	HW849	1450	IJ101
5	1352	HY370	1386	IA220	1417	IB15	1451	IJ163
	1353	HY374	1387	IA64	1418	IB19	1452	IJ167
	1354	HY404	1388	IA69	1419	IB22	1453	IF28
	1355	HY419	1389	1A86	1420	IB28	1454	IF376
	1356	HY435	1390	HW936	1421	IB36	1455	1F456
10	1357	HZ103	1391		1422	IB49	1456	IF87
	1358	HZ109	HW10	17	1423	IC103	1457	IJ1201
	1359	HZIII	1392		1424	IC126	1458	IJ1220
	1360	HZ115	HW10	44	1425	IC132	1459	IJ1237
	1361	HZ71	1393		1426	IC142	1460	IJ1240
15	1362	HZ76	HW10	59	1427	IC155	1461	IJ1247
•	1363	HZ88	1394	HW430	1428	IC54	1462	IJ1287
	1364	HW115	1395	HW432	1429	IC87	1463	IJ1292
	1365	HW128	1396	HW440	1430	IC92	1464	IJ1299
	1366	HW477	1397	HW456	1431	IE146	1465	IJ583
20.	1367	HW483	1398	HW518	1432	IE147	1466	1J592
	1368	HW491	1399	HW591	1433	IE149	1467	IJ5 9 7
	1369	HW499	1400	HW598	1434	IE169	1468	1J629
	1370	HW507	1401	HW627	1435	IZ6	1469	1J638
	1371	HZ116	1402	HW646	1436	JE33	1470	IJ640
25	1372	HZ162	1403	HW649	1437	JE44	1471	IJ642
	1373	HZ185	1404	HW693	1438	JE52	1472	IJ6 8 6
	1374	HZ201	1405	HW695	1439	IE10	1473	IG25
	1375	HZ224	1406	HW697	1440	IE47	1474	IG35
	1376	HZ262	1407	HW711	1441	IE73	1475	IH40
30	1377	IA106	1408	HW715	1442	JA37	1476	IH54
	1378	IA110	1409	HW730	1443	JA78	1477	IJ288
	1379	IA114	1410	HW732	1444	JB12	1478	IJ76
	1380	IA153	1411	HW741	1445	JB23	1479	IF292
	1381	IA157	1412	HW750	1446	1E352	1480	IF513

	1481	IF548	1515	1Q58
	1482	IJ1043	1516	15488
	1483	IJ1048	1517	IS564
	1484	IJ1054	1518	IT23
5	1485	[]1088	1519	IT44
	1486	IJ 777		
	1487	1J887		
	1488	IJ907	•	
	1489	1J928		
10	1490	1J942		•
	1491	IL1		
	1492	IL100		
	1493	IL112		
	1494	IL28		
15	1495	IK11		
	1496	IK14		
	1497	IK20		
	1498	IK203		
	1499	IK209		
20	1500	IK212		
	1501	IK343		
	1502	IK73		
	1503	IO134		
	1504	IO138		
25	1505	IO151		
	1506	1O202		
	1507	IO209		
	1508	IO31		
	1509	IO356		
30	1510	10420		
	1511	1062		
	1512	IQ15		
	1513	IQ45		
	1514	IQ55		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selection "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

10

15

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplpasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides disclosed herein.

20

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions, most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

	Stringenc y Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	В	DNA:DNA	< 50	T _B *; 1xSSC	T _B *; 1xSSC
	С	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	a	DNA:RNA	< 50	T _D *; 1xSSC	T _D *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	RNA:RNA	< 50	T _f *; 1xSSC	T _F *; 1xSSC
	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	Н	DNA:DNA	< 50	T _H *; 4xSSC	T _H *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	<50	T _j *; 4xSSC	T,*; 4xSSC
15	К	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	< 50	T _L *; 2xSSC	T _L *; 2xSSC
	М	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50	T _N *; 6xSSC	T _N *; 6xSSC
	0	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	P	DNA:RNA	< 50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50	T _R *; 4xSSC	T _R *; 4xSSC

5

10

15

20

25

35

[‡]: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

*: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

* T_B · T_R : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m (°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m (°C) = 81.5 + 16.6(log [Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The soluted polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

10

15

20

30

sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac[®] kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA

Sepharose[®]; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

15

20

30

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

and the second s

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

10

25

30

The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as porbes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise antiprotein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligand. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

15

25

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

10

15

20

30

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ, Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto, 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

10

15

20

30

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

eri Pagas Pagas San

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

15

3.0

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

10

15

20

25

30

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

10

15

25

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigenpulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991: Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

25 <u>Hematopoiesis Regulating Activity</u>

15

20

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemo:herapy,either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

15

20

30

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

5

10

15

20

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-liketissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-liketissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

10

25

30

plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

10

15

20

25

30

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

5

10

15

20

30

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15 Receptor/Ligand Activity

10

25

30

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusioninjury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

20 <u>Tumor Inhibition Activity</u>

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

30

5

10

15

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

15

ADMINISTRATION AND DOSING

15

20

25

30

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

5

15

20

can directly signal T cells. Alternatively antibodies able to bind surface immunolgobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

20

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about $0.01~\mu g$ to about 100~mg (preferably about 0.1~ng to about 10~mg, more preferably about $0.1~\mu g$ to about 1~mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

15

25

30

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem. Soc. 85, 2149-2154 (1963); J.L. Krstenansky, et al., FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

25

30

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses(including hydroxyalkylcelluloses),including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose,the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorbtion of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

25

30

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

Sel.	Species	Tissue	Call Tyme
AA	Human	Kidney	Cell Type 19-23wks., M/F pool of 5
AB	Human		
AC AC		Fetal Lung	Fetal Lung
	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
AI	Human	Blood	Adult PBMC/TH1or2
AJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
AZ	Human	Colon	Caco-2 Adenocarcinoma
В	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	
BM			10-61yrs., pool of 11
	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
BO	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1or2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C	Human	Blood	PeripheralBloodMononuclearCell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC T	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	SalivaryGland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	PeripheralBloodMononuclearCell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney

DL	Human	Brain	N/A
DM	Human	Brain	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP ·	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	***
EX	Human	Testes	26yrs., 1 specimen
EY	Human	Brain	10-61yrs., pool of 11
EZ	Human	Fetal Kidney2	19-23wks., M/F pool of 5
FA	Human	Brain	Fetal Kidney
FB	Human	Placenta	19-23wks., M/F pool of 5
FC	Human		26yrs., 1 specimen
FD	Human	Testes	10-61yrs., pool of 11
FE		SalivaryGland	N/A
	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA

FG	Human	Desim	NT/A
FH	Human	Brain Brain	N/A
FI	Human	Small Intest	19-23wks., M/F pool of 5
FJ	Human		Adult I man CA
FK	Human	Lung CA	Adult Lung CA
FM	Human	Kidney	Adult Kidney
FN	Human	Brain	N/A
FO		Brain	19-23wks., M/F pool of 5
FP	Human	Brain	N/A
	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX	Human	Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human	Placenta	26yrs., 1 specimen
G CA	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	Fetal Kidney
GV	Rat	Retina	Newborn Retina
GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GX	Human	Brain	N/A
GY	Human	Testes	10-61yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
Н	Human	Blood	PeripheralBloodMononuclearCell

HA Human Fetal Kidney2 Fetal Kidney HC Human Brain 19-23wks., M/F pool of 5 HD Human Brain N/A HE Human Brain 19-23wks., M/F pool of 5 HG Human Brain 19-23wks., M/F pool of 5 HG Human Brain N/A HI Human Brain N/A HI Human Brain N/A HI Human Brain N/A HK Human Brain 19-23wks., M/F pool of 11 HJ Human Brain N/A HK Human Brain 19-23wks., M/F pool of 5 HL Human Brain N/A HK Human Brain 19-23wks., M/F pool of 5 HL Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Brain N/A HT Human Brain N/A HT Human Brain N/A HX Human Brain 19-23wks., M/F pool of 5 HU Human Brain N/A HT Human Brain N/A HT Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Brain N/A HT Human Brain N/A HT Human Brain N/A HT Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Brain N/A HT Human Brain Hippoca Adult Brain Hippocampus HY Human Brain Thalamus HY Human Brain Thalamus HY Human Brain Thalamus Adult Brain Thalamus I Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HC Human Brain 19-23wks., M/F pool of 5 HD Human Brain N/A HE Human Testes 10-61yrs., pool of 11 HF Human Brain 19-23wks., M/F pool of 5 HG Human Fetal Kidney2 Fetal Kidney HH Human Brain N/A HI Human Brain N/A HK Human Brain 19-23wks., M/F pool of 5 HL Human Brain 19-23wks., M/F pool of 5 HL Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Brain N/A HT Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Fetal Kidney2 Fetal Kidney HV Human Brain 19-23wks., M/F pool of 5 HU
HID Human Brain N/A HE Human Testes 10-61yrs., pool of 11 HF Human Brain 19-23wks., M/F pool of 5 HG Human Fetal Kidney2 Fetal Kidney HH Human Brain N/A HII Human Brain N/A HII Human Brain N/A HK Human Brain 19-23wks., M/F pool of 5 HL Human Brain 19-23wks., M/F pool of 5 HL Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HM Human Brain N/A HN Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Brain 19-23wks., M/F pool of 5 HQ Human Brain N/A HS Human Brain N/A HS Human Brain N/A HT Human Brain N/A HT Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Brain N/A HT Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Brain N/A HT Human Brain Hippoca 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Brain Thalamus I Human Brain Thalamus I Human Brood PeripheralBloodMononuclearCell IA Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HE Human Testes 10-61yrs., pool of 11 HF Human Brain 19-23wks., M/F pool of 5 HG Human Fetal Kidney2 Fetal Kidney HH Human Brain N/A HI Human Testes 10-61yrs., pool of 11 HJ Human Brain N/A HK Human Brain 19-23wks., M/F pool of 5 HL Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HM Human Testes Adult NCCIT TeratoCA HN Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Fetal Kidney2 Fetal Kidney HV Human Fetal Kidney2 Fetal Kidney HV Human Brain N/A HX Human Brain N/A HX Human Brain N/A HX Human Brain Hippoca HY Human Brain Hippoca HY Human Brain Hippoca HY Human Brain Thalamus I Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HF Human Brain 19-23wks., M/F pool of 5 HG Human Fetal Kidney2 Fetal Kidney HH Human Brain N/A HI Human Brain N/A HK Human Brain 19-23wks., M/F pool of 5 HL Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Fetal Kidney2 Fetal Kidney HV Human Brain N/A HX Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Fetal Kidney2 Fetal Kidney HV Human Brain 19-61yrs., pool of 11 HW Human Brain N/A HX Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocarnpus HY Human Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HG Human Fetal Kidney2 Fetal Kidney HH Human Brain N/A HI Human Testes 10-61yrs., pool of 11 HJ Human Brain N/A HK Human Brain 19-23wks., M/F pool of 5 HL Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Brain N/A HX Human Brain N/A HX Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HG Human Fetal Kidney2 Fetal Kidney HH Human Brain N/A HI Human Testes 10-61yrs., pool of 11 HJ Human Brain N/A HK Human Brain 19-23wks., M/F pool of 5 HL Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain 19-23wks., M/F pool of 5 HU Human Brain 19-24 Adult Brain Hippocampus HY Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Brain Thalamus I Human Brain Thalamus Adult Brain Thalamus I Human Brain Thalamus Adult Brain Thalamus I Human Brain Thalamus Adult Trachea HZ Human Brain Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HH Human Brain N/A HI Human Testes 10-61yrs., pool of 11 HJ Human Brain N/A HK Human Brain 19-23wks., M/F pool of 5 HL Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HN Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Fetal Kidney2 Fetal Kidney HV Human Fetal Kidney2 Fetal Kidney HV Human Brain N/A HX Human Brain N/A HX Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HI Human Brain N/A HK Human Brain 19-23wks., M/F pool of 5 HL Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HM Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Brain 19-23wks., M/F pool of 5 HU Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Brain N/A HX Human Brain 19-23wks., M/F pool of 5 HU Human Brain 19-23wks., M/F pool of 11 HW Human Brain 19-23wks., M/F pool of 5 HU Human Brain 19-23wks., M/F pool of 11 HW Human Brain 19-23wks., M/F pool of 11 HW Human Brain 19-23wks., M/F pool of 5 HU Human B
HJ Human Brain N/A HK Human Brain 19-23wks., M/F pool of 5 HL Human Fetal Kidney2 Fetal Kidney HM Human Testes Adult NCCIT TeratoCA HN Human Brain N/A HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Brain 19-23wks., M/F pool of 5 HU Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Trachea Adult Trachea HZ Human Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HK Human Brain 19-23wks., M/F pool of 5 HL Human Fetal Kidney2 Fetal Kidney HM Human Testes Adult NCCIT TeratoCA HN Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain N/A HX Human Brain N/A HX Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Trachea Adult Trachea HZ Human Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HL Human Fetal Kidney2 Fetal Kidney HM Human Testes Adult NCCIT TeratoCA HN Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Brain N/A HS Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Fetal Kidney2 Fetal Kidney HV Human Brain N/A HX Human Brain N/A HX Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Brain Thalamus HY Human Brain Thalamus I Human Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HM Human Testes Adult NCCIT TeratoCA HN Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain N/A HX Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocarnpus HY Human Trachea Adult Trachea HZ Human Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HN Human Fetal Kidney2 Fetal Kidney HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocarnpus HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HO Human Brain N/A HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HP Human Brain 19-23wks., M/F pool of 5 HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocarnpus HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HQ Human Testes 10-61yrs., pool of 11 HR Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocarnpus HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HR Human Brain N/A HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HS Human Brain N/A HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HT Human Brain 19-23wks., M/F pool of 5 HU Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocarnpus HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HU Human Fetal Kidney2 Fetal Kidney HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HV Human Testes 10-61yrs., pool of 11 HW Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocarnpus HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HW Human Brain N/A HX Human Brain Hippoca Adult Brain Hippocampus HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HX Human Brain Hippoca Adult Brain Hippocampus HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
HY Human Trachea Adult Trachea HZ Human Brain Thalamus Adult Brain Thalamus I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
I Human Blood PeripheralBloodMononuclearCell IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
IA Human Thyroid Adult Thyroid IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
IB Human Embryonal CA Fetal NT2-D1 IC Human WER1-Rb1 line Adult Retinoblastoma
IC Human WER1-Rb1 line Adult Retinoblastoma
ID Human Muscle N/A
IE Human Brain 19-23wks., M/F pool of 5
IF Human Uterus N/A
IG Human Testes 10-61yrs., pool of 11
IH Human Muscle N/A
II Human Brain N/A
IL Human Retina 16-75yrs., pool of 76
IM Human Various Various
IN Human Prostate Adult Prostate
IO Human Brain 19-23wks., M/F pool of 5
IP Human Fetal Kidney2 Fetal Kidney
IQ Human Prostate Adult Prostate
IR Human Brain Hippoca Adult Brain Hippocampus
IS Human Trachea Adult Trachea
IT Human Brain Thalamu Adult Brain Thalamus

SEQUENCE LISTING

(1) GENERAL	INFORMATION
١		/ GENERAL	THEORMALTON

- (i) APPLICANT: Jacobs, Kenneth McCoy, John LaVallie, Edward Racie, Lisa Merberg, David Treacy, Maurice
 - Spaulding, Vikki Agostino, Michael
- (ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
- (iii) NUMBER OF SEQUENCES: 1519
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy Disk
 - (B) COMPUTER: IBM PC Compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
 - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8224
 - (B) TELEFAX: (617) 876-5851
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAGATGTTG	AGGTGGCTGC	TGACCTTGGG	TCTCATCTCC	TTGATTTTCT	TTATCTTCTT	60
CATTGCCGTC	CTCTCTAGGC	TGTCTTTGGC	GAGGAGGCC	CCTGCGGAAT	CGTGGTCTAT	120
ATCCCCGATA	CATATTCTGC	CTCACTGGTC	TACCTTGTTC	TCCTGCACCC	TGGTTGTCAG	180
CACCCTCCAT	CACTTCTCCC	TGCACAGGAG	GGTTGGAATA	CTGTGGTCGA	CGCCCATAGG	240

GGCCTTCGGG	GTAGTAAGGT GGGAACCTTC GCCTGCGGTA GGGCCGGCGT TGTTGGGCCT AGCACTCTCC GATCCCTCGT TCTTTTCCCC ACTCTCACTA TTCTGGTAAT ATTGCGTGGA GGAGAACAGG TAGACTCGAG	300 360 400
(2) INFORM	ATION FOR SEQ ID NO:2:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:2:	
TTTTGGAAAA	CCAGCACTTT AAAAATTGGT ATAGTTCACA TAAATATTCT GAATTCAGGC GTTGTGGACC CAAGAATACT AGGCCCGCAT TTTCTTACGT CAACATTCTT TGAATGGACT GTTCTCTTTG GCCCCCTATC TCGAG	60 120 165
(2) INFORM	ATION FOR SEQ ID NO:3:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 299 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:3:	
	CCTTCCTCTC CTACTCCCTT CCTTAGGCTC CTGAACTCGT TTGCTCCTAA	60
TTCTCTGTCT TTATCCTCAA	TTCTTTTTCT CTGGATTTTG GTTTCTTTTG GCTTTCCCTT GCCTTCCCCT CCAACACTCT TTCCCCATGT CTTTCTGGCT GTCTCTATGT TCCTCTTCTC CTTTCTGTCC ATTCGGGCCT CCTCCCCACC TCCCACGCCC CAGCCCCTCC TCCTTTTCGA TATGCCAAAC CAATTTTGGG TCGAGTGCAT TCCCTCGAG	120 180 240 299
TTCTCTGTCT TTATCCTCAA CTCCTTGGTC	CCAACACTCT TTCCCCATGT CTTTCTGGCT GTCTCTATGT TCCTCTTCTC CTTTCTGTCC ATTCGGGCCT CCTCCCCACC TCCCACGCCC CAGCCCCTCC	180 240
TTCTCTGTCT TTATCCTCAA CTCCTTGGTC (2) INFORM	CCAACACTCT TTCCCCATGT CTTTCTGGCT GTCTCTATGT TCCTCTTCTC CTTTCTGTCC ATTCGGGCCT CCTCCCCACC TCCCACGCCC CAGCCCCTCC TCCTTTTCGA TATGCCAAAC CAATTTTGGG TCGAGTGCAT TCCCTCGAG	180 240
TTCTCTGTCT TTATCCTCAA CTCCTTGGTC (2) INFORM	CCAACACTCT TTCCCCATGT CTTTCTGGCT GTCTCTATGT TCCTCTTCTC CTTTCTGTCC ATTCGGGCCT CCTCCCCACC TCCCACGCCC CAGCCCCTCC TCCTTTTCGA TATGCCAAAC CAATTTTGGG TCGAGTGCAT TCCCTCGAG ATION FOR SEQ ID NO:4: SEQUENCE CHARACTERISTICS: (A) LENGTH: 241 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	180 240
TTCTCTGTCT TTATCCTCAA CTCCTTGGTC (2) INFORM (i)	CCAACACTCT TTCCCCATGT CTTTCTGGCT GTCTCTATGT TCCTCTTCTC CTTTCTGTCC ATTCGGGCCT CCTCCCCACC TCCCACGCCC CAGCCCCTCC TCCTTTTCGA TATGCCAAAC CAATTTTGGG TCGAGTGCAT TCCCTCGAG ATION FOR SEQ ID NO:4: SEQUENCE CHARACTERISTICS: (A) LENGTH: 241 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	180 240
TTCTCTGTCT TTATCCTCAA CTCCTTGGTC (2) INFORM (ii) (xi) (xi) GCGATTGAAT ATGACTAAGT TTAATTTCGT	CCAACACTCT TTCCCCATGT CTTTCTGGCT GTCTCTATGT TCCTCTTCTC CTTTCTGTCC ATTCGGGCCT CCTCCCCACC TCCCACGCCC CAGCCCCTCC TCCTTTTCGA TATGCCAAAC CAATTTTGGG TCGAGTGCAT TCCCTCGAG ATION FOR SEQ ID NO:4: SEQUENCE CHARACTERISTICS: (A) LENGTH: 241 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear MOLECULE TYPE: cDNA	180 240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCC	TTCATGGCCT	AGGAAATGAC	TTTATTGTGG	TTGAATTAGT	TAAAGGGTAC	60
TTACATTACG	TGTTTGATTT	GGGAAATGGT	GCTAACCTCA	TCAAAGGAAG	CTCAAATAAA	120
CCTCTCAATG	ACAATCAGTG	GCACAACGTG	ATGATATCAA	GGGACACCAG	CAACCTCCAC	180
ACTGTAAAGA	TTGACACAAA	AATCACAACG	CAAATCACCG	CCGGAGCCAG	GAACTTAGAC	240
CTCAAGAGTG	ACTTATATAT	AGGAGGAGTA	GCTAAAGAAA	CATACAAATC	CTTACCAAAA	300
CTTGTACATG	CCAAAGAAGG	CTTTCAAGGC	TGCCTGGCAT	CAGTTGATTT	AAATGGACGG	360
CTCTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCGGCC	TTCATGGCCT	ATAAAATTTA	AAAATGCTAA	GGATCTGGCC	CCACAGGCCC	60
CAAAGCTTTC	ACAGAGCTCC	TCTTAGACAT	GAAGATGCCC	ATTGGCCTCC	TAGGTCCCAG	120
GAGGTGTGGG	CAGGACTGCC	CTTCCTCCGT	TCTCATTGCG	GGGCTCCTGA	AGGGGGTATC	180
TGAAAGTATG	TAAATCTGAT	GGGAGGTCTG	ATCCTCCTTT	TGCTAGCCCC	TGAACTCTGT	240
GGTGGAGTCT	GGCTGATGGC	CAGGGCCATG	TCCTAGAGGG	GACTCCCCTG	CAGGAGGCGG	300
GCTCTAAAGG	GAGTGGTGTC	CCTTTAGGCC	AGGGTTCACA	GTCGGGGTGG	TCTGGAGACT	360
GCAGGACTCA	GGGCCTGGGG	GTGGCATCAG	TCTGGCCAGG	CCCTGCGTCA	CTTGCACCCA	420
CTGTCTCGAG						430

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGTGGCTCA	TGCCTGTAAT	CCCGGCACTT	GGGTAGGCCA	GGGCAGCAGG	ATCGCTTGAG	60
CCCGGGAGTT	CGAGACAGCC	TGGGCAACAT	GGTGAGACCC	TGTCTCCATA	ATTTTTTA	120
AAAAATTGCC	AGGTGTGGTC	GTGTGTGCCT	GTGAGGCTGA	GGTGGGAGGC	TCGCTTGAGC	180
CCAGGGGTCA	AGGCTGCAGT	GAGCCATGAC	TGCACGCCAC	TGCACTCCAG	CGTGGGTGAC	240
AGAGTGAGAT	ACTGTATAAA	AAAAAAAAGC	TAAAACAAAA	CAAGAAGTAT	TATCTTAAGC	300
ATGTTATTTA	GAAATATGGA	GATAAATAAA	AATAACTGAA	AGTAGGTCGT	TGCTTCTGAG	360
GAGAGAAATT	GGGAGTTGGC	AAGGTCTCGA	G			391

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 351 base pairs

 (B) TYPE: nucleic acid

 (C) STRANDEDNESS: double

 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTTTTGGAG	CTGCTAAAAT	GCCGGATTAC	CTCGGTGCCG	ATCAGCGGAA	GACCAAAGAG	60
GATGAGAAGG	ACGACAAGCC	CATCCGAGCT	CTGGATGAGG	GGGATATTGC	CTTGTTGAAA	120
ACTTATGGTC	AGAGCACTTA	CTCTAGGCAG	ATCAAGCAAG	TTGAAGATGA	CATTCAGCAA	180
CTTCTCAAGA	AAATTAATGA	GCTCACTGGT	ATTAAAGAAT	CTGACACTGG	CCTGGCCCCA	240
CCAGCACTCT	GGGATTTGGC	TGCAGATAAG	CAGACACTCC	AGAGTGAACA	GCCTTTACAG	300
GTTGCCAGGT	GTACAAAGAT	AATCAATGCT	GATTCGGAGG	ACCCACTCGA	G	351

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTGATGTGTC	ACCCCAAGTG	CTCCACGTGC	TTGCCAGCCA	CCTGCGGCTT	GCCTGCTGAA	60
TATGCCACAC	ACTTCACCGA	GGCCTTCTGC	CGTGACAAAA	TGAACTCCCC	AGGTCTCCAG	120
ACCAAGGAGC	CCAGCAGCAG	CTTGCACCTG	GAAGGGTGGA	TGAAGGTGCC	CAGGAATAAC	180
AAACGAGGAC	AGCAAGGCTG	GGACAGGAAG	TACATTGTCC	TGGAGGGATC	AAAAGTCCTC	240
ATTTATGACA	ATGAAGCCAG	AGAAGCTGGA	CAGAGGCCGG	TGGAAGAATT	TGAGCTGTGC	300
CTTCCCGACG	GGGATGTATC	TATTCATGGT	GCCGTTGGTG	CTTCCAAACT	CGAG	354

- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCGGCC	TTCATGGNCT	AGGAGGAGGA	AGAGGAGTAC	GAGGATGACG	AGGGAGGAGG	60
GGGAAGACGA	GGAGGAGGAG	GAGGCTGCGG	CAGAGGCTGC	CGCGGGGGCC	AAACATGACG	120
ATGCCCACGC	CGAGATGCCT	GATGACGCCA	AGAAGTAAGG	GGGGCAGAGA	TGGATGAAGA	180
GAAAGCCCAC	GAAGAAAAA	GCCTGGTTTT	GTTTTTCCCA	GAATATCGAT	GGACTTAAAA	240
AGGCTCAGGT	TTTTGACCAA	AATACAATGT	GAATTTATTC	TGACATTCCT	AAAATAGATT	300
AAATTAAAGC	AATTAGATCC	TGGCCAGCTC	GATTCAAATT	TGACTTTCAT	TTTGAACATA	360
ATAAATATAT	CAAAAGGTGT	TAAAGAAAAC	TGAATTAAAC	CCAAAATTAT	GTTTTCATGG	420
TCTCTCCTCG	AG					432

(2) INFORMATION FOR SEQ ID NO:11:

en Sagen e^r en ster S

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 687 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTATTTTACA	TGCCCACCAG	CATTGTATGG	GGCTTCTCAC	TTGTCCACAT	GCTTGCCTGT	60
GTCATATTTG	ACTTAAAGCT	TATTTTGACG	GGAAACCAAT	TTGTCCTTTT	TTTGGAAAGG	120
GATGGCACCA	CAGATGTGAC	GCGGACAATG	CATTTTGGGA	CCCCTACAGC	CTACGAGAAG	180
GAATGCTTCA	CATATGTCCT	CAAGGGCCAC	ATAGCTGTGA	GTGCAGCCGT	TTTCCCGACT	240
GGAACCAAAG	GTCACCTTCT	TGACTCCTTT	GCCCGTTCAG	CTTTATGGGA	TTCAGGCCTA	300
GATTACTTGC	ACGGGACTGG	ACATGGTGTT	GGGTCTTTTT	TGAATGTCCA	TGAAGGTCCT	360
TGCGGCATCA	GTTACAAAC	ATTCTCTGAT	GAGCCCTTGG	AGGCAGGCAT	GATTGTCACT	420
GATGAGCCCG	GGTACTATGA	AGATGGGGCT	TTTGGAATTC	GCATTGAGAA	TGTTGTCCTT	480
GTGGTTCCTG	TGAAGACCAA	GTATAATTTT	AATAACCGGG	GAAGCCTGAC	CTTTGAACCT	540
CTAACATTGG	TTCCAATTCA	GACCAAAATG	ATAGATGTGG	ATTCTCTTAC	AGACAAAGAG	600
TGCGACTGGC	TCAACAATTA	CCACCTGACC	TGCAGGGATG	TGATTGGGAA	GGAATTGCAG	660
AAACAGGGCC	GCCAGGAAGC	TCTCGAG				687

- (2) INFORMATION FOR SEQ ID NO:12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATTCGGCC	TTCATGGCCT	AGTCGGTGGG	TGCCTGTAGT	CCCAGCTACT	TGGGAGGCTG	60
AGGGAGGAGA	ACTGCTTGAA	CCCGGGAGGC	AGAGGTTGCA	GTGAGCCGAG	ATTGTGCCAC	120
TGTACTCCAG	CCTGGGCCAC	AAAGCAAGAA	TCTGTCTCAA	ААААААААА	AAGAAAAGAA	180
AAGAATAAAT	TTCTTTTCCC	CTTGAAGAAG	TTGATTTAGG	CACAGACTCT	GGACTCTGGA	240
TTTCCCACAA	TGTCTTATCT	AGTCAACTCA	AGTATCTGGA	CTACAATTTT	CTTGAAAGCA	300
AAGCCCATAT	ATTAATAATC	TTTACTTGTA	TATAAATATT	CAATAAATCA	TTAAGTAAAT	360
GTGTAGAAGA	ATTTTATGCT	CAATAAGATC	CACCCGATCA	TGCATTTGAA	AATTCTCGAG	420

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

60	CATTTTGGGG	GTCAACATCC	CTGCTTTTCT	AGCACATACT	TTCATGGCCT	GAATTCGGCC
120	CCAGTTGTCC	ACTTGTTCTC	CAGTTTTTTA	TCCTGCACCC	TCATATTTAT	AAAGGAAAAG
180	ATTCTCCTTT	TTATATATAT	GGAAAAAAAA	AAGGGAAATT	TGGGTGTAAG	CCCTCTTCTC
240	GTTACACAGC	ACCCTAACTT	CAGCAAGTCC	AGAGGAGAGA	CCCCTACTCC	TAATGGTGGG

ACATACCACA	GGTTCTGGAA	TTCTCATCTT	CGAACCTAGA	GAAATAGGTG	CTATAAACAG	300
GGAATTAAGC	AAAATGCTGG	ATGCTATAGA	TCTTTTAATT	GTCTTAATTT	TTTTTCTATT	360
ATTAAACAAC	AGGCTCGAG					379

- (2) INFORMATION FOR SEQ ID NO:14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTCATGGCC	TACGGAAAGT	CAGCATGGAT	AACAGACTGA	TGGAACTCTT	TCCTGCCAAT	60
AAGCAAAGTG	TTGAACACTT	CACAAAATAT	TTTACTGAGG	CAGGCTTGAA	AGAGCTTTCA	120
GAATATGTTC	GGAATCAGCA	AACCATCGGA	GCTCGTAAGG	AGCTCCAGAA	AGAACTTCAA	180
GAACAGATGT	CCCGTGGTGA	TCCATTTAAG	GATATAATTT	TATATGTCTA	GGAGGAGATG	240
AAAAAAAACA	ACATCCCAGA	GCCAGTTGTC	ATCGGAATAG	TCTGGTCAAG	TGTAATGAGC	300
ACTGTGGAAT	GGAACAAAA	AGAGGAGCTT	GTAGCAGAGC	AAGCCATCAA	GCACTTGAAG	360
CAATACAGCC	CTCTACTTGC	TGCCTTTACT	ACTCAAGGTC	AGTCTGAGCT	GACTCTGTTA	420
CTGAAGATTC	AGGAGTATTG	CTATGACAAC	ATTCATTTCA	TGAAAGCCTT	CCAGAAAATA	480
GTGGTGCTTT	TTTATAAAGC	TGAAGTCCTG	AGCGAGGATG	CCCTCGAG		528

- (2) INFORMATION FOR SEQ ID NO:15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 466 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCC	TTCATGGCCT	AGCCCAGGCC	ACGCTACACT	CTGCCCACAC	TGGTGAGCAG	60
GAGGTCTTCC	CACGCCCTGT	CATTAGGCTG	CATTTACTCT	TGCTAAATAA	AAGTGGGAGT	120
GGGGCGTGCG	CGTTATCCAT	GTATTGCCTT	TCAGCTCTAG	ATCCCCCTCC	CCTGCCTGCT	180
CTGCAGTCGT	GGGTGGGGCC	CGTGCGCCGT	TTCTCCTTGG	TAGCGTGCAC	GGTGTTGAAC	240
TGGGACACTG	GGGAGAAAGG	GGCTTTCATG	TCGTTTCCTT	CCTGCTCCTG	CTGCACAGCT	300
GCCAGGAGTG	CTCTGCCTGG	AGTCTGCAGA	CCTCAGAGAG	GTCCCAGCAC	TGGCTGTGGC	360
CTTTCAGGTG	TAGGCAGGTG	GGCTCTGCTT	CCCGATTCCC	TGTGAGCGCC	CACCCTCTCG	420
AAAGAATTTT	CTGCTTGCCC	TGTGACTGTG	CAGACTCTGG	CTCGAG		466

- (2) INFORMATION FOR SEQ ID NO:16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCGGCC	TTCATGGCCT	AGCGTGATCC	TGGAACGTGC	TCTAGTTCGA	GAGAGTGAGG	60
GCTTTGAGGA	GCATGTACCA	TCTGATAACT	CTTGAAGATA	CAGAGAGAAA	TCCATCTTTT	120
CCCAGGTCTC	CTTCACTGAA	AACAAAAATC	TACTTACATA	CACTGTCACC	TTAGCATCAG	180
AGTCGGATTA	ATGAACTGCG	GAACAAGAGG	TTGTGAGAAT	CTAAGATGGA	ACCTTTCTTT	240
CTTTCTTTCT	TTTTTTTAA	ATTTTGTATT	TTCCATCCAA	CACTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:17:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGCC	TTCATGGCCT	AGGGCTCTGC	TTATAAACTT	CAAAGTTACA	CTGAAGGATA	60
CGGTAAAAAC	ACCAGTTTAG	TAACCATTTT	TATGATTTGG	AATACCATGA	TGGGAACATC	120
TATACTAAGC	ATTCCTTGGG	GCATAAAACA	GGCTGGATTT	ACTACTGGAA	TGTGTGTCAT	180
CATACTGATG	GGCCTTTTAA	CACTTTATTG	CTGCTACAGA	GTAGTGAAAT	CACGGACTAT	240
GATGTTTTCA	TTGGATACCA	CTACCTGGGA	ATATCCAGAT	GTCTGCAGAC	ATTATTTCGG	300
CTCCTTTGGG	CAGTGGTCGA	GTCTCCTCTT	CTCCTTGGTG	TCTCTCATTG	GAGCAATGAT	360
AGTTTATTGG	GTGCTTATGT	CAAATTTTCT	TTTTAATACT	GGAAAGTTTA	TTTTTAATTT	420
TATTCATCAC	ATTAATGACA	CAGACACTAT	ACTGAGTACC	AATAATAGCA	ACCCTGGTCT	480
CGAG						484

- (2) INFORMATION FOR SEQ ID NO:18:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

^ > > mmod.com	mas maaaams	~~~~~~~~~~~	GW3 3 GG GW3 G	> ma > ma > amm	N COMO COMO CON	60
GAATTGGCCT	TCATGGCCTA	GGAGATATAC	CTAATGCTAG	ATGATGAGTT	AGTGGGTGCA	
GCGCACCAGC	GTGGCACATG	TATACATATG	TAACTAACCT	GCACAATGTG	CACATGTACC	120
CTAAAACTTA	AAGTATATAT	AAAAAAAAA	GACNTCGCTA	GTGAGCACGC	TGTATACGAC	180
ATCGCTAATG	AGGACACCAT	ACAAGGCATC	GCTAACGATG	ACGCTGTACA	CAACATCACT	240
AATGATGACA	CCGTATAAGA	CATCGCTAAT	TATGACGCTG	TATACGACAT	CGCTAATGAC .	300
ACCGTACGAG	GCACGCTAAC	AAGGATGCTG	TACACAACAT	CGCTAATGAG	GACAGTGTAC	360
AAGCCATCGC	TAATGAGGAC	ACTGTATATG	ACATTGCTAA	CGAGGACACT	GTACAAGGCA	420
TTGCTAACGA	GGACGCTGTA	CACAACATCG	CTAATGACAC	CATATAAGAC	ATCACCAATG	480
AGGATGCTGT	ATATGACATC	GCTAATAACA	CCGCTCGAG			519

- (2) INFORMATION FOR SEQ ID NO:19:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCAGCTCTCA	TCCTCGTCTC	CCCAACACCA	TAACGTCCTC	ATCCCGCCTC	CAACCCACAC	60
CAGGCCGAAG	CCCTCAGAGA	GTGTTTTCAT	CAGGAACCAC	TCTCGAACCT	GAAGGTTGAC	120
TTTAGCGTTT	AGCAACCCAG	GGCGGTGTGT	GTGTTTCCCG	TTTTGTTTTC	TGAGTGGTAG	180
CAGTGATCAC	CGTAATTCCA	TGTAGCCATG	TGCTAGCAGA	ACCCCTGTGT	CCTCACCGTG	240
GCCCGTGTGA	CCCCAGCCGA	CGAGTGCCCG	GCGGAGTCCC	CGCTGCCTTC	CCATGGTCCA	300
GTGAGCTGCC	AGGGCATCAC	ATGACTCTCA	GCTGGGCTCG	AG		342

- (2) INFORMATION FOR SEQ ID NO:20:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

${\tt GAATTCGGCC}$	TTCATGGCCT	AGAGCAGCTC	TGAGGTAGAA	ATTACAACGA	TGAAAAGAGC	60
ACAACGTACA	AAACCAAGAA	AGAGTCTGTT	GTGTGAAGGG	TCATTCGATG	AAGAAGCTTC	120
TGCACAGTCC	TTTCAGGAAG	TGTTAAGTCA	ATGGAGAACC	GGAAATCATG	ATGACAACAA	180
GAAACAGAAT	TTACATGCAG	CAGTAAAAGA	CTCATTGGAA	GAATGCGAAG	TACAGACTAA	240
TCTGAAAATT	TGGAGAGAAC	CACTTAATAT	TGAACTTAAA	GAAGACATTC	TATCCTATAT	300
GGAAAAATTA	TGGCTTAAAA	AACACAGGAG	AACTCCACAA	GAGCAACTTT	TTAAAATGCT	360
ACCAGATACG	TTCCCACATC	CACATGAAAC	CACTGGTGAT	GCACAGTGTT	CTCAAAATGA	420
AAACGATGAA	GATAGTGATG	GTGAGGAGAC	CAAAGTACAA	CACACAGCTC	TTTTATTGCC	480
AGTAGAAACA	TTAAACATAG	AGAGACCTGA	ACCATCTCTA	AAGATAGTCG	AACTGGATGA	540
TACTTATGAA	GAGGAATTTG	AAGAAGCAGA	ACATCTCGAG			580

- (2) INFORMATION FOR SEQ ID NO:21:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAATTCGGCC	TTCATGGCCT	AGAAAGATCT	AATTATCATG	GACCTGCGAC	AGTTTCTTAT	60
GTGCCTGTCC	CTGTGCACAG	CCTTTGCCTT	GAGCAAACCC	ACAGAAAAGA	AGGACCGTGT	120
ACATCATGAG	CCTCAGCTCA	GTGACAAGGT	TCACAATGAT	GCTCAGAGTT	TTGATTATGA	180
CCATGATGCC	TTCTTGGGTG	CTGAAGAAGC	AAAGACCTTT	GATCAGTTGA	CACCAGAAGA	240
GAGCAAGGAA	AGGTTTGGAA	AGATTGTAAG	TAAAATAGAT	GGCGACAAGG	ATCGGCTCGA	300
G						301

- (2) INFORMATION FOR SEQ ID NO:22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAATTCGGCC	TTCATGGCCT	AAAAAAAGGA	TGGTGTGTTG	AGACCAGAAG	CAGCAGCAGT	60
CCTCGACATC	AACTACAACT	TTCCTTCGCA	CAGTGCATAC	CCTCTGATAT	ACTGAACCCA	120
ACGCCTATCC	TCCAGCCCCC	TAAGAACTAG	AGAGGGAGCC	TCACAACATT	CCAATTTAAT	180
CCTTCAGAAA	ATTCATTACT	CTTCAAAGTT	GTCTGTGGTT	TTGTGACAAC	GATATGACTA	240
GGTGCAAAAT	GGCTTGCAAC	TAATTAACAA	ACATAGAAGC	ATCCAACAAA	CATATACGTG	300
CACAATCTGA	GGATTTAGGG	ATGAAGCTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO:23:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCGGCC	TTCATGGCCT	ACCAGCCTGG	GCGACAGAGC	AAGACTCAGT	CTCAAAACAA	60
AACAAAACAA	AACAAAAAGA	GAAGGCTATT	ATTAACATTC	GAGATAATGT	GCCAGACTGC	120
TTCCATGTAT	TTTCATTATT	CTGTCCCAAA	TCTGGTGAAG	TGGGTATCTG	CACAGCTTTC	1.80
TCTAGATTGA	ACAACTAGTA	AGGGGGCTGG	CCCTGGAGAA	AGTTACCTCC	TGCCTCGAG	239

- (2) INFORMATION FOR SEQ ID NO:24:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATTCGGCC	TTCATGGCCT	ACTTTTATAT	TGTTATTTTT	GTAAAGCATC	TTTTCTTCAA	60
TTCTTGTTGG	CATTCTGGGC	CAAAATATTT	CAGGTTGGTT	CGGTGTGGAG	TTAAGAAAAG	120
CAGGCGTTTT	AGTGGAGAAA	TGGGGAACAG	CATCAAGAAA	GGCTTTTTTC	CTTTTTTCTT	180
ተተተተተተተተተርር	AGACAGAGTC	חתככככתכתכ	ACCCAGGCTG	GAGTGCAATG	GTCTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAATTCGGCC TTCATGGCCT AGATGGATTT CTTAATTGAA GTACTTTTAT AATCACAGTG

ATGTCCTTCC T	GAGGGTTAC TTTACTATAC TGTGTATGGT GTATAGCCAC AGAAAGTCAG TTCAATGTG TAAGTGTGAT GCATTCAACC CAGATCTCGA G	180 231
(2) INFORMAT	ION FOR SEQ ID NO:26:	
(i) SI	EQUENCE CHARACTERISTICS: (A) LENGTH: 307 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) !	MOLECULE TYPE: cDNA	
(xi) \$	SEQUENCE DESCRIPTION: SEQ ID NO:26:	
ATTGTCTGTG T ATTTTGGACC T TGCTAGTCCT T	TCATGGCCT ACACAGAGTA TATTTATAGC TATCTCAGGG TCCTTGTCCA CATTTCTC ATCTGCTTCT ACTGATTTT TCTGCTTCTG TTTACTCTTC ATTTTCCCT TATTTGGTGC TTTGCATACA ATTTGTTGGG ACTGGATCTT TAAATGTTT TTAAGCTTTG TTTTGGGATG CAGTTAGGTG ACTCAGAAAC ATTTGATCC TTTTATGTCT CTTAAGCTTT GTTATAGGCA GGACCAGAGC	60 120 180 240 300 307
(2) INFORMAT	ION FOR SEQ ID NO:27:	
(i) S	EQUENCE CHARACTERISTICS: (A) LENGTH: 253 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) I	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:27:	
TTCAGTCTTT C	TCATGGCCT ACAATAATAG CCTCCCACCT GGTCTTCCTT CTTCAGTCTC CCCAAAGCTC TTGAATCCTA CATGAACCCA TGCCTCGGTC AAAATATTAC CAATCTTCAA GTGGCATACA GGCCAAACAT CCATTTATAA TATGGTTGGA CATTTTATCA TAGATCTAAT GCCATACAAT AGGTGGAGGT TAGATCCTCA CAG	60 120 180 240 253
(2) INFORMAT	TION FOR SEQ ID NO:28:	
(i) S	EQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:28:	
TCTCCTCGCT C	TCATGGCCT ACAGAGAACT TGTGTTCCGG TTTATTGAAG TTCAGACACT CATTCTGTC CACATTTGTG TGAGCACATC TGGACACTCC TGGGAAAGCC ATGAATGCTT CATGGCCTGT GGCAGGTCCT GTTAATGAAG TTTTAATACA TATCTTATGG AAGTAACACA TGACCTTAGA CTACGACTCA AGAACTATAT CGAG	60 120 180 240 254

- (2) INFORMATION FOR SEQ ID NO:29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 211 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATTCGGCC	TTCATGGCCT	ACGAGAAGGA	GTGGAAGAGT	AAGCAGACTA	GGAAAATACA	60
GTACAACCAT	CAGGCAGCAT	TACAGACCCA	CTTAAGGTTT	GTGGCCATGT	GTGGTTGTGT	120
GGTTTTTTT	CTGGCCATGC	TCAGTTACAT	AGGGGCAAGT	GCAAAAAAA	CCCCAGAGTT	180
TGTTTTAACT	AGAGCTCTGG	TTTTGCCAAA	C			211

- (2) INFORMATION FOR SEQ ID NO:30:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATTCGGCC	TTCATGGCCT	AGGATCAGGT	TCGTCCTTTA	GTGTTGTGTA	TGGTTATCAT	60
TTGTTTTGAG	GTTAGTTTGA	TTAGTCATTG	TTGGGTGGTG	ATTAGTCGGT	TGTTGATGAG	120
ATATTTGGAG	GTGGGGATCA	ATATAGGGGG	AAATAGAATG	ATCAGTACTG	CGGCGGGTAG	180
GCCTAGGATT	GTGGGGGCAA	TGAATGAAGC	GAACAGATTT	TCGTTCATTT	TGGTTCTCAG	240
GGTTTGTTAT	AATTTTTTAT	TTTTATGGGC	TTTGGTGAGG	GAAGTAGGTG	GTGGAGCACA	300
GGCACTGCAG	GTCAATGGAG	GTGGAGTACA	GGGACTACAG	GTCAATGGAG	GTGGAGCACA	360
GGGACTAAAG	GTCAATGGAG	GTGGGGCACA	GGGACTACAC	GTCAGTGGAG	GTGGAGTCAC	420
AGGGACTACA	GGTCACTGGA	GGTGGAGCAC	AGAGACTACA	GGTCAGTGGA	GGTGGGGCAC	480
AGAGACTACA	GGTCAGTGGA	GGTGGAGCAC	AGAGACCACA	, G		521

- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAATTCGGCC	TTCATGGCCT	AAAATTTCCT	CTAAGTACTG	ATTTAGCTGC	ATTGTATAAG	60
TATATGCTTC	CATTTTCATT	CATTTCCAAA	TATTTTCTAA	TTTCCTTTGC	AATTTTTTTT	120
TCAGGAATTC	GGGCCTTGCT	GTGTTGCCCA	GGCTGGAGAG	CAGTGCCACT	ATCACAGCTC	180
ACTATAAACT	CAAACTCCTG	GGCTCAAGCA	ACCCTCCCAC	CTCCCAACTC	CCCTCGAC	238

- (2) INFORMATION FOR SEQ ID NO:32:
 - (i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 257 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:32:	
TTGTGATTAC ACTTCTCCTA	AAAAAAAAA AAAAGGAATT TGATCCAGAG CAATTTTTCT CAATTAAAAT ATTTCTGAGT TTCCATGGCA GAGTTGTGAG TGGGGCTGTG ATATAATTTA AATTGCTGAC ACCGATAACC CTATAAATTA ACAGATGGCG GAGGGAAATC TTCCTGGCTA GTTTTTTTA ATGGTCTGAT TTTTGTAATA GGGGTTTTGA ACTCGAG	60 120 180 240 257
(2) INFORM	ATION FOR SEQ ID NO:33:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 251 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:33:	
TAGTGTGTTG AATTTTGCTT	TTCATGGCCT AAAGACTTAC GTTATATTTT CATATACTCC TTCCCACTCT TCAATATACA TTTTGTTTTA CATGTAAAAA CACCACAGTA TATTGTTCTT TTAATAGTAA ACTGTCTTAT AACAAATTAT GAAAATGGAA AAAAACATGT TGCCCTCATA TTTATCCATT TAGGCACTCT TCCTTTTTCC CTTTCATTCC G	60 120 180 240 251
(2) INFORM	ATION FOR SEQ ID NO:34:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 245 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: CDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:34:	
CATTGAGATT TCTTAATTCT	TTCATGGCCT ACTAACATTT ATGAAAATTA TTTGTAAATA AAATAAGAGG AAAATTGGAG ATAAAGTTGC TGATGTGTTG TTTTCCTGAA GTATTTTTT GATCTTTGTT TCCCAATACA ATCACACTCA CACCCTTGCA GTTCAGTTTC TCTAGTGTGC CAGATCTGTG TTTCTATGTC AGTGATCTGT TCCCCATCTC	60 120 180 240 245
(2) INFORM	ATION FOR SEQ ID NO:35:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 383 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAATTCGCTT CATGGCCTAC	CGAGAAATGG	GTGTGATTGC	TGCCATGAGA	GATGGTTTTG	60
GTTTCATCAA GTGTGTGGAT	CGTGATGTTC	GTATGTTCTT	CCACTTCAGT	GAAATTCTGG	120
ATGGGAACCA GCTCCATATT	GCAGATGAAG	TAGAGTTTAC	TGTGGTTCCT	GATATGCTCT	180
CTGCTCAAAG AAATCATGCT	ATTAGGATTA	AAAAACTTCC	CAAGGGCACG	GTTTCATTTC	240
ATTCCCATTC AGATCACCGT	TTTCTGGGCA	CGGTAGAAAA	AGAAGCCACT	TTTTCCAATC	300
CTAAAACCAC TAGCCCAAAT	AAAGGCAAAG	AGAAGGAGGC	TGAGGATGGC	ATTATTGCTT	360
ATGATGACTG TGGGGGTCTC	GAG				383

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 base pairs
 - (B) T'PE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCGGCC	TTCATGGCCT	ACTGCCGCTC	CTGGTGCTGC	TTGTGTGCTC	GTTTGGTGCG	60
GACCTGGTAC	CTCTTTTGTG	AAGCGGCAGC	TGAGGAGACT	CCGGCGCTCG	CCATGGCCGA	120
CGAAAAGCTC	GAG					133

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCGGCC TTCATGGCC	T AAGGTAGTCT	AGGCTCATCT	TCATGAGGGA	ACTGAGGTCT	60
TGGGGGGTGG GGGTTACCC	A AATAGGTTCA	CAGAAGAACC	AGAAATAAAA	CCTGCCTTTC	120
TAGACTGTAA GTCTTGTGA	T TGTCATCTAA	ATGGTTGTCT	CTATACAGCA	ACTCATCTCT	180
AGAACTGAAA ATAAGTTTA	A ATCCCTCCTC	CATCCCCAAT	AATTCAAGCT	GCATTTCAGA	240
GAAAACCAGG ACTTTGGAA	T CAGACAGCAA	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

and the second of the second o

TTATCAAGGA CACATCATGA CCTGAAAACG CCCCTGCCAC	TCTTAGAGTA GGAGTTGGAA CTATAGGA TCTACTCACT CAGTTTCCCT AAAGCTCT CAGATGTTCC GGCTACATTT ACCCAGGC GTCAACAAAC AATCACTAAA ATCAGTGA ACTACAGGGT AGAACCCAGT CTGGAAGG GAAAATTACA AGGGAACAGA CTCGAG	CT CTCCAGATCG IG AGTGTAATGG GG AATTGACTGA	GATTCAACCG GGATAAACCA TGTGGACAGC	60 120 180 240 300 336
(2) INFORMA	TION FOR SEQ ID NO:39:			
(i) S	GEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ ID	10:39:		
GCAGGATGTT TAGGAAGGTC TGAGGGGGTT TGGTGATCTA TGGACGGTGC	TTCATGGCCT AGTCGGAGAA GGACATCC GATATGGTGT TTGCGTCATT CATCCGCA CTGGGAGAGA AGGGAAAGAA CATCAAGA CGGAGGTTTG ATGAAATCCT GGAGGCCA GGCATTGAGA TTCCTGCAGA GAAGGTCT AACCGAGCTG GGAAGCCTGT CATCTGTG CCCCGCCCCA CTCGA	AG GCATCTGATG IT ATCAGCAAAA GT GATGGGATCA IC CTTGCTCAGA	TCCATGAAGT TCGAGAATCA TGGTGGCTCG AGATGATGAT	60 120 180 240 300 360 385
(2) INFORMA	TION FOR SEQ ID NO:40:			
(i) S	EEQUENCE CHARACTERISTICS: (A) LENGTH: 245 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ ID 1	10:40:		
GGTTTTCTTA AAATGAGTGA	TTGCTAAAAA AAAAAAAAA GAGGCAAG TCTATAAATA CTGATTAAAA AAAAAAGT ATACAGGCAA AATGCCTTAC ATTTTACT TATGATGACA ATTATGATGA TGATGATA	AC ACTGTCTGCC TT ACATTTACTA	TTATAAGCTA AGCACCCAGA	
(2) INFORMA	TION FOR SEQ ID NO:41:			
(i) :	SEQUENCE CHARACTERISTICS: (A) LENGTH: 247 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: CDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ ID	NO:41:		
	TTCATGGCCT AAATAAAGAT GATTTTTC GCAAAACTCT TTCCCAATTC AGTCGCTA			60 120

	CATTTTGTGT GTACAGTGCT GTGTGTAAGC TTATCAGTGT GTTTTTTTAT CATGAAAGTC CTGTTAGGTA TCCAGAGTTC TATTTATCTA GCTGTACAGA	180 240 247
(2) INFORMA	ATION FOR SEQ ID NO:42:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:42:	
	ACTGAGAACC ATTTTCTAGT TGAGATAACT CATGTACAGG GGGGGTCACA ACACACAGAG CACAGAAGAG AACCAACAAT CTCGAG	60 106
(2) INFORM	ATION FOR SEQ ID NO:43:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 237 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:43:	•
TTAGATGATA TTGGCATCTT	AAGTGTATGT ATTTCTAAAG ATAGATTTTT TAAAAACAAA AAATCTTAAT AGCGATTTTT ACCTTTTTT TTTTTCAAA GCAACTTGAT CCTGTAAGTT AAGTGGAAAT GTTCATGCAG TTTTGCTGGA TCTTCGCTAA GGCAGTAAAA CACTGTGGTT AAGAGTGCAG AACGGAGTCA GTCAGCCTGA ACTCGAG	60 120 180 237
(2) INFORM	ATION FOR SEQ ID NO:44:	-
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 476 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xí)	SEQUENCE DESCRIPTION: SEQ ID NO:44:	
TGTGTCTGTG AATGGAGGAC TGGTATTTCT TGATGTAAGA GTTATGTGTC TGGATGAAGC	TTCATGGCCT ATAGGCCATG AAGGCCGGCC TTCATGGCCT AGGGAGTNGG CATTTATTTG GATCATGGAA GGTTGTAGAT GTGTATTTCT AACTGTAGAT ACATATTTGG GGGAGTTTGAA GAGGATGTGT ATGTGTGTG	60 120 180 240 300 360 420 476

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAATTCGGCC	TTCATGGCCT	AGGCAAACTC	TGCTGGACTT	AACTTCATCA	ATGTAGTGGG	60
CTCTGTTTGT	GGGGCCCAGG	CTTTGATGAG	TGGTTCAAAC	CCCATGCTGG	GCTGTAACAC	120
TGGTGCCATA	ACTCCTGCAG	GAATAAACCT	GAGCGGCCTT	${\tt CTACCCTCAG}$	GAGGTCTGCT	180
ACCAAATGCA	CTGCCCAGTG	CAATGCAGGC	AGCTTCTCAA	${\tt GCAGGTGTTC}$	CATTTGGTTT	240
AAAAAATACT	TCAAGTCTCA	GGCCCTTAAA	TCTACTCCAG	CTTCCAGGTG	GTTCACTTAT	300
TTTTAACACT	CTGCAGCAGC	AGCAACAGCA	GCTCTCCCAG	TTTACACCAC	AACTCGAG	358

- (2) INFORMATION FOR SEQ ID NO:46:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAATTCGGCC	TTCATGGCCT	AATCATTTTG	ACTTTCAGTG	CTTTCAATGA	CCAGTGGCCT	60
CCAGGGATAA	AGCAACTGCT	TGGTTTGCAG	GGCGTCCTCT	GCGCTGCTGA	GCCATCAGCC	120
TCCAATACGC	CAATGCCCAT	AGATGCTAGT	TACAGCCCTG	CTTCCTCCTA	CATAGGGTTC	180
TGTCATCACT	GAGTCTCACC	ATTTCCCTCT	CCCCAGTGTC	TTTATTATGT	GACACACA	240
CACGGCACTA	TGTTTAAAAA	AGCGTGCTCA	CTGGCAACCT	CTTGGCGTTG	TGTGTTCATT	300
CTGTGTTTTG	TATTGGTGGT	ATCTTGGGGT	CGACCGAAAG	AGTCAACCTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:47:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B). TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAATTCGGCC	TTCATGGCCT	AGGGAGCTAC	CAGATGCTGA	AGAAAGGGCC	CTGGCAGACT	60
GGGTTCAAAC	TCAGCCATTG	TCAGCTTGGT	AACCTTGACC	AAGTGTCTTC	CCCTCTGTGA	120
GCCTCAGTTT	TCTCAATAGT	AAGAGGGGAT	AACACACTTA	CCTCTCATAG	CTGTGGACAT	180
GGAGGTGAAA	GTGCCGCATA	CACTGTAAAG	TGTTATATAC	GTGTAAGAGA	AAAAATCGGG	240
CCAGAGGCTG	GGCTTGTGTT	AATTGATTCA	GGAAATTCAC	CAGAGGCCCC	CTAGATGCAA	300
CGTCCTTTGG	GTGTCTGGCA	GTGGGCACAA	AGATGAACAA	AACAGTGCCC	CACCCTCACC	360
CCGTCAACCG	TCAGTGCAGC	AGTGGGCTGG	GTGCTTGCGT	CCCACAGTGA	GGAAGGCAGA	420
AGGGGTCCCT	GCCCTCAAAG	GAGGACGATA	CTCGAG			456

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GAATTCGGCC	TTCATGGCCT	AGCTGCCCCG	CAGCACTTAC	CGGAGCGACC	ATGAGGGTGA	60
CGATTTGAAG	CACACACAGG	CTTCCCGCCA	CCTCCTTTAA	ACCGCCGCTG	GCTTGCCAGG	120
GACAGACGGC	GCGGTTGGCT	CCCCAAAATT	CCGACTGATA	CGCGCCTCGG	CGAGCGAAAG	180
CAAACGCGGG	ATACTCTCGC	GTTCCTGATT	GGCTGCAGTT	GGAATTGATC	ACACCTTTTC	240
AGTTGTACTT	CAATCCTGAA	TTAATCTTTA	AACACTTTCA	AATATGGAGA	TTAATCACCA	300
ACTTCTTATT	TTTTGGGCCA	GTTGGATTCA	ATTTTTTATT	TAACATGATT	TTTCTATATC	360
GTTACTGTCG	AATGCTAGAA	GAAGGCTCTT	TCCGAGGTCG	GACAGCAGAC	TTTGTATTTA	420
TGTTCCTTTT	TGGTGGATTC	TTAATGACCC	TTTTTGGTCT	GTTTGTGAGC	TTAGTTTTCT	480
TGGGCCAGGC	CTTTACAATA	ATGCTCGAG				509

- (2) INFORMATION FOR SEQ ID NO:49:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAATTCGGCC	TTCATGGCCT	AAAGCAAGTG	ATTTTCTTTT	TTTTAAAGAC	AGGGTCTCAC	60
TTGGTCACCC	AGGCTGGAGT	ACAGTGACAT	CATCACGGCT	CACTGCAACC	TTCGCCTCTT	120
${\tt GGGCTCAAGT}$	GATTCCCCCA	TCCCCCACCC	CCCTTCTCAC	CCCCAGATTG	GACTATAGGC	180
${\tt GTGTACCACC}$	ACGCCTGGCA	GAGACCGGGT	TTTGCCGTTG	CCCAAGCTGA	TCTCGAACTC	240
CTGAGCTCAA	GCGATCTGCC	CGTCTCAGCC	TCCCCTAAGC	AAGCATTTTT	AAGTTTCTAT	300
${\tt GCTGTTTAAT}$	TTTTTTTAAC	TGATTAATTT	ATTTGCATTG	TGTGGTCATG	GAATATGTTT	360
TTATGATATT	GGTTGTTTGA	GATTTGGTGA	GTCTTTCTTT	GTAACCTAGT	TAAACCATTC	420
${\tt CATATCTTTT}$	TAAAAGGATG	TATATTCCTT	ATCTGTTAGG	GCTCGAG		467

- (2) INFORMATION FOR SEQ ID NO:50:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GAATTCGGCC	TTCATGGCAG	AGTGGAAGGG	GTTGTAAATA	TTAGGAGAGA	GATAATTCTT	60
AGTGCATTTC	TCTGAGGATG	AAGCATGAGA	TGAATCCATG	GCACGAATGG	AACAGCTGGG	120
GAAAGCAGGT	CAGAATGGAT	ATGGATATAA	ATACTGTGAG	TTCTCGAG		168

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
GAAGTAAATT ATTACGATTT CCTTAGGTGG TTAATAAATT ACCATTATTT TCTCTATTTT ACAGATCACG AAATGATAAG TAACTTACCG AAAGTTACAT TATTTAAGTT AATCAAATGT TTATTGATTG CCAGACTTTT TTCTAGGCTT AAGCAAAATGT TGGAAAATAC TTCTCTGAGC TTTCAAAAAAT GTTATTCTA CTTGTCAGTG CTGCAGGAGT CTCTCGAG	60 120 180 228
(2) INFORMATION FOR SEQ ID NO:52:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 247 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	
GCAGAGTCAA TAGATACTTT AAATTGAAGT AAAGAATTAA AAAAGGAAGT GGATAGTTTG GGTATTAGTT TAGCTAGAAA TACAAAGAAA CTTGACTTCT AGGGCAGTAC AAATTCAAGC CTTCCACAAA CAAACAGTTG AGAGTATGTT TATCTTCTTA AAATGTGTGG GTGCCTTCCC ACCACTTCAC CTGCTCCTCA CTGGTGCTTT GTCCCCTCCC TACTACCATT CCTGTCCCGG TCTCGAG	60 120 180 240 247
(2) INFORMATION FOR SEQ ID NO:53:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
GGCCAAAACA AAGCTTATAA AGGTTCCTGC TCCCAACGTA ATTACCTCCA ATCGGCATTT AAAGACATCC GCATTGCTTA CAGCACATCC TAGCCTCATG CTTGCCCAAG GATGGACTCG AAATGAACTA TTTCCAGAGC GACTTATTCA GGCATTCTGT GGAGCCTCCG TTGCCCTGTC CATCACCGGA GCTTTTGTAA TTGCAGCTAT GCCATTGGCC TCCGGCAACC TCGAG	60 120 180 235
(2) INFORMATION FOR SEQ ID NO:54:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 231 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GAATTCGCCT TCGTGGCCTA AAAAGAAAAA ATCTAAGGTA GATTGTGCCT TCCTCTGCTC AAGACCTTTC AGTGGCTTCC CACTTCACTC AGTAAAAGGC ATTAAAAACC TACAAGGCAT TATGTTACCC ACATTGTCCC TGCTCCCCTA AAGTCTATGA TCTTTTACC ATTCCTTGTA CAAAGGATTT TCACTGGCTG	AAAAAGTCCT 120 CATTGTACTC 180
(2) INFORMATION FOR SEQ ID NO:55:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 330 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
GAATTCGGCC TTCATGGCCT AGAAATATTT TCCTACAAGA GTACTGAATT GGATAGAGCT TCTAACCAGT GTATTCCGTC AAGTAAGATA ATAACAGCTG AGCATTACAG GGAGATTCTT TGCTCAGCTA ACACATTTCT GTTTTTCAAA AATTGTAGCT GTTATTCTAA TTTGTGACAT GGAACTAACT CATGCTTCAA AGCAAAAACTC AGAACAGGTT ATGTAAAAAAT ATAGTCTGGC TTTAGAATTT CTGCTTTGCC ACAGAAAATG GAGACTCGAG	ACCTGCCAAC 120 ATTGATGCTT 180 TCCTTGATAG 240
(2) INFORMATION FOR SEQ ID NO:56:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 230 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
GAATTCTAGA CCTGCCTCGA GATCTGAACT ATAATCTTTT CCATTCTATC CCTAAGTCCT CTCCTCCTAA CGTGGAACTC TCCTAAAATC TTCTCCTTAT GAGACATGAG GCTGTCTTTT TGGGCCTTTT GCGTTGTCAC AGTCCCAGAC TCTCTCTTCC CCAGGACAGG ACATTCTCTC TTCCCCAGCG CTCCCTCGAG	ACTAGGGTTC 120
(2) INFORMATION FOR SEQ ID NO:57:	
(i) SEQUENCE CHARACTERISTICS:	

- - (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAATTCGGCC	TTCATGGCCT	AAAGGGAAAG	TGGGAATATA	CACAATGCAN	ACACTAGCCA	60
CATGCAATCA	TGGGAGAACA	GAGCCTACTT	AAAAATCANA	CCCAAGCTTT	GCTTCAGAAA	120
TAAGTGGAGT	TGAACCCATT	CGATCATTTA	CGCATGACTT	TGCAAAGGTT	CTCTGGAGGG	180

GGAAGAGGAT CAACCTTCTC TCATACCGCA CAGCAAGGGA ACCAAAGTAA TATAAATCAC

TCTTAAAAAT GTCATGTTAC TTTAAGAATA AGCCATACTG CTGGCACCTA GAATATTTTT

GTGGGTCCCC ATCTCTGGCT TTTCTTGTTC AAATGGCCCC CAGGCTAAGA GGCAGCTGCT

CACATCCCTG CAACAAACAT GTTCTTTCCT TTCTGCATAG CCTTCCATTT CTCGAG

(2) INFORMATION FOR SEQ ID NO:58:

240

300

360

416

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 289 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
GAATTCGGCT TCATGGCCTA CTAGACCTGC TCAGTCGTTC CTAATGAATA AAAATCAAGT GCCAAAGCTT CAGCCCCAGA TAACTATGAT TCCTCCTAGT GCACAACCAC CACGCACTCA AACACCACCT CTGGGACAGA CACCTCAGCT TGGTCTCAAA ACTAATCCAC CACTTATCCA GGAAAAGCCT GCCAAGACCA GCAAAAAGCC ACCACCGTCA AAGGAAGAAC TCCTTAAACT AACTGAAACT GTTGTGACTG AATATCTAAA TAGTGGAAAG TCACTCGAG (2) INFORMATION FOR SEQ ID NO:59:	60 120 180 240 289
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 382 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
GAATTCGGCC TTCATGGCCT AATTTGAGGC CTGGGTGGAA CTGACAGGTG GAGTTTGAAG GCACATCTGC TAGCTCACAT AGGAAACAGA ATCTCCCAGG GAAAAGACAT AGGACCTCTG ACTCTAACTG AGGTTCTGGA TTATTATGAG AGATTTTCAG AAATGGTCTA ATGGTGTTGG CTTGCTCCAT ACCATAGATT TTAAGAGACA GTAGAGCTTC TGCGATGAGA TTCCCCCATA AAATAATTAT GGATCTGCAC TGGCAAGCTG GTCTTGGCTC CAAAGACCAA GAGTTGGTTT GTGGTGCTGA TTCTGAACCC TTGCGATGCA ACTGTCTGGT AGTAAAATGG CTTTGTATGG TAAGAAAAGCT TTAATCCTCG AG	60 120 180 240 300 360 382
(2) INFORMATION FOR SEQ ID NO:60:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 196 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
AAAAAAAAAC CAAACCCTAT TATTTCATTG ACAGATTGTC TTAGAGTTGA TAGCATTTAA FAATTGAGTA AGTACAGTCC TTCCTTGTTC CCAACGTGCC CTATTTTTTC TTTCTTCTC ACTTTTGCAT ATGCATTTTC CCTCTTTCTT GTTTCTTGGT GAATTCCTAA ACCTTTTTTT FCAAAAATCAC CTCGAG	60 120 180 196
111	

2	INFORMATION	FOR	CEO	TD	NO . 61 .
٠.	TIME OFFICE TATEOU	rvr	320	10	MO: DI:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAATTCGGCC	TTCATGGCCT	AACCACATTT	TTCTAATTAG	TGTTCTAGAC	TGGCTAGATA	60
AATCAACAAT	GAATCAACAG	TCTTTAAGCA	CATATACAGG	TATGATAACT	CTGTAGTTAA	120
CTCAAATCCT	TGTGCTATGT	${\tt ATTATTTTGC}$	TGCGTAACTC	AGAATTCAGG	AAGCTACCCA	180
CCCAATCAGT	CTTTAGCTGT	TTTATTTCAG	TAACAAGTTT	ATGCAGAACC	TTCCATATCT	240
CTCATAAAAC	CAGAGCATTC	ATAGAACCAG	AAACTCTCGA	G		281

- (2) INFORMATION FOR SEQ ID NO:62:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAATTCGGCC	TTCATGGCCT	AAAAGATTTG	AGCATTTCAA	AATTTTAAAC	ATAAAAGCAT	60
AAACGTAGAT	AAAATGAAGG	TGTACTATGA	TATCTTCAGT	TTTATCAGAA	ATGATGTAAA	120
AATTACAACC	TCTTTAAAAA	GTAGTGTTAA	TCATTAAGTT	AGAAAATATA	TAGCTGGGCA	180
TGGTGGCAGA	TGCCTGTAAT	CCCAGCTACA	TGGGAAGGTG	AGGTGGGAGA	ATCGCTTGAA	240
CCCAGGCAGT	GGAGGATGCA	GTGAGCCAAG	ATCATGCCAC	TGCACCCCAG	CCTGGGTGAC	300
AGAACAAGAC	TCCATNTCAA	GGAAAAAAA	AAAGAAAAAT	ATATATATGA	ACTTCAGAAT	360
CTGAGGTCAT	ATATAGACAG	GTCTTCCCCC	CGTCCTCGAG			400

- (2) INFORMATION FOR SEQ ID NO:63:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GAAACCATAG	TGGCAGATTT	GTAGCAAAAA	GAATCTTTGT	AACCTTCCCT	TTAGATGTCC	60
				GTGTTTATCT		120
				CCCCATGCAA		180
				TATTGATACA		240
GTTATGAAGT	GCATTGTA	CATTATCTTC	TIPLAATTITC	ACAACACTCT	TCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:64:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGTCGCAGAA	GAGTGTCAGA	ACAATCAGTT	AAAGAAGCTC	AAAGAAATCT	GTGAGAAAGA	60
AAAGAAAGAA	TTAAAGAAGA	AAATGGATAA	AAAGAGGCAG	GAGAAGATAA	CAGAAGCTAA	120
ATCCAAAGAC	AAAAGTCAGA	TGGAAGAGGA	GAAGACAGAG	ATGATCCGGT	CATATATCCA	180
GGAAGTGGTG	CAGTATATCA	AGAGGCTAGA	AGAAGCGCAA	AGTAAACGGC	AAGAAAAACT	240
CGTAGAGAAA	CACAAGGAAA	TACGTCAGCA	GATCCTGGAT	GAAAAGCCCA	AGGGGGAAGG	300
TTCCTCCTCA	TTCTTGTCGG	AAACTTGCCA	TGAGGATCCC	TCTGTTTCCC	CCAAACTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GAATTCGGCC	TTCATGGCCT	ACTGGGGGAA	GAAGGCTGCT	TTATGTTTAT	TTTTCAAGAC	60
TTTAAAAATA	TTTTTTGGTT	GTATTGCACT	AGGAAATCTC	TCCCACCTCT	CCCTTTTCTC	120
TTTCTTTCCC	TATACAAAAT	AAAAGGCCCA	CCATAGAGAC	TAGGCGGCCG	AAAGACTAGG	180
AGGGCTGAGG	AAAAGAAATA	GGTCTCTGGA	GGTGGAACTA	AAACTGTGCA	GCTGCCTCTT	240
CCTGGCGGTG	GATGCTGCTT	TGGGAGGGCC	AGGGAGGCTG	CAGGGGGACA	GTGTTGGGAT	300
TGTCAAGGAA	AAAGGGGTAG	GAAGGAAGGT	GGAGGGATTG	ATCTAGTACC	AGGGAGAATA	360
TTCCACTGAA	CTGTGATTCT	ATGCGGCCTC	GAG			393

- (2) INFORMATION FOR SEQ ID NO:66:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GAATTCGGCC	TTCATGGCCT	AATTTGTTAT	TGCTAGAAAA	TACACAGTTT	TGAGATTTTT	60
${\tt GGGCATAATT}$	GGCCTTAGTG	TGTCACTTCT	GCATTAAAAT	ATAGGTTAAT	AATCAGATGA	120
AAGCAGCCAA	TAACCTATGG	CTTCTGTACT	TTCTGGTGAA	AGTTTTGTTA	ATGTTTTTAA	180
TTTGTATTTT	TCTGCTTATA	AATTTGTCCT	TAAATCACTC	CCCTCCTTCC	CGCCCCCCG	240
ACTCCTTCTC	CCTCCTTCCC	GCCCCCCAA	CTCCTTCTCC	CTCCTTCCCG	CCCCCGCGAC	300
TCCTTCTCCC	TCCTTCCCGC	CCCCCGATCC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:67:
 - (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
GGTGACATAT TTATTGCTTC TGTTTTCCAA CTACATCACT TCAACTAGAA GTAAAGCTAT	60
GATTTCCTG ACTTCACATA GGAGGCAAAT TTAGAGAAAG TTGTAAAGAT TTCTATGTTT TGGGTTTTTT TTTTCCCTTT TTTTTTTAA GAGTATAAGG TTTACACAAT CATTCTCATA	120 180
ATGTGACGCA AGCCAGCAAG GCCAAAAATG CTAGAGAAAA TAACGGGATC TCGAG	235
(2) INFORMATION FOR SEQ ID NO:68:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 257 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
GAATTCGGCC TTCATGGCCT ACCACAATCT GTTTGCTTTT CCTCTTTAGA TTCCAAAAAT	60
AACACCCCAA AGGCTACCTT TTCAAATATT CTACAACATC TGCAAAAATC TTTAGTACTC	120
TGTCCTTGGA GTCAGTCAAG AAATTCCACC CCAGAAGTGT AAAAACCAAT CAATAATATA TGACACTGAT TTTCTCTAAA TTATTATTTT TCTTATGGTT GAGTCTCCTG CCAACTTTAT	180 240
GTTTCCCAAT CGGCTCG	257
(2) INFORMATION FOR SEQ ID NO:69:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 261 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
GAATTCGGCC TTCATGGCCT AGCTGGGCAT GGTGATGCAC GCCTGTAATT CTAGCTACTC	60
AGGTGGGGGG TTAAAGGTGA GGCAAGGTCA GCGGTGAAGT GCAGCTCAGA GGGAGGGGTC	120
AAACATAAAC CAGAACTTAT AGGTCTAGAG GTAAAATGGG ATTCATGGGG GGCAGAGGTC	180
AAAGGTGAAG CAGAAGTCAG GGGTGAAGGA AGGTCTGCAA AGTTAAAGGT GCGGTTTCCA GAGTCAGAAG GGGTGCTCGA G	240 261
(2) INFORMATION FOR SEQ ID NO:70:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 279 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
114	

(A) LENGTH: 235 base pairs

(xi) SEQUENCE DESCRIPTION: SEO ID NO:70:

(AL) SEQUENCE PERSONAL LEGIS, SEQ EP NO. 10.	
GAATTCGGCC TTCATGGCCT AGATTGAATT TTTAACACAG TCCTCTCAGA AACTGACTAA AACAGGTTTT AAAATTAGCA AATATTAAGA ACATACGAGT AAAAGTCAGT TTATTTTAGA TAAGTAGGGA TTTAAATTCA ACAAAAATAA ACACATTTTA AACTCCTATA ATACATTTAT TTAAAATAAA TATTATTTTG CCAAAAGAAG TGTAAGTTCA AAGAGTTAAC ATACAGATTA TATCCTATGA GATATAATAA TATTAGAAAC TGGCTCGAG	60 120 180 240 279
(2) INFORMATION FOR SEQ ID NO:71:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 255 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
GAATTCGGCC TTCATGGCCT AGTTACATTT ATAATCAGTG AGGAAAATAT AAACTATACA ATAAATGAAA GGGTCATTGG CCAATTGTTT GGAGGGAAAA AATACACCAT GTTCTAAAAT AAATTTCTAG TGATTTATTG TGACTTTCAT GCATTTGGAT GATTTTAAAG ATTTATATA AAAATGAAAC CATAGCCTTA CGAGAAGAAA ATATAAAGAA AAACTTGTAT AGTCTTGGGA GGGGGGATTC TCGAG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:72:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 138 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	
GCGATTGAAT TCTAGACCTG CCTCGAGATC GTCTTTTCTA CCTGGATGAG AGCTCTACCA CTTCTTTCCT TTTGCACACT CATCTCATTC TATGCACTCT TGGGCTGTAA CTGTCATTTC TTTTCCTGTA CACTCGAG	60 120 138
(2) INFORMATION FOR SEQ ID NO:73:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 208 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	
GAATTCGGCC TTCATGGCCT ATCACATTGC ATTAAATCTG TAGATTACAT TGAGCATTAT	60

120

180

208

GGACATCTTC AAAATATTTC AAATTTTGAA CAGGAGCATG CTGAAGAGTG TGTTGTTTAA

TTTCTATGTA TTTGTACATT TTTTTCTCT ATCTTATACT GCCGAGACCA GCTCAGTCGG

GGAGACCCTA ACCCAACGGC AGCTCGAG

(2)	INFORMATION	FOR	SEO	ΤD	NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GAATTCGGCC	TTCATGGCCT	ACATGAAACT	GTTAGTCACT	TCATTTCTGT	TTCTTCCCTG	60
TTGCAACAGC	CCATCTTCGT	GGGAAGAACC	AAGCTTTAGG	CTTGGCTCTG	AACAGCCACA	120
AAGTGACTTG	GCTGAGGTCC	TGCCATTTCG	CTCATGCTCA	GCAGGGGGCA	GCAGACCAGG	180
GCAGTTCAGA	GTATGGGGTC	AAACCCAGGT	CCCTGTCCCC	ACTCCACCTG	TGGATTTACC	240
CTGGATTGGG	CAAGCCCCAT	TACTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:75:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GAATTCGGCC	TTCATGGCCT	ACGTGAACAA	GACCCTCCCA	AACCTTCAGG	TAGTCAACCA	60
CCAGCAAGGC	CCCCACCACA	GACACATCCT	GAAGCTGCTG	CCGTCCATGG	AGGCCACTGG	120
GGGCGAGAAG	TCCAGCACGC	CCATCAAGGG	CCCCAAGAGG	GGACATCCTA	GACAGAACCT	180
ACACAAGCAT	TTTGACATCA	ATGAGCATTT	GCCCTGGATG	ATTGTGCTTT	TCCTGCTGCT	240
GGTGCTTGTG	GTGATTGTGG	TGTGCAGTAT	CCGGGAAAAG	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 199 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GAATTCTAGA	CCTGCCTCGA	AAATACACTG	TTACTATCTT	AATCTCAAGA	GTGTCATTAC	60
AGTGAGAATC	TCATTTAAAA	GCATACCAGT	GAAATTAATA	GCAGTGCTTA	TCAAAGAACA	120
CTGAAATCTG	TGAGAATCTT	TCTAGGAGCA	TTCTTTTCTT	CTTTTAGTTC	CAAGTTCCAG	180
${\tt GTAGGCCATG}$	AAGGTCGAG					199

- (2) INFORMATION FOR SEQ ID NO:77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GATTGAATTC	TAGACCTGCC	TCGAGTTCCA	CGTCCATGGC	CATCCTGAGC	ATGCTGCAGG	60
ACATGAATTT	CATCAACAAC	TACAAAATTG	ACTGCCCGAC	CCTGGCCCGG	TTCTGTTTGA	120
TGGTGAAGAA	GGGCTACCGG	GATCCCCCCT	ACCACAACTG	GATGCACGCC	TTTTCTGTCT	180
CCCACTTCTG	CTACCTGCTC	TATAAGAACC	TGGAGCTCAC	CAACTACCTC	GAG	233

- (2) INFORMATION FOR SEQ ID NO:78:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GAATTCGGCC	TTCATGGCCT	AAGAATAGAG	AAAACGTTTT	CAGCAGGCTT	CACAGAGAAA	60
CCAAACAATA	TTTAGAATAT	GACAGCATAT	GAAGAGTCTG	CTACTCTCCC	AGTGACCCAT	120
ACTTTCTCTT	CCATCTCTGC	TGGTTCTCTC	TACTACCGAT	TCTTTCTTGC	TGTTCTCCTT	180
CTCCATCACC	GTGACTTCTA	TTGCCTTACT	CTAATGTCTT	GTCTTCTGTG	TTACCCTTCT	240
GTGTGTTTTG	CATTCAGAAC	TCCCCCTCCG	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GAATTCGGCC	TTCATGGCCT	ААААААААА	AAAAATCCCT	GGCTGAGAAC	TATTGGATTA	60
GGGCCTCCNG	TACCTATCTT	TGAGGGGGAA	AGGATGCTAC	CATCAACTTT	TCTGAATGCC	120
AGGAATGCCT	TTTAGTATAG	TTATTTCACT	TACTATTTTA	TAGCATATTT	TAATTGTATA	180
GTAAGCATTG	TGTCTGTTTT	ATGGTAAGGA	AACTAAAATT	GAGAGATTAG	GCTGCTCGTG	240
GTGGCTTATA	CCTTGTAATC	CCAAGCACTC	GAG			273

- (2) INFORMATION FOR SEQ ID NO:80:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TTTTAGAAGA AAGTGATACG TTAATGACCT	TTCATGGCCT AGCGAAATGA CGAAATCTAG CCCTTTGAAA ATAACATTG GGACAAATCC TTAAAAGTAA CATCAGACCC AAAGGTTGAG CAGAAAATT TGAAATTGAG ATGATGTGG ATGATGATGA TATCAATAGT TCGAAAGTA CTTCAGTGAT GTCCTAGAGG AAGGTGAACT AGATATGGAG AAGAGCCAA TCAAGCATTA GCAGAAAGCA GCGAAGGGCT CGAG	G 120 A 180								
(2) INFORMA	ATION FOR SEQ ID NO:81:									
(i)	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 284 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 									
(ii)	MOLECULE TYPE: cDNA									
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:81:									
AGGGCCAGAG GGAGCCAGGA TTCTGGCAAG	GGAAAACCAT CACAAGATGG AGTGCCAGCA AAAACTGATC AAGGAGCTGG GGAAACCCAG AGAGTGGCTT TGACCCACCT TACGCTGGAC CTAGAAGAA GCTGCAGGCA CAAAGCAGCC AGATCCATGA CCTGGAGAGC CACAGCACCC AGAGCTGCAG GAGAGGGACC AGGAGGTGAA GTCTCAGCGA GAACAGATCC GAGGCAGAAA GAGCATCTGA CTCAGGATCT CGAG	A 120 3 180								
(2) INFORMA	ATION FOR SEQ ID NO:82:									
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 311 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear									
(ii)	MOLECULE TYPE: cDNA									
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:82:									
TGAAGCACAG CTCTGCTCTT GCACATGATA	TTCATGGCCT ACTGTGTGA CTTGGTGGCT TGCTTGATAA GAAGGTTTT CAGATATCTC AGCTGCTAAT CCTGTAAGCC CTTTACCCAT TCTCGCTTT GCCACATCAT GAATAGATTG GTATACTATT GTGGGATACT TCTAGTTTT TAGGTTATGG TTAATGTTCC TTTCCATCTT CCTGGTTACT GATAATGTTC GATGGGTCTA TCGATGGAA GAGTTTCAGC TTTGTTCGTG TTATTTCCCC G	T 120 A 180 C 240								
(2) INFORMA	ATION FOR SEQ ID NO:83:									
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear									
(ii)	MOLECULE TYPE: cDNA									
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:83:									
GGTTCTACAT ATGTTGCTTT	TAAGAGAACC TCAGCATTGT GCACGATAAG AGAATGTGTC AGTATTTCA TTTATCTGTA AAATGTGACT TTTTTTTTTT TTTATCACAA CAGAAGTAA GTACCTGGTG TCTTTTATTA AGAATTTACT CCCCCCATTT CTCACAGAG GGAGTCATTG TCACAATATA ATAGAAATGT TAGCAACCAG ATTCATGTA	A 120 A 180								

GGACTAAGTG GTCCTCATGA ATTGCATTAA GACTCTGTAC TGCTCATATT ACACTCCATC CTCTCTGTAG TTTGCTGGGT ATTCTCGAG

(2) INFORMATION FOR SEQ ID NO:84:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 312 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
GAATTCGGCC TTCATGGCCT AGAAAGACAT CATTTAAGTN CTTTTAACAT TTAGTTTGTG GTCATAAGTT GACCTTTATG TGCTTTCTGA ATTGGAACTT AAAATAATCT TTAATTCATT ATTTTTTCTA CTTCTAGGCC AGTTTTGAGT TTAATATTTA TAAAAGGTTA GATAGTTATA GATAGGATTA TTTTGCAGTT TTGAAACAAC ATACAAATTG TTATAGATTT CAGAGTAGGG CTAATCACAG GAAAGACAAA AGTCAGAATG CTTNAGGTAA GCCCCTTCTC ATTATATAAG ATCAAGCTCG AG	60 120 180 240 300 312
(2) INFORMATION FOR SEQ ID NO:85:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
GAATTCGGCC TTCATGGCCT AAAAACTTTC AACTTAGAAA AACTAGCAAG GGATTGTTCA CCCTTACCCC AGTGGTTGGT GCTAGAGAAA AAATGGAGGA TGTCTGTTCC ACGCAGACCC TGGTGGTTTA AAACACACAT ATAGATGGCT CTGGGACCAT CAAAATAGCA GCAGCAAAGA GCCACTCCAC CAGCCTCCCC TCCACTCCCC CAGGCCCCC ACAGCAGAAG GCTCCAGCCA CTTTTTGGAA GCCTGTAGCC TGGCTCCATC TTGCCCTGTG CCACAAATGC CCATGGCCCT CGAG	60 120 180 240 300 304
(2) INFORMATION FOR SEQ ID NO:86:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 291 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	
GAATTTTGAA CACTAAAGCT TTGGATACAC AAATTTATAA CATCTTATTT ATAAATCAGT GGTGTACAGA AAGCAGAGAT CCCCATAATCA AGCATGGCAA ACATGTTGAA GAATATGCTT ACAATGATTT CTGCTATAGA TTTCATAATG GGGATTCAGA GAAGTAGAGT TATGGTGCTG GTTCACTGCA TTGATTGGAT CAGGCGCTGG AAACTCTCCC TGATAGATTT TATTCTCACC TGTTGGGCAA TTTCCAGAAT ATTCTGCTGT AATTTTACAT GTGGGCTCGA G	60 120 180 240 291

(2)	INFORMATION	FOR	SEO	TD	NO:87:
12/	TILL CHURST TON	LOK	250	12	1,0.01,

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GAATTCGGCC	TTCATGGCCT	AGCTAGAAAA	ААААААААА	AAGCCCTTTT	CAGTTTGTGC	60
ACTGTGTATG	GTCCGTGTAG	ATTGATGCAG	ATTTTCTGAA	ATGAAATGTT	TGTTTAGACG	120
AGATCATACC	GGTAAAGCAG	GAATGACAAA	GCTTGCTTTT	CTGGTATGTT	CTAGGTGTAT	180
TGTGACTTTT	ACTGTTATAT	TAATTGCCAA	TATAAGTAAA	TATAGATTAT	ATATGTATAG	240
TGTTTCACAA	AGCTTAGACC	TTTACCTTCC	AGCCACCCCA	CAGTGCTTGA	TATTTCAGAG	300
TCAGTCATTG	GTTATACATG	TGTAGTTCCA	AAGCACATAA	GCTAGAAGAA	GAAATATTTC	360
TAGGAGCACT	ACCATCTGTT	TTCAACATGA	AATGCCACAC	ACATAGAACT	CCAACATCTC	420
GAG						423

- (2) INFORMATION FOR SEQ ID NO:88:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GCGATTGAAT	TCTAGACCTG	CCTCGAGCTT	GGGGGGATTA	CAGTTCAACA	AGAGATTCAG	60
GCAGAGACAA	ATATTCCAAA	CTATATCAGG	AATTAAGTAG	GCTTTGCTGT	CCTTTTGCAG	120
CTTTGAGTCA	ACCCATATGA	${\tt GAGTGAATTC}$	TCCGATCCTG	TACATACTCG	AG	172

- (2) INFORMATION FOR SEQ ID NO:89:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTCGGCC TTCATGG	CCT ACCCGTGTTG TO	CCAGTATAC CTTATAACA	TTAGCCACTT 60
CTCCCCACCC TCCAGAA	GGG GTCCACGTTG A	ATTCTGAAT CATCTTGAAA	ATAAGATTCC 120
AACCACAAAA AAAATTT	AGC CATTTCTTTA CT	TAAAAAAAA CCAAAAAAC	AATCTGTTTT 180
ATAATCACAG ATTTTTA	GAC AAATTTCTTG TA	ATCAGGAAG AAATACAAA	TTTGTCATGT 240
TTCTCAAGCA GTGTCTC	GAG		260

- (2) INFORMATION FOR SEQ ID NO:90:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs

AGTACTCGAG

- PCT/US98/06956 (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90: GAATTCGGCC TTCATGGCCT AAACTAAGAT AAAAATAAAC AGATAGGAGA GCTGAATTCC ATTTCAAGTC CTCATGTATA TGCTTACAAA GTTCCAAATT AAGCTTGGGA CTGGTTCTTA 120 CATGGCAGGT AATCCAAACC TTTTCTATTT ACTGAAGATT TTCAGCTCTC TTACAGAAAT 180 ACACAGGCTA CCATTAAAAT TGTAGGGATA AATTTTAAAT TGAATTTGAA AATAAGAGCA 240 250 (2) INFORMATION FOR SEQ ID NO:91: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91: GAATTGAAAC ACAGAGTTGT TCTGCTGATA GTTTTGGGGA TACGTCCATC TTTTTAAGGG 60 ATTGCTTTCA TCTAATTCTG GCAGGACCTC ACCAAAAGAT CCAGCCTCAT ACCTACATCA 120 GACAAAATAT CGCCGTTGTT CCTTCTGTAC TAAAGTATTG TGTTTTGCTT TGGAAACACC 180 CACTCACTTT GCAATAGCCG TGCAAGATGA ATGCAGATTA CACTGATCTT ATGTGTTACA 240 AAATTGGAGA AAGTCTCGAG 260 (2) INFORMATION FOR SEQ ID NO:92: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 354 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAATTCGGCC	TTCATGGCCT	AATTTCATCT	TTTTTTCCTG	GTGCTGCATA	AACATATATT	60
${\bf AAATGTTGTT}$	ACTGATCCCT	AGTACTGTTG	ATTTGTGACC	CTTCTCCTGA	GGGAGACTAA	120
AGCTGCTTGA	GCTAAAGGCT	TTTGAGACAT	CCCATACGGT	TCCCTGAACA	AAGTTTTCTC	180
TCCTGACCTC	AGTTCTCTTG	ATGACCTTGG	CAAGTGGGCC	CGACTAGTTG	GACACTAATG	240
AGGCATCGTA	ACATGCCGGC	CCCATCCTGT	CCATTCTGTT	CTCTTTGCCA	TCTAGCATTC	300
AGTGTTGTGT	CTTCCTAGTG	GGCATGAAGA	CGGCTTTAAA	ACCATCCACT	CGAG	354

- (2) INFORMATION FOR SEQ ID NO:93:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GCTGAAAATG	CAAAACATGA	AGAAAGTGAT	TGAGGCAATT	CGAGTGGAGC	TGGTTCAGTA	60
CTGGGACCAG	TGCTTTTATA	GCCAGGAGCA	GAGACAAGCT	TTTGCCCCTT	TCTGTGCTGA	120
GGACTACACA	GAAAGTCTGC	TCCAGCTCCA	CGATGCTGAG	ATTGTGCGGT	TAAAAAACTA	180
CTATGAAGTT	CACAAGGAAC	TCTTTGAAGG	TGTCCAGAAG	TGGGAAGAAA	CCTGGAGGCT	240
TTTCTTAGAG	TTTGAGAGAA	AAGCTTCAGA	TCCAAATCGA	TTTACAAACC	GAGGAGGAAA	300
TCTTCTAAAA	GAAGAAAAAC	AACGAGCCAA	GCTCCAGAAA	ATGTTGCCCA	AGCTGGAAGA	360
AGAGTTGAAG	GCACGAATTG	AATTGTGGGA	ACAGGAACAT	TCAAAGGCAT	TTATGGTGAA	420
TGGGCAGAAA	TTCATGGAGT	ATGTGGCAGA	ACAATGGGAG	ATGCATCGAT	TGGAGAAAGA	480
GAGACTCCTC	GAG					493

- (2) INFORMATION FOR SEQ ID NO:94:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GAATTCGGCC	TTCATGGCCT	ACACACGGCC	AAATTTGAGG	GCATTCTCAC	ATGTGTTCTT	- 60
CTCTCAAAAC	CACTGGGGTT	GACAGATCCA	GGAGGCTAAA	AAAAAGTGAC	CTCTATAATT	120
CTTTAAAGGT	GCTATTTTTA	GAANATTGTA	TAATTTATTC	ACAGTATATC	TAAAACAGAA	180
TTAAGGACAA	TTAAAATATC	TTATGTGACA	GCCTTTATGT	CTAGTCACAT	TTGATGAAAT	240
AAAAAACTTC	TGAATCTGAA	TAGAAGTTCT	ACTGTNTCAG	GATTGAACTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:95:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GAATTCGGCC	TTCATGGCCT	AAAAAGACAG	GAAAATAAGT	CTCTTTGTAT	CCTTATTAAT	60
CATTTGAAAT	TATGCTATAA	TATTTTTTAA	AACTCACCTG	TTTGGTTCTG	GGTGAAGCAG	120
TTCCTGAAGG	AGTGTTTTGT	CAGAATATAT	TGTTAGGTGA	ATAGAGGGTT	CTGTGGCCAA	180
GTAAGTTTGG	GAAATAGTGG	GTTAGACAAA	GTTGAGTTAC	TGTTGGCCTT	TCAGACCTTT	240
GATACGCTAA	TGTGCATTTT	AAATCTCCAA	GAAGCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:96:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GAATTCTCCA	GCCTGGGTGA	CAGAGTAAGA	CTCCATCTCA	AAAACAAAAA	AACCCAACAG	60
					ATCTAGGTAC	120
TGTATAGTGT	GTATTAGTTG	GGGTTCCTTT	TTTGAAACTT	AATCTTGCCT	ATAAAACACA	180
AAAGAGTTTA	AGATGATATT	${\tt GAGACTCCTC}$	CTGTCCTCAT	TCCTTTTCCT	TCCTAATAGC	240
TCAGTCCTGA	AGCTCTTAGG	TGAGGCAGAA	CAACTCGAG			279

- (2) INFORMATION FOR SEQ ID NO:97:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GAATTCGGCC	TTCATGGCCT	AGGATACCTT	CATTTCAAGG	AGCCTCTTTA	CAGTAACTGG	60
GCTAAACATT	TTGTTGTCGT	CCGTCGGCCT	TATGTCTTCA	TCTATAACAG	TGACAAAGAC	120
CCTGTGGAGC	GTGGAATCAT	TAACCTGTCC	ACAGCACAGG	TGGAGTACAG	TGAGGACCAG	180
CAGGCCATGG	TGAAGACACC	AAACACCTTT	GCTGTCTGCA	CAAAGCACCG	TGGGGTCCTT	240
TTGCAGGCCC	TCAATGACAA	AGACATGAAC	GACTGGTTGT	ATGCCTTCAA	CCCACTTCTA	300
GCTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:98:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAGCTGTGTC	AGCATCGATC	AGGGGTCTGT	AGACAAAAAT	TCCCAAAGAT	TTGAGACTTT	60
ATTGGGGGAA	ACAGATCACT	GGCGGGGAAT	AAGCCACAGG	CCAAAGGAGG	AAATGCTGGG	120
ACCAGAAGTC	CCGCTTGCCG	CCTTTTGCTA	AAAGTTCCGC	ACGCCTGCTC	GGCGTGGGCG	180
CAAGCATAGT	GTCGTCGGGG	CTCTGCGACG	TCTGATTGGC	TCTCTGCAGT	GCACCGTCGA	240
GGTAGAAGGC	TCAGCTCCTA	GTCGCTCCCA	AATTACTTTG	TTGGTGCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:99:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCCTCTCTGT	TCTGGTTCTC	TCATTTTATA	AAGTGCCTTC	TTCCTTTCTG	CATTTATAAG	120
TAAACATGAG	AAAAATCTGA	AAAGACTTCT	TCAGGATGTT	TAAGGAAACA	AATGTTGCTT	180
TCCTTGGGTT	GGGTCGTTTC	ATAAGAGTGA	TGTTTGCCAT	AAAACTGGAG	CCTCATAGAC	240
GATCCTGCAG	GGAGGAAGCT	TTCCTTGGTC	ACCTGACTCA	TGTGTTTATA	TATAGTATAG	300
AGGAGAGGTA	TTCCAAAAGA	CCCGTCGCTT	TTCCTGTGTC	CCACAGCTGC	CTGTAGAGTT	360
GTGGCACCAT	AAACTTTAGC	AGCTGGAAAT	CCTCGAG			397

- (2) INFORMATION FOR SEQ ID NO:100:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GAATTCGGCC	AAAGAGGCCT	ATTAATTTAA	TAAAGCCATA	TCATACCTCT	CTTTAACATT	60
GTTAAAAGGA	AACTGTGTGT	GTGTATTTGT	GTTAATGTTA	ANTTCTCTTC	ATTTTTGTGC	120
TTGGGGGGCT	${\tt GTTTATTTGA}$	GGATGGTCGG	GGGGCGGGTG	GGTCAGACCC	ATCCATCCCC	180
CATGGAAGAC	CAGACCCATC	CATCCCCCAT	GGAAGACCAT	TCCCGTGTGT	TCAGACTGGC	240
AGGGTACTTC	CATAGACAGG	AACATTCTGG	ATGCTCTGAT	GCTGAACACT	ACCAGAATCG	300
GCCATGGATT	TGCTTTGAGC	AAACACCCCG	CAGTCAGGAC	TTACTCCTGG	AAAAAGGACA	360
TCTTCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:101:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GAAAAAAATA	GACAAAACTA	TGATGTAAAA	ATGCTTAAAA	ACAATTATTC	CTCTCTGCTA	60
ATTTTAATGC	AAAATAAATG	ATGCTAGCAT	TTAATATGTT	TATATGATCT	TGTTTTTAGG	120
ATTGAAATTT	TAATACAATG	GCCTTTTGTA	ACTATTTTA	CTATTATAGC	TCAGGTGTTT	180
GAATTCTCTC	TACCCCACCT	ATCACCCCTA	TCCCCTAACA	AAGAGTCTGG	CTTCATAAAT	240
ACTGTTGAAT	GAAAATTGGT	TCTCTAAATG	GTTAACAAGA	TGAATCCACA	TAAATCATAA	300
TTCAGTACTG	AGGAACCGAA	TTTATACCCA	GCGTCTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:102:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

The second of th

AAGGGCAGAG AAATTTCAGG GGTGAAGAGA GCAATGGTAG	AAGTAGCTGG TGGGATTTGA CTGGAGGTGC	GAACTGAGAA ACAGAGATGT GGGGCAAGTA	TGTTTAGGAG GAACTTTGGC GTGGTGATCT TGGAAGCATG TTAACTGGAG	TGTTATTCTA GACTTGGTTC GAGACCATTA	GTAAGACTGA ATTCTGCTGT ATTTATGGGG	120 180 240 300 360	
GCCACTCGAG						370	
(2) INFORMATION FOR SEQ ID NO:103:							

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCGATTGAAT	TCTAGACCTG	CCTTGAGATC	ACCGAGTGCT	TCATCTCTGA	CAGTTCCTCT	60
GACCAGATGA	CCACAGGCAC	CAACGAGAAC	GCCGACAGCA	TGACATCCAT	GAGCACACCC	120
TCAGAGCCTG	GCATCTGCCG	CTTTACCGCC	TCACCACCCA	AGCCCCAGGA	TGCGGACCGG	180
GGCAAAAACG	TGGCTGTGCC	CATCCCTCAC	CGGGCCAACA	AGAGTGAGTG	CTCAGACCAC	240
CTCCCAGGCA	GTGCCCCCC	GACTCTCGAG			•	270

- (2) INFORMATION FOR SEQ ID NO:104:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAATTCGCCT	TCATGGCCTA	ATATGCTTAT	GAATATGATG	TTGATGGACA	GCTCCAAACA	60
GTTTACCTCA	ATGAAAAGAT	AATGTGGCGG	TACAACTACG	ATCTGAATGG	AAACCTCCAT	120
TTACTGAACC	CAAGTAACAG	TGCGCGTCTG	ACACCCCTTC	GCTATGACCT	GCGAGACAGA	180
ATCACTCGAC	TGGGTGATGT	TCAATATCGG	TTGGATGAAG	ATGGTTTCCT	ACGTCAAAGG	240
GGCACGGAAA	TCTTTGAATA	TAGCTCCAAG	GGGCTTCTAA	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:105:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GAATTCGGCC	TTCATGGCCT	ACTTAAATCT	TAGATGCTAA	TGGGAGAAAC	TGATTTTTTA	60
AAAAACAGGG .	AAACTAATTA	ACATTTTATC	AGATATGCTA	TGAAGTAAAC	AGTTGAAGAC	120
TGACAGTCCA						180
CAAGGGGAGA	GCTGAGACCT	GAATATGAGG	AGAAGCCAGG	CGAGCACACA	ATAGGGCAGA	240

AAGGAGCAGT AGGTCAAAGC CTGAGGCAGG AGAGAGCTTG ACTGACTCGA G

291

(2) INFORMATION FOR SEO ID NO:106: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106: GAATTCGGCC TTCATGGCCT AGAAATGGTT CTGAAAGCGA CAGTAGAGAG ATGCAGTTGT GATGATTTCA ACAACCTGGA TGTTTTCTTT CTCCTCTTTG CTTCCATTCA TCTCTGTTGG 120 CTGCTGTTGA TGGAGTCAGA CAGTAAACAC GTGGCTTGGA TAACACCCAT CATCCTATGA 180 AGAATATAGG GAGTACTTGT TCTCTGTTGA TTCAACTTTT ATGTCTCCAG TAACATTGCG 240 CTTATGAAGG TACCTGTATT TGTATGGACT CTGAATAAAG AAGAATTCAT TTGTTTAGCA 300 AGTATTAGTT CAGCAACCAC TGAGAAACAA GCACTCGAG 339 (2) INFORMATION FOR SEQ ID NO:107: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 439 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107: GAATTCGGCC TTCATGGCCT ACATCATGTC AAAGAGTACT ACATACAGTT TGGAATCTCC TAAAGACCCG GTACTACCAG CTCGTTTCTT CACTCAACCT GACAAGAATT TCAGTAACAC 120 CAAAAATTAT CTGCCTCCTG AAATGAAATC ATTTTTCACT CCTGGAAAAC CTAAAACAAC 240 CAATGTTCTA GGAGCTGTTA ACAAGCCACT TTCATCAGCA GGCAAGCAAT CTCAGACCAA ATCATCACGA ATGGAAACTG TAAGCAATGC AAGCAGCAGC TCAAATCCAA GCTCTCCTGG 300 AAGAATAAAG GGGAGGCTTG ATAGTTCTGA AATGGATCAC AGTGAAAATG AAGATTACAC 420 AATGTCTTCA CCTTTGCCGG GGAAAAAAAG TGACAAGAGA GACGACTCTG ATCTTGTAAG 439 GTCTGAATCG GAGCTCGAG (2) INFORMATION FOR SEQ ID NO:108: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 298 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108: GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCC TCGAGAGGCA GGTCTAGAAT 120 TCCAAATGTA AAATTTACTA AGGCTTTTCA TGTGGAAGTA GAATGCATAT ATCTTTCTTG ATATAACAAA TGAATTTGGT TGTAGCTAAC GTGTTGTACT AGTAAAGGTC CACCTGCTAA 180 240 ACTITITCTT TTTTGTTGAG GTATAGACAG TAGAGTGATA CCGATACATG AGGAAAATGA GAACTGGAAT GCAGGCCAAA AGCTGGTCCT TTCCAGATGA ATGTAACCAA GACTCGAG 298

andre Transport de production de la company Transport de la company

- (2) INFORMATION FOR SEQ ID NO:109:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GAATTCGGCC	TTCATGGCCT	ACACTCTCAA	ATATGTGGCC	TTTAACGGGA	CCAAAGTAGG	60
AAAGCAGATA	GTGGAAAACT	TCTCTCCCAA	TCAGACCAAG	TTCACGGTGC	AAAGAACGGA	120
CCCCGTGTCA	CGCTACCGCT	TTACCCTCAG	CGCCAGGACG	CAGGTGGGCT	CTGGGGAAGC	180
CGTCACAGAG	GAGTCACCAG	CACCCCGAA	TGAAGCTTAC	ACCAACAACC	AAGCAGACAT	240
CGCCACCCAG	GGCTGGTTCA	TTGGGCTTAT	GTGCGCCATC	GCCCTCCTGG	TGCTGATCCT	300
GCTCATCGTC	TGTTTCATCA	AGAGGAGTCG	CGGCGGCAAG	TACCCAATAC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:110:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GAAAAAACTG GGTCAAAGAA	TTACGGAAAA	TGTTGGGAAA	TGAAATCTGT	TTATGTATAG	60
TTGGTAATAA AATAGACTTG	GAAAAGGAGA	GACATGTTTC	CATTCAAGAA	GCAGAGTCGT	120
ATGCAGAATC TGTGGGAGCA					180
AGGAACTCTT TCTTGACCTT					240
CAAAAGGCAA TGGCTCTAGT					300
ATGAACCTCA AGCCCAGACC	AGTGGTGGAG	GGTGCTGTTC	TTCTGGATAA	CTGTTCACGC	360
CTAAGAAATT AAAAGACAGA					407

- (2) INFORMATION FOR SEQ ID NO:111:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

033mmaaaaa	##CX#CCC#	******	አሮአጥጥአአአርሮ	AACTTGCATC	TCAAAACAAT	60
						120
				CCTCCTCTGA		
ATGGGTAAAG	TTGTCTAAAT	ATGGGATTCC	TTAGAATCCA	TCCTCCTTCC	CAAGCATTTC	180
				GGCAGAGCTG		240
AGCCTTCTCT	GAAGTATTGA	GGGAAAGTCT	GCTAAACGGC	TAAACTACTT	AAGGAGCTAA	300
				TTTCTAATTA		360
	GTCAAAGGTA					395

4545/	101/05	90/00930
	(2) INFORMATION FOR SEQ ID NO:112:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 301 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:	
	GAATTCTAGA AACTACAGTA GTGGGACACA TAACATAGAA GTAATCGTCC AGGATTCTGGAAGAAGT AAGAGTGTTC ACCACATATT TTCTGTTCAA GAGAATAATC ATCTCAGGTGATCCCCTG GCATCATTTA TTCTCCGTAC TGATCACTAC ATCATGGCCC GGGTCCTTGTGCTGATT GTGCTGAGCC AGCTCACCAT TCTCATTATT TTTAGATATC GAGGATAAAAGAGCTTAAAA GAACCTTCAG GGTTTATAAA TCTGACCTCA TTTTCTCTTC AATGTCTCG	TTT 120 TTT 180 CCC 240
	(2) INFORMATION FOR SEQ ID NO:113:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 268 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:	
	GAATTCGGCC TTCATGGCCT AAGCATGCTG TCTTGTGATG GTGATTCAT GTGTTTT CATGGGATTA TTAACGGCAT CCATTTTCTT GGGCGTCAAG TTGTTGCAGG TGTCCAC TGCGATGCAG CAGCAAGAAA AACTCATCCA ACAAGACAGG GCACTGCTAA ACTTTAC ATGGAAGAGA AGCTGTGCCC TTCAGATGAA ATATTGCCAA GCCTTCATGC AAAACTC AAGTTCAGCC CATAACAGCA GTCTCGAG	CAT 120 AGA 180
	(2) INFORMATION FOR SEQ ID NO:114:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:	
	GAATTCGGCC TTCATGGCCT ACCCGCATCC CAGCTCTATT TAAAAAAATA AAGAAG	

- GAATTCGGCC TTCATGGCT ACCCGCATCC CAGCTCTATT TAAAAAAATA AAGAAGAAGA
 TAATTCATTT CCTTAAGCTG CCCTTACACT ATTAGTCAGG AATGTTTGTG TTCACTTCCA
 120
 CTACATACCT TACGATCTCT TTTGCTTTGC TTTTTTTCAG TCAAGTCTCT ATTTATGAGG
 180
 TGGACAAGCA AGATTGTCGC AAATTTTGCA CTACTGGCAT CGATGGAGCC ATGACAATTT
 GGGATTTCAA GACCCTCGAG
 260
- (2) INFORMATION FOR SEQ ID NO:115:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGGCC TTCATGGCCT	AAACATTTTC	TGAAAAACGT	GATAGAAAGA	AGGAGGAGCT	60
GTTTCTAGGA GGGAAATAAA	TAATTTGGCA	GGAGACTTTT	TGAACTAGAT	ATCTATTGAA	120
TAACAAAGTG ACAATGTTCC	CCATCCTCTC	ATTTCCATTC	CCAATTTTAC	TTCTCGTCCC	180
AATTCAAATC ATTCTTACTT	ATGATCGGCG	CTATGTCAGT	GCCTCTCAGC	TGGTCTTCCC	240
AGACCCAGTC ACCCTCGAG					259

- (2) INFORMATION FOR SEQ ID NO:116:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAATTCGGCC	TTCATGGCCT	AATTACATTT	ATGCAACCAA	GCTATCAAAA	GGACTGGCTG	60
TCCTTGGGAA	TGAAACGTAA	CAAAATCGTC	AATAGAGTAT	TATTGGAAAA	GATTGTTTTC	120
AGTCATGAAC	TAGCTATTTA	AATGAGAAAA	CAAATGTAAT	GATGCTTTCT	GTCATGATTT	180
AAATAAATAT	TGTCAATTGT	AGGAAATTGG	TAAAATAAAT	GAAAAAGAAA	AACTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:117:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GAATTCGGCC	AAAGAGGCCT	ACCCTAGACC	TGTTTTCTGT	TCTCTACTCT	TGAAATGCTA	60
ATGACCTTCA	TGACCAGAGT	CCGCTATTGC	AGTTTGTGGT	TGACAGGCAT	CTCTCACTCA	120
CTGTGCTGCA	ACTCAACTCT	TTATCTTCAA	CCAAACAGGG	CCTCCCCGCA	GCTTTCCCAC	180
TGCCACTCAG	TGGCACTCCA	TCCAGGGTTT	CCAAAGTGTA	AGACCCCGGA	ATTTATCTTT	240
GACACTTCCA	TCTCCCTCCA	CCCCTCATCC	AATTCATCA			279

- (2) INFORMATION FOR SEQ ID NO:118:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 656 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAATTCGGCC	AAAGAGGCCT	AGTTATAATG	ATGGAAGAAG	TGGAAAAACT	TTGTGATCGG	60
CTTGAACTGG	CAAGCTTACA	GTGCTTGAAT	GAAACACTCA	CATCATGCAC	AAAAGAATAG	120
GAAAGGCTGC	TTTGGAAAAA	CAGATAGAAG	AAATAAATGA	GCAAATCAGA	AAAGAGAAAG	180
AGGAAGCTGA	GGCTCGTATG	CGACAAGCAT	CTAAGAACAC	AGAGAAATCA	ACTGGTGGAG	240
GTGGAAATGG	AAGTAAAAAT	TGGTCAGAAG	ATGATCTACA	ATTACTAATT	AAAGCTGTGA	300
ATCTGTTCCC	TGCTGGAACA	AATTCAAGAT	GGGAAGTTAT	TGCTAATTAC	ATGAACATAC	360
ATTCTTCCTC	TGGAGTCAAA	AGAACTGCCA	AAGATGTTNT	TGGCAAAGCA	AAGAGTCTCC	420
AAAAACTTGA	CCCTCATCAA	ANAGATGACA	TAAATATAAA	GGCATTTGAT	AAGTTCAANA	480
AAGAACATGG	AGTGGTACCT	CAAGCAGACA	ACGCAACGCC	TTCAGAACGA	TTTGAAGGTC	540
CATATACAGA	CTTCACCCCT	TGGACAACAG	AAGAACAGAA	GCTTTTGGAA	CAAGNTTTGA	600
AAACATACCC	AGTAAATACA	CCTGAAAGNT	GGGAAAANAT	AGCAGAAAGT	CTCGAG	656

- (2) INFORMATION FOR SEQ ID NO:119:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 523 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GAATTCGGCC A	AAGAGGCCT	AGAGACAAAT	AGGTGATACT	GAATTTTATA	CTGTTTTCTA	60
CTTTTCCATT A	AAACATTGG	CACCTCAATG	ATAAAGAAAT	TTAAGGTATA	AAATTAAATG	120
TAAAAATTAA T	TTCAGCTTC	ATTTCGTATT	TCGAANCAAT	CTANACTGTT	GTGATGAGTG	180
TATGTCTGAA C	CTGTAATTC	TTAAAANACT	TCTTAATCTT	CTAGAAGAAA	AATCTCCGAA	240
GAGCTCTCTC T	AGAAGTCCA	AAATGGCTAG	CCATTATGCT	TCTTTGAAAG	GACATGATAA	300
TGGGACCAGG A	TGGTTTTTT	GGAGTACCAA	GCAAGGGGAA	TGGAGCACTT	TAAGGGCGCC	360
TGTTAGTAAC A	TGAATTGGA	AATCTGTGTC	GAGTACCTCT	GATCTAAACG	GTAAAACAAG	420
CTGCCTGGAG A	GCAGCTGTA	CCTAACAATA	CTGTAATGTA	CATTAACATT	ACAGCCTCTC	480
AATTTCAGGC A	GGTGTAACA	GTTCCTTTCC	ACCAGATCTC	GAG		523

- (2) INFORMATION FOR SEQ ID NO:120:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAATTCGGCC AAAGAGGCCT AATTTCTTC TGTGATATGA GAATTTCTTT TCTTTCAGCA 60
GCTTTACCTG CATTTGGCTT TGGCTTTTGC AATCGGCCCC TCATTCTCGA G 111

- (2) INFORMATION FOR SEQ ID NO:121:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

e de la composition della comp

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GAATTCGGCC	AAAGAGGCCT	AACCGCGGCC	GCTACTTCGG	CCTCTTTGGA	AAAAAAAAG	60
TGAAAGAAAA	NATCACAATA	CAGGGAAAAG	TGAGCTAAAA	ATCCCGGCAT	TAAAAAGCCC	120
TTGATGTGGT	CCTGAATCGG	CTATTTCTAT	CTGTTCCCTG	AGCCTAACCT	CAGCGCTGGC	180
CTCTCTAAAC	CTCTTTTCAG	TCCTCTCATT	TTGAAAACAG	${\tt GGCCCATTAC}$	ACATTCTCTG	240
AAAGCTTGCT	GAGTGATTTA	ACCACATAGT	CTAGGGGAGG	CACTCATCAA	ACATAAGGCC	300
TCTCTTTTTG	ATTTTTATCC	TATAGTGGTA	TCTATCTAGA	GGCTGGTGAA	GACAGTGTGG	360
TGGAAGGAAA	GTGGGAAGGA	TACACTGAAA	TAGGACATAG	ACGTAGAGGG	GAGTCGATGG	420
TCATCTGGCT	TGATAGGGAA	AGTTAGAGAG	CTCTCCTGAA	CCACAGTTAC	AGAGCTTGGG	480
ATTATAACAC	ACACAGCCCC	AGAGAAAACA	CTTTGTTTAC	CATATTTCCT	CTTCTGCTGG	540
GGCTCTGGCA	CCTTAATTGG	TCAAAAGGCA	GCACTCGAG			579

- (2) INFORMATION FOR SEQ ID NO:122:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GAATTCTAGG	AATGGGTCGG	GAAGTTGAGA	ATCTTATATT	AGAAAATACA	CAACTGTTGG	60
AAACCAAAAA	TGCTTTGAAC	ATAGTGAAGA	ATGATTTGAT	AGCAAAAGTG	GATGAACTGA	120
CCTGTGAGAA	AGATGTGCTG	CAAGGGGAAT	TGGAGGCTGT	GAAGCAAGCC	AAACTGAAAC	180
TAGAGGAAAA	GAACAGAGAA	TTGGAGGAAG	AGCTTAGGAA	AGCTCGGGCA	GAAGCTGAAG	240
ATGCAAGGCA	ACTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:123:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATTCCTGT AACTCGGAAA AG	GATATCAGA	GGAATGTTCG	TGGCATCAGA	GAGAAAGATG	60
AGAGCTCACC AGGTGCTCAC C	TTCCTCCTG	CTCTTTCGTG	ATCACCTCGG	TGGCCTCTGA	120
AAACGCCAGC ACATCCCGAG G	CTGTGGGCT	GGACCTCCTC	CCTCAGTACG	TGTCCCTGTG	180
CGACCTGGAC GCCATCTGGG G	CATTGTGGT	GGAGGCGGTG	GCCGGGGCGG	GCGCCCTGAT	240
CACACTGCTC CTGATGCTCA TO	CCTCCTGGT	GCGGCTGCCC	TTCATCAAGG	AGAAGGAGAA	300
GAAGAGCCCT GTGGGCCTCC A	CTTTCTGTT	CCTCCTGGGG	ACCCTGGGCC	TCTTTGGGCT	360
GACGTTTGCC TTCATCATCC A	GGAGGACGA	GACCATCTGC	TCTGTCCGCC	GGTCACTCGA	420
G					421

- (2) INFORMATION FOR SEQ ID NO:124:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid

Superior State

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTCTAGA CCTGC	CTCGA GAAAATGAAA	GTCTTTTCTC	AAAAAACTTC	TTCCCAGGTC	60
TGTGAAGCAG CACAG	TGGCC CCTTCTGGCT	CTCACCTTGT	ACCTCGTCCT	TGTTTGCCTC	120
GAG					123

- (2) INFORMATION FOR SEQ ID NO:125:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GAATTCGGCC	TTCATGGCCT	AAGATGGCGT	CTCACAAATC	ATATGCCAAT	TACTGAAATT	60
GGAGGTGAAA	ATATTCTAGA	TTTATTGTGG	GATATATA	TTTTATGGTG	TATGGCTCCC	120
AACACCACAT	GCCACTGAAC	TATATAAAAC	TTTATGTCAG	AACACTTACT	TGTGTCATAT	180
GTAACCCTCT	TGCAAATAAT	ATTCCCTTAC	TACAGATCTG	TCCCACTGTT	CTCAGAAAAT	240
AAAACATGGG	AACGTTGGAA	TGTCTCCTTG	CTATAAGATA	TTGAATTCTA	GACCTGCCTC	300
GAG						303

- (2) INFORMATION FOR SEQ ID NO:126:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GAATTCGGCC TTCATGGCCT AATGAATACG CAATTAGAAC TGTTAAAAAA CTACAAGAAG ATATCTGCAA AAGCAATTAG CCAAAATATC ATTGAGGCTA AGAGCTTTTA CAGTTGAAAG TGAAGCATCA GCTAAGGAAC	TTTCAGAACA AGATTGAGAA ACGCTACCAC ATTCTCAGCA CTATACACCA ATGAAGCAGA	ACTTAAATTT AATTAGGCCA TGATGAAAAG TTACCAAAAA AGAAGAGGTG GATAAATAAG	CAGAACAACT GGCTTTGAGG AAGGAAACAG AATATTAATA AAAGAGTTGA TTGAACGAGC	CTGAAGATAA AGCAAATTTT TTACTCAACT GTTTGCAGGA TGTGCCAGAT TAAAAGAGAA	60 120 180 240 300 360 420
TGAAGCATCA GCTAAGGAAC CTTAGTAAAA CAATGTGAGG AGAAAATTTA AGGAAAGCCA	CAAGTGAAAA				480 508

- (2) INFORMATION FOR SEQ ID NO:127:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 713 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GAATTCGGCC	TTCATGGCCT	AGCGGCAGTC	CAGATCACGG	TTACTGTGAC	CTGACTGGAG	60
AAAAATTATG	TGTCTGCAAT	GATAGTTGGC	AAGGTCCTGA	TTGTTCTTTG	AATGTTCCCT	120
CTACTGAGTC	TTACTGGATT	CTGCCAAACG	TTAAACCCTT	CAGTCCTTCT	GTAGGTCGGG	180
CTTCACATAA	AGCAGTTTTA	CACGGGAAAT	TTATGTGGGT	GATTGGTGGA	TATACTTTTA	240
ACTACAGTTC	TTTTCAAATG	GTCCTAAATT	ACAATTTAGA	AAGCAGTATA	TGGAATGTAG	300
GAACTCCATC	AAGGGGACCT	CTCCAGAGAT	ATGGACACTC	TCTTGCTTTA	TATCAGGAAA	360
ACATCTTTAT	GTATGGAGGC	GCCCCAAGGC	CCGACCCCTC	CCCCAAAGGG	GCAGTCCCCT	420
TCTTGCAGGT	CTCAGCTTGC	GGGGTGGGGG	GAGTCATGCC	CAGGGGAGGA	GACTTTTTAT	480
CTGGAGGGGA	GAGAAGGATT	CTAGGGGTGT	GGAGTTGGAG	AAAGAGGCTT	CCTTGAGCCA	540
CCCTTCCCAC	CCCAGCCCTT	GNTGGTCCCT	AGGCCAAGCC	ACCAAGTGAA	ACCTTCCAGG	600
ATACTAGCCC	GCCAGCTGTG	GGCCCCAGAA	AGCCAGCCTG	CCTTTTAGCA	CTTGGATACA	660
CACAGACCCA	CGGAGCTCTC	TGTGTTTGGC	CTCTCACACA	CACACAACTC	GAG	713

- (2) INFORMATION FOR SEQ ID NO:128:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GAATTCGGCC	AAAGAGGCCT	AAGAGATTCA	GGACCTGCAG	AGTCGCCAGA	AGCATGAAAT	60
TGAATCTTTG	TATACTAAAC	TGGGCAAGGT	TCCCCCTGCT	GTCATTATTC	CCCCAGCTGC	120
TCCTCTGTCG	GGGAGAAGAA	GGAGACCCAC	TAAAAGCAAA	GGCAGCAAGT	CTAGTCGCAG	180
CAGCTCATTG	GGCAATAAAA	GCCCACAGCT	TTCAGGCAAC	CTGTCTGGTC	AGAGTGGAAC	240
TTCAGTCTTA	CACCCCCAAC	AGACCTCCAC	AGTCGAG			277

- (2) INFORMATION FOR SEQ ID NO:129:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 670 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GAATTCGGCC	TTCATGGCCT	AAGGCTACCG	ATATTGGAGA	AGCTAACTAT	GGGTTTTACC	60
ACACGTAACA	GCTTTTTGGT	GAAATCAGTT	GTTATACTAA	TAAGCTTTCC	TCTAATTGAT	120
TTGAGTTTTG	GTTTTTGTGT	TTGTATTTGC	GGGTTTTGTC	TCTTTTGTTT	TCTTGTTTTT	180
AGTAAATTGG	TTTTTCTTCA	ATGTATTTTC	TTAAAGTAGT	CTAGCTTTAC	CCAGTTTCCT	240
TGGCAAATTG	AAATTTAGGC	CATGAAGGCC	GAATTCGGCC	TTCATGGCCT	ACTCAGCCTC	300
CCCAAGTAGC	TGGGACTACA	GGCGTGTGCC	ACTATTCTCA	GCTGATTTTT	GTATTTTTAG	360
TGGAGACGGG	TTTTTGCCAT	GTTAGTTGGC	CAGGATGGTC	TCTCTCTCGA	CGTCGTGATC	420
CGCCCGCCTC	GGCCTCCCAA	ATTGCTGTGA	TGACAGGCGT	GAGCCACCCC	GCNTGGCNTG	480
TCCTACCTCT	TTTTTAAGAC	CTCTTCCTGT	AAGCACTGGA	TAATCTACTT	CTAGTAATGT	540
GAAACTGACT	ATATNTTGAA	TTCATATGTT	TTCAATCAAC	CTGTTGCAGT	TTATATTTCA	600
CACCCTGCTC	CCTTTTGACA	GTTTAAGTAC	AGATAGTCTC	AGCAGTTCTG	GAGACCATGT	660
AAAGCTCGAG						670

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATTCGGCC	TTCATGGCCT	ACGACTCTGC	TCTATTTACC	ACTATCAGGC	CAATCCTCCT	60
GACATGCTGT	TAATATTTAG	AAATATTTCT	CCAACATTCA	GAGTGCCTGG	GTACCACACA	120
TGGATGCGAC	TAAGATTCTT	AAGTCTGGTT	TCTAAGAGCT	TCTTCAATGT	CTCCAACTAT	180
CTTTTCAGGC	TCATGTTTGA	GACCTTCCTT	TCAAGAATAA	TTTGCTTGTG	ATCTGGTTCA	240
AGCTGAACAG	AGATTTTCAG	ATGACTCCCA	AACTATCTGC	AACACATCAG	CCCTATTAAC	300
TCTTCTCAGA	ATGCTCATAC	AGAAGCCATG	CCAGTGCACA	AAAGCCACTT	CTGACACCTG	360
GCCCTGTCTG	ACTCATGGAT	TTCTTCCAGG	ATTGCTCTTT	CTATCTGCTT	TAAACCTCCT	420
TGTCAATTGA	CTTTCCTTGG	CTCCCAACCC	ACTTTACTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:131:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 535 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GAATTCGGCC	TTCGTGGCCT	ANATATTCTA	AGCATTCAAT	TTGTCAGTTT	CTGAGATTTT	6 D
CTTTCCATCT	TAGTTTTTTA	GAAGTCAGAA	AATGACTTTT	CACATTCAGT	TAGGGTATAT	120
AACAATGTTA	ACGTAAGTTT	ATGAGCTGAG	TAGGTAGTTA	ATAAACATCC	TTTTAAGTTG	180
TAATGCTTTG	AAATAGCATA	TTAAAGGGTT	GCAAGGGAAA	ATTGGAACAT	CAGTGTGAGT	24.0
TATTTTACAG	TCATTTGTAG	GTCTGTTTGT	GACCTTGGCC	TTTTCACACT	TGTTTGTCTA	300
TCACCTTTAG	TATATTACTC	TTTGGCACAG	GTTGTCTAAT	CACATTAATT	TTTGCATCAA	360
AAATCCCTTG	GTTTAGTGAT	TCTTAATGAT	GTTTATTTTG	GAAAGTCATG	GACCTGAATT	420
CTTTGAGTAG	TTCATGAAAA	CCATATACCT	TTCCCAGAGA	AATGGGGTGC	ATATAATTTC	480
AGGAAGTTCA	AGGTAGGGAA	AACAAGCTAA	AAATCCCAAC	TTATTTCATC	TCGAG	535

- (2) INFORMATION FOR SEQ ID NO:132:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

G	AATTCGGCC	TTCATGGCCT	AAGGGGATCA	TCAAAGATGT	TGGACACCTT	GTGTTCAAAT	60
C'	TTGGTTCAG	GTGCGGCCTG	TGCAGATCGG	CTTTTTGGTT	TGGTTGTCTT	GGCCTGGATA	120
C	CAGTGGAGA	AGATGTCATC	CATATCATCA	TCAAATATAG	ACTTGGTTTC	CACTTTCTTT	180
T	TGGACTTTT	CTTTTGGTTT	TACAGTTAAG	TCAGCAAAGA	TATCAATGTT	ATCATCAAAT	240

AAATTAGATT CCAATGTTTT CTCCTTCTCT CTGGTTTTCT GAGAGGGTTT AATTGCTTCC 300
GTAGCAAATA TATCATCCTC AAAAATATCT TGTGTTGTTA ATATGACATC CTGCTGACTA 360
CTGGATTTTG TCTCATTCTT CTTGACTTTC TGATCCTCGA G 401

- (2) INFORMATION FOR SEQ ID NO:133:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GAATTCGGCC	TTCATGGCCT	AGTAGATGAA	CTAGAAGATG	GATAAACGAA	GATAGATAAA	60
ATGAAGAAAA	ACAAAAGTCA	AGGAGAACTC	AGGCGTCCAA	GAGTGTGTAA	ACAACTTCTG	120
GTGTGAGACG	CGCTACATTG	CGCTAAATGG	CCTGTGCGCT	TCTGGTTTTT	CCCTTCCTCT	180
GTTGATTTTT	TATAGTTGTC	TTTTATTTTA	AACACGCCTC	CCCCCCCCT	TTTTAAACTG	240
ATTTTACCAT	CACTCTCTCT	AGCCCTGCCT	CCCTAGAATT	AGCTGCTTCT	TACCTCCCTT	300
GGATCTGGAA	CTTAAATATT	AACGTGTATA	TAAGTTAATA	GTAAGTAGAC	CGTGAATTTA	360
GAAGAGTAAA	ACAGAATCAT	GAGTACGTAG	TCACTGTGGC	CCCTTTTTTG	CTGGATTTCA	420
AGTTCGTAAG	CATTTTTGGA	AGAGAGTCGA	AGGGGAAGGG	GTGGCTTGCC	AGTCAGTTGA	480
GTGATGCATG	GCTCGAG					497

- (2) INFORMATION FOR SEQ ID NO:134:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAATTCGGCC	TTCATGGCCT	AGGCTGGTCA	TTGAGAGTGT	TGGTGCAGTC	AAACTGGAAC	60
ACGATGTGAT	TGGTAAACAT	GTGCTTGATA	CATCGAACAA	AATATTCTGT	CTCTGCTTCT	120
${\tt GTAAGTTGAA}$	CAGGCTCAGA	AGACTTGAAC	${\tt AAGGGTCCTA}$	TATTCAGAAA	CTCAGGAATG	180
GCAGCCAATT	GTTCTTGGGG	ATATATTTCT	AATGAAGTGC	TAGACTATCC	AATTACTTAA	240
TTTCTTATAC	CTTTAGATAA	TCAGTATGAA	AAGTTCCCAT	TTATAATGGA	AATGAAAATT	300
CTTAACTAAA	CTATACATGT	AATATGTATT	TCTAGAAGAG	AATAAAAACC	CAAGTCCTCG	360
AG						362

- (2) INFORMATION FOR SEQ ID NO:135:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

in the second of the second of

CATCTTCTGT	CACTGCTGGA	GTTGCCAGTT	CACTCTCAGA	AAAAATAGCC	GACAGCATTG	120
GAAATAACCG	GCAAAATGÇA	CCATTGACTT	CCATTCAAAT	TCGTTTTATT	CAGAACATGA	180
TACAGGAAAC	GTTGGATGAC	TTTAGAGAAG	CATGCCATAG	GGACATTGTG	AATTTGCAAG	240
TGGAGATGAT	TAAACAGTTT	CATATGCAAC	TGAATGAAAT	${\tt GCATTCTTTG}$	CTGGAAAGAT	300
ACTCAGTGAA	TGAAGGTTTA	GTGGCTGAAA	TTGAAAGACT	ACGAGAAGAA	AACAAAAGAT	360
TATGGGCCCA	CCTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:136:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCC	TTCATGGCCT	AAGCAAACTT	CATGCAGCTG	GTGGAACTAG	ATGTGTCTCG	60
AAATGAGATT	CCTGAAATTC	CAGAAAGCAT	TTCATTCTGT	AAAGCACTGC	AGGTAGCTGA	120
CTTCAGCGGA	AACCCACTGA	CTAGGTTGCC	AGAAAGCTTT	CCTGAATTAC	AGAATTTAAC	180
ATGTCTTTCT	GTAAATGACA	TCTCACTACA	${\tt GTCTCTACCT}$	GAAAATATTG	GCAATCTTTA	240
TAACCTGGCT	TCACTGGAAC	TGAGAGAGAA	TCTTCTTACA	TATCTTCCTG	ACTCTCTTAC	300
CCAGCTGCGA	AGACTAGAAG	AACTTGACTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:137:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GAATTCGGCC AAT	GAAGCCT ACTTTAG	TAT TTTGGCAC	TT CCTAATTGAC	ACCTTGGGAG	60
ACTGCAGGAA GGG	GAACGAGA ATCATTI	INTA GGNTATTI	GT GTGTGTGTGT	GGTTTTTTTT	120
TTTTTTTGGA AGA	ACAGAGTC TCACAC	TTTT GCCCAGGC	TG GAGTGCAGTG	GCGTGATCTC	180
GGCTCACTGC AAC	CTCTGCC TCCAGG	TTC AAGCGATT	CT CTTGCCTCAG	CTTCCCGAGT	240
AGCTGGGATT ACA	AGGCACAC GCCACA	ACGC CTGGCTAA	TTTTATATTT TT	TAGTAGAGAC	300
AGTCTCGAG					309

- (2) INFORMATION FOR SEQ ID NO:138:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 599 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAATTCGGCC AAAGAGGCCT	AAACTCAGAA	TGGTGCTACT	TGAAGACTCT	GGATCTGCTG	60
ACTTCAGAAG ACATTTTGTC	AACCTGAGTC	CCTTCACCAT	TACTGTGGTC	TTACTTCTCA	120

GTGCCTGTTT	TGTCACCAGT	TCTCTTGGAG	GAACAGACAA	GGAGCTGAGG	CTAGTGGATG	180
GTGAAAACAA	GTGTAGCGGG	AGAGTGGAAG	TGAAAGTCCA	GGAGGAGTGG	GGAACGGTGT	240
GTAATAATGG	CTGGAGCATG	GAAGCGGTCT	CTGTGATTTG	TAACCAGCTG	GGATGTCCAA	300
CTGCTATCAA	AGCCCCTGGA	TGGGCTAATT	CCAGTGCAGG	TTCTGGACGC	ATTTGGATGG	360
ATCATGTTTC	TTGTCGTGGG	AATGAGTCAG	CTCTTTGGGA	TTGCAAACAT	GATGGATGGG	420
GAAAGCATTA	TTGCAATCAC	AATGAAGATG	CTGGCGTGAC	ATGTTCTGAT	GGATCAGATC	480
TGGAGCTAAG	ACTTAGAGGT	GGAGGCAGCC	GCTGTGCTGG	GACAGTTGAG	GTGGAGATTC	540
AGAGACTGTT	AGGGAAGGTG	TGTGACAGAG	GCTGGGGACT	GAAAGAAGCT	GAACTCGAG	599

- (2) INFORMATION FOR SEQ ID NO:139:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GAATTCGGCC	TTCATGGCCT	AACCTTCCTG	AATATCTGCC	GTTTGTCCTG	CAAGAAATAA	60
CTAGTCAACC	CAAAAGGCAG	TATCTTTTAC	TTCATTCCTT	GAAGGAAATT	ATTAGCTCTG	120
CATCAGTGGT	GGGCCTTAAA	CCATATGTTG	AAAACATCTG	GGCCTTATTA	CTAAAGCACT	180
GTGAGTGTGC	AGAGGAAGGA	ACCAGAAATG	TTGTTGCTGA	ATGTCTAGGA	AAACTCACTC	240
TAATTGATCC	AGAAACTCTC	CTTCCACGGC	TTAAGGGGTA	CTTGATATCA	GGCTCATCAT	300
ATGCCCGAAG	CTCAGTGGTT	ACGGCTGTGA	AATTTACAAT	TTCTGACCAT	CCACAACCTA	360
TTGATCCACT	GTTAAAGAAC	TGCATAGGTG	ATTTCCTAAA	AACTTTGGAA	GACCCAGATT	420
TGAATGTGAG	AAGAGTAGCC	TTGGTCACAT	TTAATTCAGC	AGCACATAAC	AAGCCATCAT	480
TAATAAGGGA	TCTATTGGAT	ACTGTTCTTC	CACATCTTTA	CAATGAAACA	AAAGTCTCGA	540
G						541

- (2) INFORMATION FOR SEQ ID NO:140:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTTCATGGCC	TAGTGGTTCT	TCTGAAATCG	GCCTTCAGAC	ACCTGTCTTT	GGTAGTACCA	60
ATATCTAAGA	AGTGGTTTCA	GTTCAATTTT	GTTTTCCTCC	ATGCCAGAGA	GAAGCCACAG	120
TTTCCTAAGC	TGGGGAGGAG	GTATATCCTT	CAAGAGATCG	GCTTGTTAGA	ATAGACCACT	180
TAACACCATA	TGAAAAAGCA	ACAGACTGAA	ACATGGATGT	CCTCAAGAAG	GGCTGCTGAC	240
ACCTATGATT	TGGCAAGGAG	ATAAATAACA	GAATGTGCAA	AGGGTCATAA	GAGTGCAGAC	300
ACCCTAATGT	CTGTTGGCTG	GAAGGTCAGA	GCAGTTCACC	AGTGAAAATG	GGTACGCCAT	360
GAAGGCCGGC	CTTCATGGCC	TATAGGCCAT	GAAGGCCGAA	TTC		403

- (2) INFORMATION FOR SEQ ID NO:141:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 439 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAATTCGGCC	TTCATGGCCT	AGTCCTCATC	TGCTGGCATT	TTGTGGGGTG	TTAGTGCCAA	60
ACTTGAATAG	GGGCTGGGGT	GCTGTCTTCC	ACTGACACCC	AAATCCAGAA	TCCCTGGTCT	120
TGAGTCCCCA	GAACTTTGCC	TCTTGACTGT	CCCTTCTCTT	CCTACCTCCA	TCCATGGAAA	180
ATTAGTTATT	TTCTGATCCT	TTCCCCTGCC	TGGTCTAGCT	CCTCTCCAAA	CAGCCATGCC	240
CTCCAAATGC	TAGAGACCTG	GGCCCTGAAC	CCTGTAGACA	GATGCCCTCA	GAATTGGGGC	300
ATGGGAGGGG	GGCTGGGGGA	CCCCATGATT	CAGCCACGGA	CTCCAATGCC	CAGCTCCTCT	360
CCCCAAAACA	ATCCCGACAA	TCCCTTATCC	CTACCCCAAC	CCTTTGCGGC	TCTGTACACA	420
TTTTTAAACC	TGGCTCGAG					439

- (2) INFORMATION FOR SEQ ID NO:142:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCGATTGAAT	TCTAGACCTG	TGTGTCTAGC	TGTGATGGAA	TCTGAAATGA	AGTTTGACAA	60
GGACCATGAT	GGACTCATTG	AAAATGGAGG	CTATGCAGAC	CAGACCTATG	ATGGATGGGT	120
GACCACAGGC	CCCAGTGCTT	ACTGTGGAGG	GCTGTGGCTG	${\tt GCAGCTGTGG}$	CTGTGATGGT	180
CCAGATGGCT	GCTCTGTGTG	GGGCACAGGA	CATCCAGGAT	AAGTTTTCTT	CTATCCTCAG	240
CCGGGGCCAA	GAAGCCTATG	AGAGACTGCT	GTGGAATGGC	CGCTTACTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:143:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GAATTCGGCC	TTCATGGCCT	AGGGAGGCTG	AGGTGGGAGG	CTCACTGGAG	GCCAGGAGTT	60
CGGAACCAGC	CTGAGCAACA	TAGGGAGACC	TCAGCTCTAC	AACTGAAAAA	AAGATAGCCA	120
GGTGTGTTCA	TGGTGGCACC	TGTCTGTATT	CCAGCCGCTT	GGGAGGCTGA	GGCAGGAGGT	180
TTGCTTGAGT	CCAGGAGTTT	GAGGTTGCGG	TGAGCTACAC	AATGAGCTAT	GGTGGCACTA	240
CTACACTCCA	GCCTGGGCCA	TAGAGTAAGG	CCCTGTCTCT	AACTGGAAGT	CCAAAGAGGG	300
ATCTACTTCC	TAGACTATTA	ATTTAATAGA	TCAATAAATT	AATCAAGAAT	ATGATTTTTT	360
TCTCATCTTT	CTCTGTAGTC	ATATTTTATA	CAGACTTTTT	GTTTAAGTAA	TCTCTCTTTA	420
TGGGCAGACA	ATGATTTCAG	AAACACCCTG	CCTCGAG			457

- (2) INFORMATION FOR SEQ ID NO:144:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

talian Talian talian Talian

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

60
L20
80
40
00
60
88
2

- (2) INFORMATION FOR SEQ ID NO:145:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAATTCGGCC	TTCATGGCCT	AGGCAGTGGA	GGCCTCTGTA	ATTCTAGCAT	ACAGGTGGCA	60
AGTTATTACA	TTATTTCTTT	CCTCCTGTCT	ACCTGCAGTT	GGTTTTATGT	GGGGCGTTAG	120
TACACTTCCC	AAAGGGCTTG	CCCGCAGGTG	AGAGGTGCAC	ATTGAACTCC	CTCACCAGGC	180
AGATGGGAAG	TGTGGCCATG	AGAGAGAGCT	TCAGGGGCCC	TGGGTTTATG	ACATCGCTGG	240
GCCAGGAATG	AGGTTAATAT	TTTTAATGGC	GAAGGGTGAG	CCCCGTTATT	ACCCGAGCTC	300
GAG						303

- (2) INFORMATION FOR SEQ ID NO:146:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAATTCGGCC	TTCATGGCCT	ACTGGATGGC	ATCTACTTCG	TATGACTATT	GCAGAGTGCC	60
CATGGAAGAC	GGGGATAAGC	GCTGTAAGCT	TCTGCTGGGG	ATAGGAATTC	TGGTGCTCCT	120
GATCATCGTG	ATTCTGGGGG	TGCCCTTGAT	TATCTTCACC	ATCAAGGCCA	ACAGCGAGGC	180
CTGCCGGGAC	GGCCTTCGGG	CAGTGATGGA	GTGTCGCAAT	${\tt GTCACCCATC}$	TCCTGCAACA	240
AGAGCTGACC	GAGGCCCAGA	AGGGCTTTCA	GGATGTGGAG	GCCCAGGCCG	CCACCTGCAA	300
CCACACTGTG	ATGGCCCTAA	TGGCTTCCCT	GGATGCAGAG	AAGGCCCAAG	GACAAAAGAA	360
AGTGGAACAA	CTCGAG					376

- (2) INFORMATION FOR SEQ ID NO:147:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GAATTCGGCC	TTCATGGCCT	AATGGAAAGG	ACAAGGAAAA	GGGAGAAGGG	GTGAGAGTCT	60
GTCCTAGGGG	CCAACGAGAA	CAGTGAGCTG	TTTCAGGGGA	GCCATTTCCT	TGTCCATGCT	120
CACAAGCCTG	TGGATTCTTC	CCCCTCTGCA	GGAAATTACC	TGATGTTCCA	AACCCCCTCC	180
AGATCCTGTA	TATCCGCAGC	ATCTCCCCTT	TCCCTGAGCT	GGAACAGTTT	CTACAGGACA	240
CTATCAAGAG	GTACTAGGGG	CCTGGAGGTT	TGGGCTCCAA	GAGAAGCTTG	ACAGAGCCCA	300
CGCCCGACCC	CTACTTCTGT	TTCTTCCTAA	GGTATAATCT	GCAGATGTTG	GAAGCTGAGG	360
GCAGCATGAA	GCAGGCCCTG	GGTGAACTGC	AGGCACAGCA	GCCCCCCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:148:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GCCTGGCCAT	CCGGAGAGCT	AAGAACCTCA	GGCGGCTGCT	GTACGTNTCA	TGCAACCCCC	60
GGGCAGCCAT	GGGCAACTTT	GTGGACCTCT	GCAGAGCCCC	ATCTAACCGG	GTGAAGGGCA	120
TTCCCTTCCG	${\tt GCCGGTCAAG}$	GCTGTGGCAG	TGGACCTGTT	CCCGCAGACC	CCTTCTTTTT	180
TCATACTTAT	ATGAAAGACT	ACATACTTAA	AATACTGGTG	ATTATATTTA	GGACCTGAAA	240
TCATAAGATT	GTGGTCTTGC	TTTTTACTTA	TTTTTGTATC	TTAGCGATGT	CTAGAGTTAA	300
TAAGTGTTGC	${\tt TTTTCTAATC}$	ACAGCAAATC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:149:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GGATTCGGCC	TTCATGGCCT	AGTGGGGCAC	TAGGATCATC	ATTTGGGTGA	GAGCCCTCGG	60
CAATGGTGGA	GAGGGAGAAG	TTATCATTGT	GGAGCTCAGA	TGGGGTCCGG	AATTTGTTGG	120
TCCTACGCAG	CTTGGTATTC	TCCGTCTTGA	${\tt GCAGGTAGAG}$	CTTCTTGGCA	AAGAACACCG	180
TCATCATGAA	GAGCAGGAGC	AGGACGAGGG	CAGCCGAGCC	CACGGCCACG	CACATCACCT	240
GGAAGTCGGT	GATGATGGAC	TCGCAGCGCA	TCCCCTTGTG	CCAGATGTAG	TCCTGCGTGT	300
TGCACCTGCA	GAAGGCCCCT	ATGTTCTCCA	CCAGGTAGCA	CTGGCCGCCA	TTGTGACAGT	360
AACTTGGGAA	GAGGTCGCAC	ACTGACCGGC	AGGAGCCGTT	ATGCCGCACA	AAGCCACTGC	420
GGCACTCAGT	GCCATTTTCA	CTGGAGGCCA	AGTCCCTGCC	TGGCTCTCCT	TAGGCCATGA	480
AG						482

- (2) INFORMATION FOR SEQ ID NO:150:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

ing the state of t

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTTCCTTACT AACTTTAATG GCCACAACAT	TTAGGCGAAA	GGGGGGCAAT	CATTGGTGGT	60
TTGGCATTCG CAGAGACTTC TGTCAGTTTC	TGCTTGAAAT	TTTCCCATTT	TTAAGAGAAT	120
ATGGGAACAT TTCATATGAT CTCCATCACG	AAGATAGTGA	AGATGCTGAA	GAAACATCAG	180
TTCCAGAAGC TCCGAAAATT GCTCCAATAT	TTGGAAAGAA	GGCCAGAGTA	GTTATAACCC	240
AGAGCCCTGG GAAATACGTT CCCCCCCTCT	CCTCGAG			277

- (2) INFORMATION FOR SEQ ID NO:151:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GCTCGCCCAC	TTTATGAAGA	GCGATTTCAC	GGCTGCTTGA	ACCATTCGAA	TTTGGATTTG	60
TGTTCAGCAC	TTTAAAAGGT	TCAACTTTTT	GCTTCTACCC	AGATTGGTCT	CAGGTCTGTC	120
TTCTCCAGAT	GACCGGTGGT	TTCCTGAGCT	GCATCTTGGG	CTTGGTGCTG	CCCCTGGCCT	180
ATGGCTTCCA	-GCCTGACCTG	GTGCTGGTGG	CGCTGGGGCC	TGGCCATGGC	CTGCAGGGCC	240
CCCACGCTGC	ACTCCTGGCT	ACAATACTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:152:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAATTCGGCC TTCATGGCCT AGGGGCC	GGTG AAACGTCCTG	AAGAGCGTCC AGCT	CGTGGC 60
CGAGAGGACT CGGGCGCTCC CCACGC	TGGA GGCCGTGGAC	CGCTCCCTTT AAAA	GTTGAA 120
ACGGCCGCCG TTCGGGACGG CCTGGCC	GGGA GGAGGGCCCG	ACGAGGGGAG GCTT	CAGGGA 180
CAACTGGGGC TTCTCGACGT CCACCC	TTTT CAGGGCGCGG	CCCCGGTAGC CCTC	GGGCCG 240
GCCCAGGTAC AGGAGGTGCT TCCCGG	GACC CCCGGAGTAC	CTGGAGGGAC CTCC	CGAGGG 300
GACTCGAG			308

- (2) INFORMATION FOR SEQ ID NO:153:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAATTCGGCC	TTCATGGCCT	ACAATCCCAA	ATGTAGGATC	ATGCCCATTG	CCCTAAGCCC	60
AGGCATGAGA	GTCGACATCT	CTCCTCTTAT	ATACAGATCC	AGTCCACAGG	TGAAGTGGGA	120
ACTCTCCAAC	CAGGATTCAG	CACACCATTG	ATGTTGCGAC	TCCTCTACTG	GAACACAGCT	180
TGGAGAAGGG	ATTGGGGCTC	TCATGGCAGG	ATGCAATCCA	CTGTTGAGAT	TGTGACTCAT	240
GCACTTGAAC	CTAAGTCTCA	GGAGTTGTTG	ACTCTTACAC	CCAGCACCCA	GGTGATAGGA	300
CTCTCATGTC	TGGTTCCTGC	CCACAGGTGA	AATTGTGACA	TATACATGGT	CACAGCTCAC	360
AGGTGAGGTG	ATAACTCACA	TACCTGGATC	CAGCTAAGAG	AACAGATTTT	GACTCTGATA	420
TCTTAGGCCA	TGAAGGCC					438

- (2) INFORMATION FOR SEQ ID NO:154:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

G	AATTCGGCT	TCATGGCCTA	CAAGATGACT	AAAGTCTTCA	CTCACCAAGG	AAAAGTGGCT	60
C	TGTATGGCA	AGCTGGTGCA	GTCAGCTCAG	AATGAGAGGG	AGAAACTTCA	AATAAAGATA	120
G	ATGAGATGG	ATAAAATACT	TAAGAAGATC	GATAACTGCC	TCACTGAGAT	GGAAACAGAA	180
7	CTAAGAATT	TGGAGGATGA	AGAGAAAAAC	AATCCTGTGG	AAGAATGGGA	TTCTGAAATG	240
A	GAGCTGCAG	AAAAAGAATT	GGAACAGCTG	AAAACTGAAG	AGGAGGATGC	TCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:155:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAATTCGGCC	TTCATGGCCT	AAATTTAGGA	AGGTCAAACG	TGAATCTCCA	TTTGACAAAC	60
GTCCAACTGC	AGCAGAGATT	AAAGTGGAAC	CCACCACTGA	GTCATTGGAC	AAAGAGGGCA	120
AAGGTGAAAT	TAGAAGCCTA	GTGGAGCCAC	TCAGTATGAT	CCAATTTGAT	GATACTGCTG	180
AGCCACAGAA	AGGAAAAATA	AAAGGAAAGA	AACACCATAT	CTCTTCAGGA	ACTATCACAA	240
GCAAAGAAGA	AAAAACTGAA	GAGAAGGAAG	AGTTGACCAN	ACAAGTCAAG	TCTCATCAAC	300
TTGTTAAATC	ACTCTCAAGA	GTGGCTAAAG	AGACTTCAGA	ATCTACCAGA	GTTCTAGAAA	360
GTCCAGATGG	CAAAAGTGAA	CAGCGTAACC	TCGAG			395

- (2) INFORMATION FOR SEQ ID NO:156:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAATTCGGCC	TTCATGGCCT	ACAGAGTACT	GAGTGGAACA	TACGATGATA	GATTTACAAA	60
TAATGTAGCA	TACTTCTACT	TCATTGTATC	TTAAGTTTCT	TGAAATATTG	CTACTGGAGA	120
TTGGAAAGAA	ATCTTAATGT	TATGGGGTAT	TGTCTAAGAA	GCTTTATTTT	AAAACCATCT	180
CATTAAATTT	TGTTGCATTT	TAGATAATCG	TCCCCAGATG	CCATGTTACC	CTAGTGCAGA	240
GTTTGGGGCT	GGATAAGTTT	TTGTTGTAGG	TGGCTATCCT	GTGTTTTGTA	GGGTATTTAG	300
CAGCATCCTG	GCCTTAAAAC	AAAAATGTTT	TCAGACATTG	CCAAATGTCC	CCCGAGCGGT	360
AAAGTCACCC	CCAAGTTGAG	AACCGCTCTA	TACAAAGAGC	TGTTATTAGA	GCCAGACTCG	420
AG						422

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAATTCGGCC	TTCATGGCCT	AGATTGCTTG	AGGCCAGAAG	TTCAAGACAG	GCTGCCCAAC	60
ATAGTGAGAC	CCCCTTCTCT	ACCAAAATTT	TAAAAATGAG	CATGCATCTG	TAGTCCTAGC	120
TATTGGGAAG	GCTGAGGCAG	GAGGATCATC	TGAGCCCAGG	AGTTTGAGGC	TGCAGTGAGC	180
TAAGAAGGTG	CCACTGCACT	GCTGTTGTCT	CTCAGCAGAT	CATTTTCAGC	TTTCTTTGGA	240
GAGTAGCCAT	TAGCAATGCA	AATGTGAAGT	TTGATAGCAC	AATAAATAA	ACACTGAAAA	300
CTGTAGATGT	TACTTATAAA	ACACTGGCAC	TCAGATAAAT	TGGGTTTGGT	CAAGAAGACA	360
GTGAAGCATA	TCCCTGTTGG	GCCAGAGGCT	GTTATCGTTT	TGCTCTGAAT	TCAAAACCTG	420
ATATGTCTCC	AAATTTGCTT	AGGGTTGTTA	TCCTGGAAAA	TAGAATCTGA	TAGAAGGTGG	480
GCACATCTCG	AG					492

- (2) INFORMATION FOR SEQ ID NO:158:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GAATTCGGCC	TTCATGGCCT	ACTGCTTTCG	TGAAGACAAG	ATGAAGTTCA	CAATTGTCTT	60
TGCTGGACTT	CTTGGAGTCT	TTCTAGCTCC	TGCCCTAGCT	AACTATAATA	TCAACGTCAA	120
TGATGACAAC	AACAATGCTG	GAAGTGGGCA	GCAGTCAGTG	AGTGTCAACA	ATGAACACAA	180
TGTGGCCAAT	GTTGACAATA	ACAACGGATG	GGACTCCTGG	AATTCCATCT	GGGATTATGG	240
AAATGGCTTT	GCTGCAACCA	GACTCTTTCA	AAAGAAGACA	TGCATTGTGC	ACAAAATGAA	300
CAAGGAAGTC	ATGCCCTCCA	TTCAATCCCT	TGATGCACTG	GTCAAGGAAA	AGAAGCTTCA	360
GGGTAAGGGA	CCAGGAGGAC	CACCTCCCAA	GGGCCTGATG	TACTCAGTCA	ACCCAAACAA	420
AGTCGATGAC	CTGAGCAAGT	TCGGAAAAAA	CATTGCAAAC	ATGTGTCGTG	GGATTCCAAC	480
ATACATGGCT	CAGGAGATGC	TCGAG				505

- (2) INFORMATION FOR SEQ ID NO:159:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GAATTCGGCC	AAAGAGGCCT	AGCCGGAGCA	GCTGTCTGGG	AGTCAAGGCT	GCAGTAGCGT	60
TTCTTCATGG	GGTGCTCCAG	GGGGTGCCAC	AGACCGACAG	GCAGCCCAAG	GGCCTGGACA	120
CCCCTCCCCA	GGCAGGTGCT	GCCCCAGGAG	GACTGTCCTC	GGGAATGAAC	CTCCCGCGGG	180
		GGCCTCGGTC				240
CAATGGTGCT	TTTGGCTTTA	GTGTACGATG	TTTGCTGTGC	TTCCCGCCGT	GGAGGGCAGA	300
GCCACCCCAC	ATCAGGATCG	GACGTGCTAC	CCCTCCCGGT	CCCGGCCCTG	GCCCAGCCAG	360
CCCAGCCCTC	GAG					373

- (2) INFORMATION FOR SEQ ID NO:160:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GAATTCGGCA	AAGAGGCCTA	ATGAATTCTC	TGATCACAAA	ACAGACCCAG	GAAAGCATTC	60
AGCATTTTGA	GCGACAGGCA	GGGCTGAGAG	ATGCTGGCTA	CACACCCCAC	AAGGGCCTCA	120
CCACCGAGGA	GACCAAGTAC	CTTCGAGTGG	CCGAAGCACT	CCACAAACTA	AAGTTACAGA	180
GTGGAGAGGT	AACAAAAGAA	GAGAGGCAGC	CTGCATCAGC	CCAGTCCACC	CCAAGCACCA	240
CTCCGCACTC	TTCACCTAAG	CAGAGGCCCA	GGGGCTGGTT	CACTTCTGGT	TCTTCCACAG	300
CCTTACCTGG	CCCAAATCCT	AGCACCATGG	ACTCTGGAAG	TGGGGATAAG	GACGGGCTCG	360
AG						362

- (2) INFORMATION FOR SEQ ID NO:161:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

${\tt GAATTCGGCC}$	AAAGAGGCCT	AGTTTTACAA	AACGCGATTT	GTAATATAAA	CTAGTTAGAT	60
AACTCAGAGG	${\tt GTTTTATTGG}$	CCATATTTTT	GTTTATGCTT	TGTCACAGGC	TTTAGTCATT	120
GCTTCCATGT	GTTTTCATCC	TTCAGGATAT	CTTCAAGAAG	CCTACTTATG	GACCAAACAA	180
GTTCTGACCA	TCATGGAGAA	ATCTCTGGTC	TTGCTCAGGG	AGGTGACGGA	TGGCTCCCTC	240
TATGAAGGAG	TTGCGTATGG	CAGCTACACC	ACTAGATCAC	TCTTCCAATA	CATGTTTCTC	300
GTCCAGAGGC	ACTTCAACAT	CAACCACTTT	GGCCATCCGT	GGCTTAAACA	ACACTTTGCA	360
TTTATGTATA	GAACCATCCT	GCCAGGTATA	GTGAGGAGTC	AGAAGTGTGA	AAACTCGAG	419

- (2) INFORMATION FOR SEQ ID NO:162:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:	
GAATTCGGCC AAAGAGGCCT ACAGGTAGTA TCTTTATAGC GGTATAAAAA CAGACTAATA CAAACAGGTA GCTCTAAATT GTGAGTTTTT CTTAACTCCT TTGATCTTCT GTGATAGCGA TTTTTCACAT TTCACACTTC CCTAATGCCA AAAATCCACC TCCAGCAGCT GTTTTGCCTC TTTCTTATCC TGCCCCTTGG AAGAATGTCA TCATTATTGC TGCCACAGCA CTGTGTTCTT TTTCAGAAGT TACAGCTCGA G	120 180
(2) INFORMATION FOR SEQ ID NO:163:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:	
GAATTCGGCC AAAGAGGCCT AGTGGTCTGG GGCAAAATTT AGTAAGACCT GGAAAGCATA GGTAATCAAA GCAGAAACTG ACAAATGAGA TGGTATCAAG CTAAAAAG	60 108
(2) INFORMATION FOR SEQ ID NO:164:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:	
GAATTCGGCC AAAGAGGCCT AGTTTAACCT CATCAGACAT TATTGCAGCC AGCTGTCAGC CAAGCTCAGT AACCTTCCAA CGCTCATTTC CATGAGGCTA GAGTTCCIGA GAATCCTCTG TAGCCATGAG CATTACCTCA ATCTGAACCT TTTTTTTATG AATGCTGATA CTGCTCCAAC ATCTCCTTGT CCTTCCATAT CTTCCCAGAA CTCAAGCTCC TGCTCCAGCT TCCAGGACCA GAAGATCGCC AGCATGTTCG ATCTGACTTC CGAGTACCGC CAGCCCCTCG AG	120 180
(2) INFORMATION FOR SEQ ID NO:165:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 135 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	•

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GAATTCGGCC AAAGAGGCCT AGCAAAAACT GTTCAAAAGA GTTGTTGATT ACTTTCATTT CCACTTTCTC ACCCCCATTC TCCCCTCAAT TAACTCTCCT TCATCCCCAT GATGCCATTA TGTGGATTCC TCGAG	60 120 135
(2) INFORMATION FOR SEQ ID NO:166:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 449 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:	
GAATTCGGCC AAAGAGGCCT AGAAAAAGTA GCACAGTGGA GTCTGAAATA GCAAGCGAAG AGAAAAAGCAG AGCTGCTGAA AGGAAAAAGGA TTATTATTAA GATGGAGCCA GAAGATATTC CTACAGATGA ACTGAAAGAC TTTAACATTA TTAAAGTTAC TGATAAAGAC TGTAATGAAT CCACTGACAA TGATGAATTA GAAGATGAAC CTGAAAGAGC ATTTTATAGA TACTATGTTG AAGAAGATGT CAGCATAAAA AAAAGTGGTA GGAAAACTCT AAAACCTCGA ATGTCAGTAA AGAGGGATGC TGAAAATGCA TCTTGTGAGC TGTGTGGACT TACAATAACC GAGGAGGACC TGTCATCTCA TTACTTAGCC AAACTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:167:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 565 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:	
GAATTCGGCC AAAGAGGCCT AAAAGGAAAC TTGGACAAGT AGAAAGTGGA TGACCCAGGC TCCGTTACAT ATACTTGGAT TCCAGCTGGG ACCTAGATTT GCTGAGGACG GAAGCCAAGG AGACAGGAAC ATGTGGCTGC TCCCAGCTCT ACTCTCTC TGCCTCTCAG GCTGTTTGTC TCTGAACGGC CCCGGCTCTG TGACTGGCAC TGCGGGGGAC TCTCTGACAG TGTGGTGTCA GTATGAGAGC ATGTACAAGG GATATAACAA GTACTGGTGC CGAGGACAGT ACGACACGTC ATGTGAGAGC ATTGTGGAGA CCAAGGGAGA AGAGAAGGTG GAGAGGAATG GCCGCGTGTC CATCAGAGAC CACCCGGAGG CTCTCGCCTT CACTGTGACC ATGCAGAACC TCAATGAAGA TGATGCTGGA TCTTACTGGT GCAAAATTCA GACAGTGTG GTCCTGGATT CATGGTCACG CGATCCCTCG GACCTGGTTA GGGTGTATGT TTCCCCAGCA ATTACAACCC CAAGGAGGAC CACACATCCA GCCACCCCGC TCGAG	60 120 180 240 300 360 420 480 540
(2) INFORMATION FOR SEQ ID NO:168:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 base pairs

 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATTCGGCC AAAGAGGCCT AGTTTCCTTT ATATGTTTGC ACTTAATTTG ATTCCATCCT TCATGCTGTT TTCATTATTC TTAGTTCATC TACACCACAT AAATTATCAC CTTTGTTTTC AGTTCCCCAA TTTCCATGTG CCACAAACAA ATCTCGAG	60 120 158
(2) INFORMATION FOR SEQ ID NO:169:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 383 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:	
GAATTCGGCC AAAGAGGCCT AGTCTCACCA TCTATTCTAA ACCTTATATT ATCAATCCTA TTCCCTCTCA CCAAAAGAAT CCCTTTATAC AAGTAATTAT CCTGTCTATG CTAGTTTCCC CACTGCAACT CTTCCCTTAA TATATGTACC TGCTCTGTA TCCCTCTCA GCTACTTCCC TATTTTCTGT TCCCCTTTAC AGGAAAACTT TTCTCCAGCA TTTCCCAATG CCATTGTCTT ACTTCCTCA ATTCTATTTT CTTCTCAAAC CATTTTTATT AGGCTTCTTT CCCCAATGGC TATTGTCAAG CTTCACTTAA TGCCGTGCAA ATCACCCTAT TCTCCAGGTC TTCTTTCTTC CCAGTCTCTC GAG	60 120 180 240 300 360 383
(2) INFORMATION FOR SEQ ID NO:170:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 282 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:	
GAATTCGGCC AAAGAGGCCT AAATATTGTC TGAAAAAAAA ATATGAGACC CATTACTCAG TCTCTCCTCC TGCCATTTAT ACTGCAGGTA TTCCCCAAGT TTCTCTTCTC	60 120 180 240 282
(2) INFORMATION FOR SEQ ID NO:171:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 350 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:	
GAATTCGGCC AAAGAGGCCT AGTGGAAGAG AAGAATGTTT CTGTCTCTC CTACGTTGAC TGTTCTTATT CCACTGGTTT CTTTAGCAGG ACTGTTCTAC TCAGCCTCT TGGAAGAAAA CTTCCCACAG GGCTGCACTA GCACAGCCAG CCTTTGCTTT TACAGCCTGC TCTTGCCTAT TACCATACCA GTGTATGTAT TCTTCCACCT TTGGACTTGG ATGGGTATTA AACTCTTCAG	60 120 180 240
147	

GATCTCTGAA AGCTCAAATG GATGGAATTT AGTTTGCGGG AACTCTCGAG

GCATAATTGA TGCAACTAGA GTCAATATGC TGTATATATT AATGATAGCT CTTGGGCATC

300

(2) INFORMATION FOR SEQ ID NO:172:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 140 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:
GAATTCGGCC AAAGAGGCCT AGGGGTGTAC ATTTTATTGG AAACCTTAAA TACTGTTCAG AAAGAATATA TCTTCAATCA AGGCTCTTGT GCAGCCTACA CAGAAAAATG AAGCTTTTTG 121 GGTTAGGTGC AACGCTCGAG
(2) INFORMATION FOR SEQ ID NO:173:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:
GTGGTCTCTC CTCCCCTGCC ACTCCCCTCT TCTTTTTTTT CCAACATGGC CTTGCTCCGC GTACATCGCC ACCCAGGAC CGCTGCCCGC CACCGTGGCT GACTTTTGGC AGATGGTGTG 126 GGAGAGCGGC TGCGTGGTGA TCGTCATGCT GACACCCCTC GCGGAGAACG GCGTCCGGCA 186 GTGCTACCAC TACTGGCCGG ATGAAGGCTC CAATCTCTAC CACATCTATG AGGTGAACCT 246 GGTCTCCGAG CACATCTGGT GTGAGGACTT CCTGGTGAGG AGCTTCTATC TGAAGAACCT 306 CGAG 304
(2) INFORMATION FOR SEQ ID NO:174:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 188 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:
GCGATTGAAT TCTAGACCTG CCTCTCTTAT ACCTCGGTGT GGCCGAAAGG AAATAAGCAG 6 AGGCGCTATT GGCAGGACCT AGAAACTTTC CTTGTAACAT AGCTAGTATG TTCCCTCTGC 12 CCCTTCTTCA TCTTTCCTC ACACTTGCTG GAGCTGGAGC AGCTATCCTG ACCGCAGGTG 18 CACTCGAG
(2) INFORMATION FOR SEQ ID NO:175:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 274 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GAATTCGGCC	TTCATGGCCT	ACTATCTGCC	TTGCGCTCCC	ACTGCCCTGA	CCTGTGCCCT	60
CTCACAGGCC	CCCGTGATGG	CTCGCTGGCC	TCCCTTCGGC	CTCTGCCTCC	TCCTGCTGCT	120
GCTGTCCCCA	CCGCCACTGC	CCTTGACAGG	GGCCCATCGC	TTCTCCGCAC	CTAATACCAC	180
TCTCAACCAC	TTGGCACTGG	CACCTGGCCG	AGGCACACTC	TATGTCGGCG	CAGTGAACCG	240
CCTCTTCCAG	CTCAGCCCCG	AGCTGCAGCT	CGAG			274

- (2) INFORMATION FOR SEQ ID NO:176:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GGTCAGCCGA	GCATGATAGG	AGACATCATC	AACCTCGGCC	TGAAAGGGAG	GGAGGGGAGA	60
${\tt GCAAAGGTCG}$	TCAACGTGGA	GATCGTGGAG	GAGCCCGTGA	GTTATGTCAG	CGGGGAGAAG	120
CCGGAGGAGT	TTTCCGTCCC	ATTCAAAGTG	GAGGAGGTCG	AAGATGTGTC	GCCAGGCCCC	180
TGGGGGTTGG	TTAAGGAGGA	GGAAGGTTAT	GGAGAAAGCG	ATGTCACATT	CTCAGTTAAT	240
CAGCATCGAA	GGACCAAGCA	GCCTCAGGAG	AACACGACTC	ACGTGGAAGA	AGTGACAGAG	300
GCAGGTGATT	CAGTGGGCGA	GCTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:177:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAATTCGGCC	AAAGAGGCCT	AAGCAATGTC	TCCACCACTG	CTGCTGCTAC	CCTTGCTGCT	60
GCTGCTGCCT	CTGCTGAATG	TGGAGCCTGC	TGGGGCCACA	CTGATCCGGA	TCCCTCTTCG	120
TCAAGTCCAC	CCTGGACGCA	GGACCCTGAA	CTACTGAGGG	GATGGGGAAA	ACCAGCAGAG	180
CTCCCCAAGT	TGGGGGCCCC	ATCCCCTGGG	GACAAGCCTG	CCTCGGTACC	TCTCTCCAAA	240
TTCCTGGATG	CCCAGTATTT	TGGGGAAATT	GGGCTGGGAA	CGCCTCCACA	AAACTTCACT	300
GTTGCCTTTG	ACACTGGCTC	CTCCAATCTC	TGGGTCCCGT	CCAGGAGATG	CCACTTCTTC	360
AGTGTGCCCT	GCTGGTTCCA	CCACCGCTTC	AATCCCAATG	TCCTCGAG		408

- (2) INFORMATION FOR SEQ ID NO:178:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GAATTCGGCC	AAAGAGGCCT	AGGAGGAATT	TCCATCTTGC	TCTCAAAGTG	AGTCTGAATG	60
TGCTCGGTGG	TGTCACCCCC	GCCGAGCTGC	CAGTGCAGAA	GGCCACTATT	GAACTCCTGC	120
ACACGCCCCA	ACTTGTCAGA	TCGGTCAACA	ACAAACAGGT	TGTTCTTTTT	GACTATCTTT	180
ATTGGCAGCT	TGTCGAACTT	ACTGGCTTGC	TTGGGCTTCT	CCTTTGGGTC	TGCAGCGGCG	240
TCCGGGGCAG	TCAGAGCGAT	GCTGCTCTTT	TCATCGCTTT	CTGTCTTCTC	GCTGTCTACC	300
TCGAG						305

- (2) INFORMATION FOR SEQ ID NO:179:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAATTCGGCC	AAAGAGGCCT	AGTGCAGCAA	TTTAGAGAGT	GTCTCAGGAG	TGTGGCTCAC	60
TGGCAGCTGC	AGCTATGTTA	GTGCTTCTTT	CTGCCTCAAG	TTCAGAAACA	AGCTGGACTA	120
TCTCAGGGTG	ATTGAATTTT	CCTGCTGTGG	AATCATAGAA	GTCTTGCAGT	CTCCCAGGTT	180
TGTGTTCAAG	GTCTTCATAT	TCAGATGCTT	GAAGAATCAT	TTCACATTGG	TCTAGCATTC	240
AATCGAG						247

- (2) INFORMATION FOR SEQ ID NO:180:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GAATTCGGCC	AAAGAGGCCT	AGTCAAGTTC	ATTTCCCAGA	GTCTTAAGAC	TAAGTTCTGC	60
CTCCTCATTG	CAGGTGTGCC	GAGAGTTTTT	TTTGAACAAC	AAAAATTACT	AAGGAACCTC	120
ACTACCTTTG	GCGGTAGAAT	TAGAAAACAG	ATTCAGCAGT	CACCTACTCC	CCTTCAGTAA	180
TTCGAGACAA	TTATTTTTCT	CCTGACACAA	CATCAGGTCC	CATGAAAAAT	GACACCGTGC	240
CTGGTGTTTT	TGGGTTCTTT	AATGCTTCTT	TTAGAGCCAC	ATTTTTCTTT	TCAAACCGAG	300
TTCCCATCGC	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:181:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GAATTCGGCC	AAAGAGGCCT AATTTTCTT CACGTTCTTT ATCACCACCA TGGTTATGTT	. 60
	GCTCACCATT TGTTTTACTG GGATGTTTGG TTTATATATA ATGTGTGTTT	
	AAAGGCTACA GGTCTCTTTC CACATCCCAA ACTTTCTATG ATGCTTACAT	
	ACCAAAGATG CCTCTGTTAC TGACTGGGTG ATAAATGAGC TGCGCTACCA	
	AGCCGAGACA AAAACGTTCT CCTTTGTCTA GAGGAGAGGG ATTGGGACCC	
	ATCATCGACA ACCTCGAG	328
		320
(2) INFORM	ATION FOR SEQ ID NO:182:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 123 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:182:	
GAATTCGGCC	AAAGAGGCCT AGTTGTGGAA AAGAAAGACT GTGAGGGTAG GCACAAGAGC	60
ACTCAAATGT	CCCAGGTAGA GAAAACAACA TGTATGATGG CCCAGAAGGA GGCAAGTCTC	120
GAG		123
(2) INFORM	ATION FOR SEQ ID NO:183:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 311 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:183:	
GAATTCGGCC	AAAGAGGCCT ACTTGGACAA GTAGAAAGTG GATGACCCAG GCTCCGTTAC	60
ATATACTTGG	ATTCCAGCTG GGACCTAGAT TTGCTGAGGA CGGAAGCCAA GGACACAGGA	120
ACATGTGGCT	GCTCCCAGCT CTACTCCTTC TCTGCCTCTC AGGCTGTTTG TCTCTGAAGG	180
GCCCCGGCTC	TGTGACTGGC ACTGCGGGGG ACTCTCTGAC AGTGTGGTGT CAGTATGAGA	240
GCATGTACAA	GGGATATAAC AAGTACTGGT GCCGAGGACA GTACGACACG TCATGTGAGA	300
GCTCACTCGA	G ·	311
(2) INFORM	ATION FOR SEQ ID NO:184:	
(4)	SEQUENCE CHARACTERISTICS:	
(1)	(A) LENGTH: 130 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCGGCC AAAGAGGCCT AGTTCAATCT GTAACAAGCC TTCTTCAATT TCCTCTCCAC 60 ATACCCTGCA TAGACTTTAA GATTCCTCTG CTCGATGCTA ATAAGAAGAC ACACCCCCT 120

CGTTCTCGAG 130

- (2) INFORMATION FOR SEQ ID NO:185:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GAATTCGGC	AAAGAGGCCT	AGGAGGGGA	AGAGAGTCCG	TTTTGCAGAA	GATGAAGAAA	60
AGAGTGAAA	A TTCCTCGGAG	GACGGTGACA	TAACGGATAA	GAGTCTTTGT	GGAAGTGGTG	120
AAAAGTACA	CCCACCTCAT	GTGAGGCAAG	CTGAGGAGAC	AGTGGACTTC	AAGAAAAAGG	180
AAGAACTAG	AAGGTTGAAG	AAACATGTAA	AAGGTCTACT	TAACAGGTTG	AGTGAACCCA	240
ACATGGCTT	CATCAGTGGG	CAGCTGGAGG	AACTGTACAT	GGCCCACAGC	AGAAAGGACA	300
TGAATGACAG	CCTGACCTCC	GCTCTCATGG	GTGCCTGCGT	CACTGCCTCG	GCCATGCCCA	360
GCAGACTGA'	GATGGAGCAT	GTTCTCTTAG	TCAGCATCCT	TCACCACTTA	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:186:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCGGCC	AAAGAGGCCT	ACTACATTTT	TACCTAAATT	TATAGAAAAT	CAATTCGGAT	60
TGACATCCAG	CTTCGCAGCT	ACTCTTGGAG	GGGCTGTTTT	AATTCCTGGA	GCTGCTCTCG	120
GTCAAATTTT	AGGTGGCTTC	CTTGTTTCAA	AATTCAGAAT	GACATGTAAA	AACACAATGA	180
AGTTTGCACT	GTTCACATCT	GGAGTTGCAC	TTACGCTGAG	TTTTGTATTT	ATGTATGCCA	240
AATGTGAAAA	TGAGCCATTT	GCTGGTGTAT	CTGAATCATA	TAATGGGACT	GGAGAATTGG	300
GAAACTTGAT	AGCCCCTTGT	AATGCCAATT	GTAACGTACT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:187:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTCGGCA AGAGCCTA	AA ATCTACAAGC	ACCAGGAAGT	CAAGATGCAA	GCACCAGCCT	60
TCAGGGACAA GAAACAGG	GG GTCTCAGCCA	AGAATCAAGG	TGCCCATGAC	CCAGACTATG	120
AGAATATCAC CTTGGCCT	TC AAAAATCAGG	ACCATGCAAA	GGGTGGTCAT	TCACGACCCA	180
CGAGCCAAGT CCCAGCCC	AG TGCAGGCCGC	CCTCAGACTC	CACCCAGGTC	CCCTGCTGGT	240
TGTACAGAGC CATCCTGA	GC CTGTACATCC	TCCTGGCCCT	GGCCTTTGTC	CTCTGCATCA	300
TCCTGTCAGC CTTCATCA	TG GTGAAGAATG	CTGAGATGTC	CAAGGAGCTG	CTGGGCTTTA	360

AAAGGGAGCT GCTGGGATTC GACTCGAG	TTGGAATGTC TCAAACTCCG TACAAGCATG CGAAGAGAGA CAGAAGAGAG CGTTCAGCAG AGCATCACCA TGGTCAGGAG CAAGATTGAT AGATTAGAGC	420 480 488
(2) INFORM	ATION FOR SEQ ID NO:188:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 163 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:188:	
GTATGGCTCC	AAAGAGGCCT AGGTCAGATG CATTAAAACA TATCAAAATG TTACAAAAAT CTTGCTGAGG CCCTGTCAGA TTATGTTAGA TGAGTAAACG CATCAGTGTG ACCAAACGTT GAATCAAGTC ATGTACTCTC GAG	60 120 163
(2) INFORMA	ATION FOR SEQ ID NO:189:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 310 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:189:	
TCTGCCTCCA GTACTTTGTA TGTGCTCAGC	AAAGAGGCCT ACCTGCTCAT ACCTGTGGCC AAAAGCATGA TGCCCCAGGC ATTCTACCAT CTTCTCCAT CTTCTCTTT TATCAGGTCT CTGCCCTCCT CTTAGATTCT CCTCTGCCAA GCCCATTCAG ACTGTGACTG GTAGGAGTGC TTTCCACTTG AGTGTTATC CAAGAAGTTG GATAACCCTC TCAAGTTATG CAGTGCGCCT CAGTCTATGG GGATGCATTC CACTCACCCT TGGGCCTAGG	60 120 180 240 300 310
(2) INFORMA	ATION FOR SEQ ID NO:190:	
(i) ;	SEQUENCE CHARACTERISTICS: (A) LENGTH: 516 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:190:	
AAGGCTTGGC TTTCTGACAT AATGAAGTGA TTGTGTATGG	TTCATGGCCT AGGGCCTCAG TCTTTTACT TTTGCGGCTG TGTTTCTCTG ATTAGTAGAT TGAAAAGAAT AACCATCTAG GGAAATGTGA ATTCAGTTTC TCTGCTCTCT ACAAGGGGAT ATTATGTACA CATAAACCTA CTTCCAAAAT GGCCTAATTC CTTACTCTTC AGAGAGCCCA CTGTGGAAGT GTCACTGACC GCTGCCCTTC ATGGCTCTGG GAGTCATTAT AAAGGGCAGC ATTTGGCGTG	60 120 180 240 300
GTGCGTCCTA . TGTTCTTGGA .	AGCCAGTGTT TCTCGGCTCT GTTCCTTAAA CATGTGTTAG TGTTAATAGA AAAAAAAAA AAAAAACAGC ATTCTGAGGT CAAACATGCT CAGAAAGCTT	360 420
	CTACGCTTCT CGTACACATT TCATATTAAA GATTTTGGAA AGTCCTGCAA	480

PCT/US98/06956

TACAGAGCCC TGTCTAATAT TGCCACAGCC CTCGAG	516
(2) INFORMATION FOR SEQ ID NO:191:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 319 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:	
GAATTCGGCC TTCATGGCCT ACTTGCTAGA TAGACAGATT AAGAATGTTG AAGACATGGT CCAGTTTATT AATAACATTT TGGATGGCAC AGTAGAAGCC CAAGGAGGTG ATAGCATTTT GCAGAGATTG AAAAGAATAG TATTTGATGC CAAATCTACT ATTGTGTCTA TATTCAAGAG CTCACCACTG ATGGGCTGCT TTCTCTTTGG CCTGCCACTG GGTGTCATCA GTATCATGTG CTATGGAATC TACACAGCCG ACACAGATGG AGGTTATATA GAAGAACGAT ATGAAGTGTC TAAAAAGTGAA AATCTCGAG	60 120 180 240 300 319
(2) INFORMATION FOR SEQ ID NO:192:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 382 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:	
GAATTCGGCC TTCATGGCCT AAGCAGAAGG ACATATTAGA GAAGGATTGT ATAGTTTTCT GGTAAAAGAT GACAGTGAAT TGTATGGGCG ATGGATTAGC CGTGGAAGGT GTTGAGTATA AGTGGTCTCC AGCCAAACTC TATGGTTACT GGAATAAGAG AGTAGGAACC TTCTCAGGCT TTATCTTTAT CTATTCTTGT CAACAGTATG TACATGTGTC CCCCAGCCCC AAATAACTGT ACAGTTTAAT GATGTTCACT CTATACAGTT CCCAGAATCC ATTGGAAATT GCTGTAACAG CATATCCTCA ATGCCCATCA ATTCTCCACG TCCAACTTCT CCATGGCCTC CTCTGCCTCT GCTGATCTGT GAACTTCTCG AG	120 180 240 300
(2) INFORMATION FOR SEQ ID NO:193:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 474 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:	
GAATTCGGCC TTCATGGCCT AATATTTTTA AAGCGAAAGC TAACTTCTAA TTTTGAAAAT TTTTATTGGG AGCAGGATAT TATAATAATA ATCTTTAGTT GTTAAACCAT TAAACATCAA GGTTTTTTAC ATTGTTCTA TGCCTCCTCC CTCAAAAAAA AAAAACCTCC TACAATAAAA CTGAAAAATT GCACAAAGAC ATATTAGTGG AAGACCACTG CTTCGTTTAC ACAAATGAAG AGTATAAAGC AGAGAAGTGC TCCTTGGGGC AAAAGGCAAT TGGCAAAAAAG CTAAGGAACA TTTTCATAAT GAATTAGAAA TACAGATCAT CAGGAATATC CAGGAAGCGA TAGTGAATAC	60 120 180 240 300 360
154	

	TAAGAGACAG GAAACATTTA GCATGTTGGT AAACCACTTT AGCACATCAG TAAACAGCTT TAGGATTGGA AATTATTGCC AGGGGGGACT CGAG	420 474
(2) INFORMA	ATION FOR SEQ ID NO:194:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 499 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:194:	
TGCACATCTT TGATCCCTCT TGGAGATAAA AGAGAAAAGA AGGTAAAGAT AAGTGAAGAA	TTCATGGCCT ACGTNNCTAT GTCTTCAAGC ACAGAGGTGT CCAGGTGTAT CATCGCACTG AGCTGCATGG ACAGCTGATT TCTGTGGAAA AAGTATAAGG CAGAAAGAAA TGAAGAAGA AAATGATGAA AAGAGTGTT CAAGAAGTTC AAAAATACGA GTGATAGAAG TAGCAAGACA CAAGCCTCTG TCAAAAAAGA TCGTCTGAGA AATCTGAAAA AAAAGAAAGC AAGGATACTA AGAAAATAGA GAGAAGAATG ATAATGGAGC AAGTGGCCAA ACATCAGAAT CGATTAAAAA AAGAAGCGAA TAAGTTCCAA GAGTCCAGGA CATATGGTAA TACTAGACCA GATCATTGTA GACCATCAAG AAGAGGAAGA TATGAGAAAA TTCATGGAAG ATGCTCGAG	60 120 180 240 300 360 420 480 499
(2) INFORMA	ATION FOR SEQ ID NO:195:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 337 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:195:	
CATTTCATAA CTTTGTACCT AAGATTACAG AGTAACAAGC	TTCATGGCCT AAGCAAAGA GCATTAAGAA GTGTCTGTTT TTGTTATTGC ATATTTTAGT AGGTGTTCAA TTTCATTGGA TATTCTTTTT TTTTAATTGT ATGATTGAAA ACAGTAGTTG GTCTATGACT TTTGAGGAGA GGGAGAACCG GAGGCCAGCA TGAGGTTGGA ACAAGAGAAT GATGACCTTG CCCATGAACT AAAATTGCTC TACGGAATGA CTTGGATCAG GCAGAAGACA AGGCAGATGT GAGCTCCTTT TGACCAAAAC CCTCGAG	60 120 180 240 300 337
(2) INFORMA	ATION FOR SEQ ID NO:196:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 386 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:196:	
ATCCTCACTG	TCATGGCCTA AAGGAAACTG ACAAATTATC CCCAGCTGCC AGAAGAAGAA GACGGCTTCC TGTTTCCTGT GGTTCATTAT CTGATTGGCT GCAGGGATGA GTTCATAGGA CTGATGATCC TCCTCACCTC TGCGTTTTCA GCCCGTTCAG	60 120 180

					GTGCACCCCT CTGGGTTGCC	240 300
CCCCAAACCA	TGTTCAGCCA	CACGCCTACC	AGTTCACCTA	CCGTGTTACT	GAATGTGGCA	360
TCAGGGCCAA	AGCTGTCATC	CTCGAG				386

- (2) INFORMATION FOR SEQ ID NO:197:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTCGGCC	TTCATGGCCT	AGTTTTTGTC	TTTTTTTCTT	TTTTGGTATT	ATTTTGTTTG	60
CCACTTATTC	CTAAAATTCA	TATTGCTATT	AACCGTACAC	ATCTTTCCAT	GTTCTTATAA	120
TAATCTACAA	ACATCTCTCC	CTTTCTGTAG	CTCTCTCTGT	CACACACACA	CACATGCACA	180
CACGCACACA	CACACACACA	CACACGCTGT	GCACTCTCCT	GAAGCATGTG	TGTACATACA	240
TACATATGTG	AGGGGTTTTA	TGACTGTTTT	ACCAAATTGT	GTTCTTAATA	TATACAATGT	300
TGGCTTCTTT	TTAGCCATTC	AGAAGTTATT	TCAGTCATGG	AATGATCTCT	AGCCATATAA	360
CTGAAAACAG	GTAAGTTTCT	TTCTTGGGGA	AGAAGGGCGA	ATGGTGATAG	AGAAAATGGA	420
GAGCTCGAG						429

- (2) INFORMATION FOR SEQ ID NO:198:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GAATTCGGCC	TTCATGGCCT	ACCAAGCTAT	GCAGGAACAG	TTGTCTAAGA	ACAAAGAACT	60
GACACAGAAA	CTCCAGGTAG	CCTCTGAGAG	TGAGGAAGAG	GAGGGAGGCA	CAGAAGATGT	120
GGAAGAACTC	CTTGTCCCTG	ATGTAGTGAA	TGAAGTGCAG	${\tt ATGAATGCAG}$	ATGGGCCGAA	180
TCCCTGGATG	CTCAGGAGCT	GCACCAGTGA	CACCAAAGAG	GCTGCAACCC	AGGAGGACCC	240
TGAGCAACTG	CCAGAGCTTG	AGGCCCATGG	AGTTTCTGAA	AGTGAGGGAG	AAGAAAGACC	300
AGTGGCAGAA	GAAGAAATTT	TGTTGAGAGA	ATTTGAAGAA	AGGCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:199:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GAATTCGGCC TTCATGGCCT	AGGGAAAGCT	CCAACTTGCT	TTACCTTTCT	AAGATATCCC	60
ATTTTCTCTA TACCATTTGT	TGACTAATAT	ATCTCTTGCC	CACTGGTTTG	TAACAGTGCC	120

TTAATTAGTT TTTGTGTTTG AAGTTCCAGA ATCTCTTCCT GGCCTATGTA TTGTGTTCCG TTGATGGATC TTTCCATCCC ATGGTACCCT TTACTATTAT TGTCTTCATT TTTATTACTA TTGTTATGCC CTTTTCTCTC TCCGTGCACA TCTTCATGTT TGAACTCTAA AAACACACCG CCAACGCTCG AG	180 240 300 312
(2) INFORMATION FOR SEQ ID NO:200:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:	
GAATTCGGCC TTCATGGCCT AATATATCCA AGTAATAGCA TGTACAGTTT GGTAAGCAAT ATAATAGAGA GATATTCACA GTGAAATAGG AAAGAGCAGT ATAGGTGCAA AGACAAAAAG CATGACACAG CTAGATACAG GGCAGCTGTT ATTGGTTTTG TATGGAGAAA ACCTGGAGAA ATGGTGAGAG AAGGGCCAGA AGATGAGAGG GGCCAGATCA TGGACTACCT GTTTGTGGCG CTCAGGAGTT TAGATGTTAT CATGCAGATA ACTAGGAGCC ATTTGAGGAA CTTAAATACA GGAGTGATAC CAGATTTATA TGTTTTTAAA ATGATTACTT GGTGGTAATT AAAGAAAAGA	60 120 180 240 300 360 385
(2) INFORMATION FOR SEQ ID NO:201:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 204 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOFOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:	
AATTCGGCCT TCATGGCCTA CGTTTTTTA AATTTTTTTA ACTACATATT TGATACGATC TTTTCCTTCT TGCCTTCTTT TTGATTACTT ACTTTCTACC ATTCTATGTT TTTCGTCACT AGTTTGAAAA TTGTATACTT TGTTTTTATT CTTTCAGTGG TTACCCTAGA AATTACAACA AACAAAAATT GCAACAACCT CGAG	60 120 180 204
(2) INFORMATION FOR SEQ ID NO:202:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 450 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:	
GAATTCGGCC TTCATGGCCT AAAATCATCA TGCATATTTA TTTCTCCAAA GCACCTTTGA CAAGCATGAT TTGGATAGAG ACTGTGCTTT GTCACCTGAT GAGCTTAAAG ATTTATTTAA AGTTTTCCCT TACATACCTT GGGGGCCAGA TGTGAATAAC ACAGTTTGTA CCAATGAAAG AGGCTGGATA ACCTACCAGG GATTCCTTTC CCAGTGGACG CTCACGACTT ATTTAGATGT	60 120 180 240

300

ACAGCGGTGC CTGGAATATT TGGGCTATCT AGGCTATTCA ATATTGACTG AGCAAGAGTC

1 C 1/ 0.07 0/ 007 30	
TCAAAGAAAT GTGTTCAGAT GTAATGTAAT TGGAGTGAAA AACTGTGGGA AAAGTGGAGT 42	60 20 50
(2) INFORMATION FOR SEQ ID NO:203:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 558 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:	
GAATTCGGCC TTCATGGCCT AACTGGTTTC TGGCTCGTGG ANTCTGTTTC AAGATCATAT AAGCCGTTGC CATTCCCAAG NAGCGCTGGG ATATGCTCCT TCTCAGATGC TGCTATTTCA 12 GTGAAGGTAT TTAATGCTTG TTCAACATTA GATTTCTGTT TGGTAGCCAT TAAGCAATAG 12 TTTTCCATTA TGCGAANCTG TACGTGACCC TGAACAGTCT GAGGTTTTAG TTCCTTAANA AGTTTTTCTG CTGTTCTTAC TGCCAGTTGC ACAGATTCTT GCTTCCAGT TGAATAACCC 30 AGGTCTCCAT CCAGGTTTTC AAATACTTCA CCTCCAACAG TTTCATTATC TGGATTCAAA 36 CAGATCTCTA TCATATTATA AAGGGCATT TGCCCAGT CACGATCTTT CCGAGCTTTA TTAAAATGTC GAAGGGCATC ATTTGGTTCT CCAGTGTACC AAAGATACAG TCCTTTACAA 42 TACTGAAATC CTGGTTCCAA TTTTGGTCTG GAGNNACGTT TCTCAGCCAT TGAGAAAAAT	30 40 00 50 20
CTTGGGACAT CCCTCGAG 55	
(2) INFORMATION FOR SEQ ID NO:204: (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 348 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:	
TCAACCACAC TCATTTCAAG CTCTGTCAGA ACAGCATCTG AATTAGGAGG ACTTTGGGAT 12	60 20 80

- CTAGGAGTGG ATGTAATATC TAAAGAGACA ACTAGGAGGA AGCTCGAG

 (2) INFORMATION FOR SEQ ID NO:205:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

CAGCCTGAAG AGACCTATAT AGACCCTACT ATGATACAAT CTTTAACTTT TCCTTTGGCC

CTTCATAATC AAAGCTCCGA TAAGACAGCT AACATTGTGG AAAACCCATG TCCTGAGATT

240

300

348

CGCTTGGGTC CAGATCTGTA TTCCCAGGGC TCATAGAGAT ATTGGCAAAC TGACAGATTT CATGGCTCAA GAAACCTAAA GACACCTACT TGAATTCCTT TGGTTGGCAG TCAAAAGCT ACTAGTGTGT TTTCAAGCTT CTATTCTTAG GCATGTTACT TCCTTTTGGA AGTCAAAAACC AACCATCTTT TAAGTAAGAG GGCTAACCAA ATATGTGCCA CACTAACTCG AG	120 180 240 292
(2) INFORMATION FOR SEQ ID NO:206:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 220 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:	
GAATTCGGCC TTCATGGCCT AAAATATTAA AATCTTTGAA GAAGAAGAAG TTGAATTTAT CAGTGTGCCT GTCCCAGAGT TTGCAGATAG TGATCCTGCC AACATTGTTC ATGACTTTAA CAAGAAACTT ACAGCCTATT TAGATCTTAA CCTGGATAAG TGCTATGTGA TCCCTCTGAA CACTTCCATT GTTATGCCAC CCATCTCGAG GCAGGTCTAG	60 120 180 220
(2) INFORMATION FOR SEQ ID NO:207:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:	
GAAAAAATGG CCAAGGCTAC TGGGAAACTA AAGCCAACTT CTAAAGATCA GGTATTGGCC ATGCTAGAGA AAGCCAAAGT TAACATGCCA GCCAAGCCTG CTCCACCCAC TAAAGCAACT CTTAAACCAA TGGGAGGGTC CGCTCCAGCC AAATTCCAGC CTGCATCAGC ACCTGCTGAA GATTGTATTT CCAGCAGTAC AGAACCCAAA CCTGATCCAA AAAAGGCCAA AGCTCCAGGA TTATCCTCTA AAGCAAAGAG TGCACAAGGG AAGAAGATGC CAAGCAAAAC CAGCTTAAAG GAGGATGAAG ACAAATCCGG GCCTATACTC GAG	60 120 180 240 300 333
(2) INFORMATION FOR SEQ ID NO:208:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 316 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:	
GGAGACAAGT TCTCCTCAGT GAACTGGCAG TACCAGTGTG GGCTTACCTG TGAGCACAAG GCCGACCTTC TCCCTATCAG TGCATCCGTC CAGTTTATTA AAATTCCTGC ACAGTTACCC CACCCCCTGA CAAGATTCCA GATCAATTAT ACAGAGTATG ACTGCAACAG AAATGAGGTG TGTTGGCCGC AGCTTCTATA TCCATGGACT CAGTATTATC AAGGGGAGCT GCATTCTCAG TGTGTTGCTA AGGGCTTACT GTTGCTGTTG TTCCTCACAT TGGCCTTGTT CCTCAGCAAC CCCCGGACCA CTCGAG	60 120 180 240 300 316

- (2) INFORMATION FOR SEQ ID NO:209:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 517 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GAATTCGGCC	AAAGAGGCCT	ATGTCCCTGT	CCATCTTAGA	GGCTGACCAA	GCCCAGCCAT	60
${\tt GGGTGGTCCA}$	AATTGCTTAG	GTGGTCCCAA	TTGCTTGGCT	GGCCCAAGAG	ATGTCTGGTT	120
CTTAACAATA	CAAGAGCCTA	TAGAAATTGC	TAAAGGGATT	TCAGCCACAA	CTGAAGCTCA	180
CCAAGAATGA	GTTTTCTGGA	ACTGGTTAAA	GTGTCACAGT	AGGGAGTAAG	GAAATAAGAA	240
TCCCCACCAA	ACATAAGAGA	ACAGAATGAT	AATAGTCCCT	ACTAGTCCAT	GACAAGGCTG	300
			ATGCTGTGAG			360
			CAAGCAGCAA			420
			TGCTACTGTA	GCATAAAAGC	AGCGATACAT	480
CCTAAACCCG	TCGATTGAAT	TCTAGACCTG	CCTCGAG			517

- (2) INFORMATION FOR SEQ ID NO:210:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 829 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GAATTCGGCC	AAAGAGGCCT	AAGAACATGA	AACATCTGTG	GTTCTTCCTT	CTCCTGGTGG	60
CAGCTCCCCG	ATGGGTCCTG	TCCCAGGTGC	AGCTGCAGGA	GTCGGGCCCA	GGACTGGTGA	120
AGCCTTCGGA	GACCCTGTCC	CTCACCTGCA	CTGTCTCTGG	TGATTCCATC	AGTCATTACT	180
ACTGGACCTG	GATCCGGCAG	CCCCCAGGGC	AGGGACTGGA	GTGGATTGGA	TATTTCTATT	240
CACCCGGGAA	CTCCAACTAC	AATCCCTCCC	TCAAGAGTCG	AGTCACCATG	TCAGTCGACA	300
CGTCCACGAA	CCAGTTCTCC	CTAAAACTCA	NTTCTGTGAC	CACTGCGGAC	ACGGCCGTCT	360
ATTACTGTGC	GAGAGACCTA	TATTGCCGTG	GGGGAACCTG	CTACCCCGCG	AGACTTGACC	420
GCTGGGGCCA	GGGAACCCGG	GTCATCGTCT	CGTCAGCCTC	CACCAAGGGC	CCATCGGTCT	480
TCCCCCTGGC	ACCCTCCTCC	AAGAGCACCT	CTGGGGCACA	GCGGCCCTGG	GCTGCCTGGT	540
CAAGGACTAC	TTCCCCGAAC	CGGTGACGGT	GTCGTGGAAT	TCAGGCGCCC	TGACCAGCGG	600
CGTGCACACC	TTCCCGGCTG	TCCTACAGTC	CTCAGGACTC	TACTCCCTCA	GCAGCGTGGT	660
GACCGTGCCC	TCCAGCAGCT	TGGGCACCCA	GACCTACATC	TGCAACGTGA	ATCACAAGCC	720
CAGCAACACC	AAGGTGGACA	AGAAAGTTGA	GCCCAAATCT	TGTGACAAAA	CTCACACATG	780
CCCACCGTGC	CCAGCACCTG	AACTCCTGGG	GGGACCGTCA	GTCTTCCTC		829

- (2) INFORMATION FOR SEQ ID NO:211:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRÍPTION: SEQ ID NO:211:

GAATTCGGCC AAAGAGGCCT AGTTAATCTG ATAAATTCAC CATCAATTTG GTAAGCTTTA

60

ATATAACTAC CCTGTTTTTT GAATACAGAT AATGCAAAAG AAAACCATTT TATACTCGGC TATATACCTT CCACCACTCG AG	120 142
(2) INFORMATION FOR SEQ ID NO:212:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 555 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:	
GAAATTCGGC CAAAGAGGCC TAGTGGAATC ATTCTGCCAC ACCATTTCCT ACTCAAATAG GTACAAACAT ACCACAGACA CTCCCATATA CACATGCTCC TCTATCCGCC AACTCTGGAA CCAAAACTAA ATTGGTCTTC AAGAGAGATG ATGGCTTTAA GAACAAAAAAT AGCCTTATCC TCTATTTTAC TTGCTGTACT GTTGTACTGT TTATTTAAGA AACAAGCTGG TGGTTGATGT CCAGGAAAAA TTATCTTTTC AAAATGAGGG AAGAGGAGGT TCACCATGTG GATATGGTGT GCCTTTCAAC ATCCTTAAGG ATTGTTGATA TCATTATTGT TAATCAATTG TTGTCAGCAC AGTGGCTGCC CAAGCTGTGC AAATGAAACA GCCAATCAGC AGGAGAAAGT GATGAAATTA AATGACCTCT TTCCTTAACC ACTCATCCGT AAGCCTTGTT ATTTTTCATA CAAACCTCGA GCCGGGGGAG GAGGGGCGC GGCGAATGCT GGGAGAGTCA GGTCTAGAAT TCAATCGTAG GCCTCTTTGG CCGAA (2) INFORMATION FOR SEQ ID NO:213:	60 120 180 240 300 360 420 480 540 555
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 97 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:	-
GAATTCGGCC AAAGAGGCCT ACGAGAAGGG CGGTGTGTAC AAAGGGCAGG GACTTAATCA ACGCAAGCTT ATGACCCGCA CTTACTGGGA ATTCCTC	60 97
(2) INFORMATION FOR SEQ ID NO:214:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 487 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:	
GAATTCGGCC AAAGAGGCCT AAGAAGAAAT TGGTAGATTG CGAGAAGAGA TAGAAGAATT AAAACGTAAT CAGGAACTTT TACAAAGCCA GCTGACTGAA AAGGACTCTA TGATTGAAAA TATGAAATCT TCCCAAACAT CTGGCACAAA TGAACAGTCT TCAGCAATAG TTTCAGCTAG AGATTCTGAA CAAGTTGCAG AATTAAAACA GGAACTGGCA ACTTTAAAGT CTCAGTTAAA	60 120 180 240
161	

CTCACAATCT GTGGAGATCA CCAAACTACA GACAGAAAAG CAGGAACTGT TACAGAAAAC 300
AGAAGCGTTT GCAAAATCAG TTGAGGTACA AGGAGAGACC GAGACTATAA TAGCCACCAA 360
AACTACTGAT GTAGAAGGAA GACTGTCAGC ATTATTACAA GAGACCAAAG AGTTAAAGAA 420
TGAAATTAAA GCTCTGTCTG AGGAAAGAAC TGCCATTAAA GAGCAGCTGG ATTCATCTAA 480
TAGTACC 487

- (2) INFORMATION FOR SEQ ID NO:215:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 584 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GAATTCGGCC AA	AGAGGCCT ACTGGGCC	IT TCAGCACCTG	CTCCAGCTTC	ACCTTGGTGA	60
ACATCAGGTT GA	AGTTCTCA GGGTGCTC	GG TGATGGCCAT	GTTGACAACA	TCCAGGGCAT	120
GCTGGTGGTG CT	TCTGGGCA GAGAAGAG	CA GTGCCAGCAG	GTGGAGGGCG	TGGGCATCAT	180
CCTTGCGTAC CT	TCAGGGCC TCCTGCAG	CT GCTCCATGGC	ACTGGAGATC	TGTCGGACGA	240
GGGCCAGCTG CA	GCGAGACA TAGAGGAT	GA CCTGGGGGTC	ACTGGGCGCC	AGCTGCTGAG	300
CCCTCTCCAG CG	TCTGCAGT GCCTTCCG	GT GCAATTCATC	TTGCTTGGAC	TTCAGGGTGG	360
CGTCGGTGGC CT	GCAGGCTA TAGGTGAG	AC CCAGAGCCAG	GTAGCCCTTG	GGGAGGAACT	420
CCCCGGCTTC CT	CTCCGAGG CTGATCAC	CA TCATGGCAAA	GTGCTCTGCT	TCCTCTAGCC	480
AGCGAAGGGA CC	CGATGCAG ACCTTCGC	GG CCATCAGGGG	CACGGTGGGG	TCCGAGGGCC	540
GCAACTTCAC AC	ACTCCCGC AGCAGGGA	CA CAGCGTAGGC	TGAC		584

- (2) INFORMATION FOR SEQ ID NO:216:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 532 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTCGGCC	AAAGAGGCCT	AGACCTGCCC	TAAAGATAGA	GTCTTGATGC	ACCGTCTACC	60
TTGTCCCCAA	CCAAGAGTGA	GTAGTGCACA	GAAGTCTCCT	GGCACCCTGG	GAATCCTGCA	120
TTTTTAATGG	ACGAGCAGGG	CAGGAAAGAA	AAAAAAAACC	CAAACCCCAT	CACTCTGCCA	180
GCCCCTGTGA	CCAAAGCAGC	CCAAATCAGT	TACCTTGACA	ACTCTCATGC	ACAGACTGCA	240
CCAGCCTGTG	TTGCAAACAT	CACTGCCCCG	CTTCTAACAG	GAAGAGATAC	TCTTTTGGGG	300
GTCTTGCAGG	GCCCAGGACC	AGAGCCCCTT	CTACCCAGGG	CCCTTCCAAA	GGCAAAGCAC	360
AGAGTCACAT	TTGGGCGTGG	CATGAGAGGG	AAATAAAGAG	ATTTGGCTGT	AGTGGGAGGG	420
AGGTTTCAGT	GCTTTTTCTG	GGGACATTGG	TGCCTATCTC	TATTCTGAGA	GTTGTTCTCC	480
TCATAGGACA	CCATAAATCG	CATCCAGGAC	CTGCTGGCTG	AGGGTACTCG	AG	532

- (2) INFORMATION FOR SEQ ID NO:217:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GAATTCGGCC	AAAGAGGCCT	AGTGTGTCCG	GGTCTTATAC	AAAAACAACA	CAGTGAATGA	60
				AAATTGTATA		120
						120
ACAATGGGAA	GCACATAGTG	AGGCTATGAG	TGATTTGGAA	ATCATGAGCG	TGCAGTGTTT	180
TGTTCACGCA	TTTCGGTTGT	GTTTTCAGAA	AGTAACTACA	ACATAGCATC	ATGTAGCAGA	240
ATTGCTGGTT	GTAAGCAAAA	AGGCTCGAG				269

- (2) INFORMATION FOR SEQ ID NO:218:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 675 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTCGGCC AAAGAGGCC	T AATTCTTTTT	CTTTTTAATT	TGAAGAAAAA	TCATCAGTCT	60
TGGAATACAG AAGAGAAA	T AGAAATATAC	GTATTTTGTT	TCACATTTGA	ACAGTCATTC	120
TTGAGGAATA CTCCATACO	T GAGTAGACAG	CCATGTGGCC	ATCGCAGCTA	CTAATTTTCA	180
TGATGCTCTT AGCTCCAAT	A ATTCATGCTT	TCAGCCGTGC	CCCAATTCCA	ATGGCTGTGG	240
TCCGCAGAGA GCTATCCTC	T GAGAGCTATC	CTATAGAGCT	TCGCTGTCCA	GGAACAGACG	300
TCATCATGAT AGAAAGTGC	C AACTATGGCA	GGACTGATGA	CAAAATTTGT	GACTCTGACC	360
CTGCTCAGAT GGAGAATAT	C CGATGTTATC	TGCCAGATGC	CTATAAGATT	ATGTCTCAAA	420
GATGCAATAA CAGAACCCA	G TGTGCAGTGG	TGGCAGGTCC	TGATGTTTTT	CCAGACCCGT	480
GTCCAGGAAC CTATAAATA	C CTTGAAGTGC	AGTATGAATG	TGTCCCTTAC	ATTTTTCTTT	540
GTCCTGGACT ACTAAAAGG	A GTATACCAGA	GTGAACATTT	GTTTGAGTCC	GACCACCAAT	600
CTGGGGCGTG GTGCAAAGA	C CCTCTGCAGG	CATCTGACAA	GATTTATTAT	ATGCCCTGGA	660
CTCCCTACAG AACTG					675

- (2) INFORMATION FOR SEQ ID NO:219:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GAATTCGGCC	AAAGAGGCCT	ACTCCCTGTT	TTGAACAAGT	TTTTTTGAGA	ATTCTTAGTT	60
TTAGTTTTTG	TTTAGCTTAC	ACACTGAAAA	TTTTGAGAAG	CATCTAAAAA	AATCCACAAT	120
TAGTGCAAAA	AGAGGGGACA	ATACTTTAAG	TCATTCCTTC	TATAAAAAGA	ATTAAGGTTA	180
CTAAATGCCA	ATTTTTAAGC	AAATATATAG	TTTCCTATTT	GCCTTCTGAA	AGACAGCAGA	240
TATAAAAATA	GTTCAATATT	AGGTTTAACA	AGGTTTGAAC	AACACATGTA	CTATCAGCTT	300
TATTTTACCT	GCAAAAATAT	TTTAGCTACA	CTTGGAAAAA	AATAAACTTG	AGAATATAAC	360
TTCACATTTC	TAAGGCCAGA	TGCAAGAATA	CTTATTTAGG	CCTCTTTGGC	CGAA	414

- (2) INFORMATION FOR SEQ ID NO:220:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GACCGTCGAT TGAATTCTAG ACCTGCCTCG AGATTGGAGA CAGAAGGTCC CGGGAGCAGA 60
AAGCCAAACA GGAGCGGAG AAAGAACTGG CAAAAGTCAC TATCAAGAAG GAAACTCGAG 120

- (2) INFORMATION FOR SEQ ID NO:221:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GAATTCGGCC	AAAGAGGCCT	AAGCAGCAGC	TGCTTATATG	CATGTGAACA	GCTGGGGAAT	60
TAATTTGGTA	TGCATTCTCA	GGAGCCACTC	ATCTGCTGGC	AGAGGTAGCA	GAAGAATGCC	120
${\tt CTTAGTGTAA}$	GTCCTCTACA	ACCATACACC	AAATGTGCTC	CCTGCATTTC	AAATTCCATT	180
GTAGAAAGTC	TCTGATAATC	TCACTTATAC	CATGAGCCAT	TCCTCAGTAT	CTGTCCTCTT	240
CCTGTTAGTG	TTCTACAATT	CCTTTCTCCT	TAATTTTTCT	CCGCTTTACA	AAATGTCACA	300
CAGACAAGTG	CATAATACTT	AAACAAGCTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:222:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 817 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GAATTCGGCC	AAAGAGGCCT	AAGAAAAGCA	CCCTTATTAA	GAATTGCAGC	AAGTAAGCCA	60
ACAAGGTCTT	TTCAGGATGA	TTTTCTTATA	${\tt TCAAGTGGTA}$	CATTTCATTT	TATTTACTTC	120
AGTTTCTGGT	GAATGTGTGA	CTCAGTTGTT	GAAGGACACC	TGCTTTGAAG	GAGGGGACAT	180
TACTACGGTC	TTCACACCAA	GCGCCAAGTA	CTGCCAGGTA	GTCTGCACTT	ACCACCCAAG	240
ATGTTTACTC	TTCACTTTCA	CGGCGGAATC	ACCATCTGAG	GATCCCACCC	GATGGTTTAC	300
TTGTGTCCTG	AAAGACAGTG	TTACAGAAAC	ACTGCCAAGA	GTGAATAGGA	CAGCAGCGAT	360
TTCTGGGTAT	TCTTTCAAGC	AATGCTCACA	CCAAATAAGC	GCTTGCAACA	AAGACATTTA	420
TGTGGACCTA	GACATGAAGG	GCATAAACTA	TAACAGCTCA	GTTGCCAAGA	GTGCTCAAGA	480
ATGCCAAGAA	AGATGCACGG	ATGACGTCCA	CTGCCACTTT	TTCACGTACG	CCACAAGGCA	540
GTTTCCCAGC	CTGGAGCATC	GAAATCTTTG	TCTCCTTAAA	ACATCTGAGA	GTGGATTGCC	600
CAGTACACGC	ATTAAAAAGA	GCAAAGCTCT	TTCTGGTTTC	AGTCTACAAA	GCTGCAGGCA	660
CAGCATCCCA	GTGTTCTGCC	ATTCTTCATT	TTACCATGAC	ACTGATTTCT	TGGGAGAAGA	720
ACTGGATATT	GTTGCTGCAA	AAAGTCACGA	GGCCTGCCAG	AAACTGTGCA	CCAATGCCGT	780
CCGCTGCCAG	TTTTTTACCT	ATACCCCAAC	GCTCGAG			817

- (2) INFORMATION FOR SEQ ID NO:223:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 587 base pairs

egine Harring de la companya de la company La companya de la compa

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GAATTCGGCC AAAGAGGCCT	AGGAGATACA	TCATCATATC	ACGGAAAGAG	ATGCAGATAG	60
ATCTTTGACC ATACTTGATG	AACAGTTATA	CTCATTTGCG	TTTTCCACCG	TGCACATTAC	120
GAAGAAAAGA, AATGGAGGTG	GGAGTTTAAA	TAACTATTCC	TCCTCCATTC	CATTGACTCC	180
CAGCACCAGC CAGGAGGACC	TTTATTTCAG	TGTTCCTCCC	ACTGCCAACA	CACCCACGCC	240
CGTTTGCAAG CAGTCCATGG	GCTGGTCCAA	CCTGTTTACA	TCTGAGAAAG	GGAGTGACCC	300
AGACAAAGGG AGGAAAGCCC	TGGAGAGTCA	CGCTGACACC	ATCGGGAGCG	GCAGAGCCAT	360
CCCCATTAAA CAGGGCATGC	TCTTAAAGCG	AAGTGGGAAA	TGGCTGAAGA	CGTGGAAAAA	420
GAAATATGTC ACCCTGTGTT	CCAATGGCGT	GCTCACCTAT	TATTCAAGCT	TAGGTGATTA	480
TATGAAGAAT ATTCATAAAA	AAGAGATTGA	CCTTCGGACA	TCTACCATCA	AAGTCCCAGG	540
AAAGTGGCCA TCCCTAGCCA	CATCGGCCTG	CGCACCCATC	TCTCGAG		587

- (2) INFORMATION FOR SEQ ID NO:224:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GAATTCGGCC	AAAGAGCCTA	AGTAGTTGCT	GCCTTTCTTC	AGATCAGGTT	ACCACAATGC	60
CTCCCCGCTG	CTGACGCTTC	ATCCCCCACA	CCTCCAGCCC	CAGTTACCTG	GAGCTTCTCA	120
GAACCCACTT	TGCCGGTGCT	AAAACACAAG	AGGGGGTGAA	AGTGGCTGCC	AGTAATGGCC	180
AGAAACCAAC	CACCAGAGGC	CAGGCTGAAA	GACAAGCTCC	GGGTGTCCAG	GGGCTGACGG	240
GCCAACCATG	TGGCAGGTCC	CAGGCCCCAC	CCACTGCGCC	ATCCGTCTCT	GAGCTCCACA	300
GTGGTCCCAC	TAATGGGAAC	CTCCTCTAGG	GAGAGTGATA	CTGCACCTTC	ACCCGTAGGA	360
CTCATATTTA	TAACAATGTG	TAATGGCTGT	AGCAAAAAGC	CCTTGTTTCT	AGATGTAAAT	420
GGTCAAAGAA	ACAAGCGCTC	TATTGTTTTG	AATAAAATAG	TTCAAATGAG	TCCTGTATCA	480
TTGTATCTCC	TATTCTGGAT	TAGTGCCTTT	TGGACAGTAG	ACTGTAACCT	CGAG	534

- (2) INFORMATION FOR SEQ ID NO:225:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 base pairs
 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GCTCCACTCT C	TCCCTATCC	ATTTGTAAGA	ACAGGCTCCC	CTCGCCGAAT	ACAGTTGTCT	60
CAAAATCATC C	TGTCTACAT	TTCCCCACAT	AAAAATGAAA	CAATGCTTTC	TCCTCGAG	118

- (2) INFORMATION FOR SEQ ID NO:226:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GAATTCGGCC	AAAGAGGCCT	AAATTTTAGT	AGAGATGGAA	TTTCACCATA	TTGGCCAGGC	60
CGGTCTCAAA	CTCTTGACCT	CAAGTGATCT	GCCCGCCTCG	GCCTCCCAAA	ATGTTGAGAT	120
TACAGGCGTG	AGCCACCATG	CCTCTCTTAC	ATTCTTTTCT	TCTGTTCACT	ACAGCCGTGG	180
AGAGCTCCGG	GTTGTCCTGC	ACATGTGCAC	TGCCCTCTCT	TTTATGGACC	TTTTAGGCTG	240
GCTGCACCCT	CCGTCTGTGT	CACCCTCCTG	CTCCTCCTCC	ACCTGGCTAG	TTCCTGTTGG	300
			CACCCTGAGT			360
TGAGCTCACT	ATGCTGGGTT	TTATCTATGT	CTCCCTCGCA	ACTAGATCAT	TCACGTCTTG	420
AAGTTAGGCA	TCATGCGTTC	TTCATTTCTG	TACCTCCCAA	CTCAATGCTT	AGCACCCAGC	480
AGGGGCTCAA	GACTGTGTGT	${\tt GGAATGAAGG}$	ATTCGTGTGA	AAATGCAGGG	AGATGGAAGG	540
CTGAGCGTTT	CTGTTCCTTG	ACCATTCCCG	GGTTGGCTCG	AG		582

- (2) INFORMATION FOR SEQ ID NO:227:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GAATTCGGCC	AAAGAGGCCT	AAAAACTTAT	AAATAAGTGA	GACTACTGCC	CCCTAGCCTA	60
AAATTCATTC	CCTGCGCTCA	CTCAACATCA	${\tt TAGTTCTTTA}$	GGAAGACAAG	TTGTTCTATA	120
GCATAAAGAT	ACAACCTATT	TAGATAGTCT	AAAGATTCTC	CTCTGTTTCT	CAAATACAGT	180
CAGTTATGCA	${\tt GCTCAAAATG}$	CCTCTCATTT	TCCTGCTTTT	TTTTCTTCTA	CTATTGTTGC	240
CTCCAGGCTT	TGCAGAAACA	CATGTTATTC	TCCCCCTAAA	ATCTGTTCCT	CTTCTAGTTT	300
TCTCTCTGCC	AGCAATGGCA	CCACACAGTC	TTTTGGTTTT	GCACCAGAGA	ATTAGAGATG	360
AACCCCTCAT	CTCTAATCTA	TCACAAGTTT	CCTCAGATTT	AAACTCTCAA	ATCAAGATGT	420
TTCTCACCAT	TTCCATTACT	ATTGTCCCCA	GCTTTCTCGA	G		461

- (2) INFORMATION FOR SEQ ID NO:228:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GCCTAAACCG TCGATTGA	AT TCTAGACCTA	TCTCGAGAAA	GAGTTGTTCT	GGAAAGAAAT	60
GAAGAAAAGA GCAGAACC	AA TCTCAAGCAG	CCAAGTGGTG	AAGTTGGATG	TATGTGACCC	120
TACGTCTCTC GAG					133

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GAAAGGGATC	AAAAAGAAAA	AGTGATCGAA	TGGAATCTAC	TGATACCAAA	CGACAAAAGC	60
CTTCTGTCCA	TTCAAGACAA	CTGGTTTCTA	AGCCACTGAG	CTCATCTGTT	AGCAATAACA	120
AAAGAATAGT	TAGTACAAAA	GGAAAGTCAG	CCACAGAGTA	TAAAAATGAG	GAATATCAAA	180
GATCTGAAAG	AAACAAGCGT	CTAGATGCTG	ATCGGAAAAT	TCGTCTATCA	AGTAGTGCCT	240
CCAGAGAACC	TTATAAGAAT	CAACCTGAAA	AAACCTGTGT	CCGGAAAAGG	GATCCTGAAA	300
GGAGGGCCAA	ATCTCCTACG	CCAGATGGTT	CTGAGAGAAT	TGGGCTTGAA	GTGGATAGAC	360
GTGCAAGCAG	ATCCAGCCAG	TCTTCTAAGG	AAGAAGTGAA	CTCTGAAGAA	TATGGCTCTG	420
ACCATGAGAC	TGGCAGCAGT	GGTTCTTCTG	ATGAGCAAGG	GAACAACACT	GAAAATCTCG	480
AG						482

- (2) INFORMATION FOR SEQ ID NO:230:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAATTCGGCC '	TTCATGGCCT	AGGGGATAAA	TGTAAGCTTG	TTAAAGTAAG	CACCACACCA	60
TGTTTCTGTC '	TCCCCAGCAC	CCAGCACAGT	GCTGTGAACC	TTGGCAGATG	CTAGATAAAT	120
GTGTGTTGAA '	TGAATGTGCC	TATGAAGCCA	CAAAGATGCC	ACATGTTAGT	ATATCAGTGA	180
GAGGTGACTC	CACAGTGCTC	TCTGGAGAAG	CAATATGAGT	GACTGAAGAG	TGGGGCCTTT	240
TGCTTTTGCC '	TGGATATAGG	GGTGCTCTTC	TACTGTAATT	${\tt GGGTGTGGAA}$	AAACTCTGGC	300
TTTATGGTAT '	TCCATTAGGT	TCTTTTCATT	TAAAGTAGTC	TTAAAATCAA	AGTATCCAAT	360
ATTTTAAAGC	CACAAAGTAG	ATTACATAAT	TAGCAGAGAT	TTTAGTCAGT	AAAATGTTAG	420
AAATCAAACT	ATAAGAAAAT	TCAAGTCCTT	TATTTTGTGT	CTTGGGTATA	TGTCATTATT	480
TTAAATTCCA	CAGCTCTCGA	G				501

- (2) INFORMATION FOR SEQ ID NO:231:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GAATTCGGCT	TCGATTGAAT	TCTAGGACTT	GACAGAATTC	GAGTTATCCT	TCTCAGAACA	60
TGTGCAGAGT	CTCTTTTTGC	CTCACCATGT	GGTCCTGTGC	TCTTTCAGGT	GGGAGTTTTG	120
GGGCCTCCAG	GGCAGCAGGC	ACCACCTCCA	TATCCCGGCC	CACATCCAGC	TGGACCCCCT	180
GTCATACAGC	AGCCAACAAC	ACCCATGTTT	GTAGCTCCCC	CCCAAAGACC	CAGCGGCTTC	240
TTCACTCAGA	GGCCTACCTG	AAATACATTG	AAGGACTCAG	TGCGGAGTCC	AACAGCATTA	300

GCAAGTGGGA TCAGAGCAAT CTCGAG

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GAATTCGGCC	TTCATGGCCT	AATCAGAAGC	TTTTCAAAAT	TCCGTCTTCA	AGAAGAAACA	60
CCCGTGGAGG	AAGAAGACAT	TATACAAAAC	AAATTTAGAA	ACTGGGATCA	TGAGTGGAAA	120
AACAAAGGCA	AGAAGGGCTG	CCATGTTTTT	TAGACGTTGC	TCTGAAGACG	CCAGCGGTAG	180
CGCCAGTGGC	AATJCTTTGT	TATCAGAGGA	CGAAAATCCT	GATGCGAATG	GGGTAACTCG	240
${\tt ATCATGGAAG}$	ATTATTCTAA	GTACAATGCT	TACACTGACT	TTTCTTCTTG	TAGGACTCCT	300
AAATCATCAG	TGGCTTAAAG	AAACAGATGT	TCCTCAGAAA	TCCAGACAAT	TATATGCCAT	360
GCTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:233:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GAATTCGGCC	TTCATGGCCT	AAAGAAGAAT	TGACACCTCT	TGGAGTCCAC	TTGGCACGAT	60
TACCCGTTGA	GCCACATATT	GGAAAAATGA	TTCTTTTTGG	AGCACTGTTC	TGCTGCTTAG	120
ACCCAGTACT	CACTATTGCT	GCTAGTCTCA	GTTTCAAAGA	TCCATTTGTC	ATTCCACTGG	180
GAAAAGAAAA	GATTGCAGAT	GCAAGAAGAA	AGGAATTGGC	AAAGGATACT	AGAAGTGATC	240
ACTTAACAGT	TGTGAATGCG	TTTGAGGGCT	GGGAAGAGGC	TAGGCGACGT	GGTTTCAGAT	300
ACGAAAAGGA	CACACTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:234:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

60	CTCTATTTGC	GTGGTGTTGG	GCTGTCATTT	CGATGAGGCT	TCATGGCCTA	GAATTCGGCT
120	TGAACAGATA	AAATCACTGC	TTTGGCTTCC	GAGCCAGGCT	GCAGAGGAAG	TGTCACTCAA
180	GCTCAAGTGC	TACAATGTTG	GTACAACATC	TGACCTTGCA	GGACGAGACC	CGCCGTGGAG
240	GCATTGTGTC	GAAGACTTTG	CTTCCCTCCA	CTGATGATTC	GTGGAACTAT	TGCATTAGAC
300	CCCACACTGT	AGCAATGTCT	TGCCCCTGCT	GGGACCGGAT	AATGTCAAAT	TGGAATGCTC
358	TCCTCGAG	TCGGCAACAA	CAACTTCACC	CTGGTTATTT	CCTCTCAAGG	GGTCCTGCGC

- (2) INFORMATION FOR SEQ ID NO:235:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GAATTCGGCT	TCATGGCCTA	GTTGTACGTA	ATGTATTTAT	ATGTTAATTT	GTTATGTATA	60
TAGATGTGCA	AGTCTTGTCA	GAATTGGCCT	CAGTGTAGTT	AAAGGGCAGA	AGGGGAAGAT	120
ACTGACTAGT	CATAGAAATA	CCTCATTCGC	CTGTGGGAAG	AGAAGGGAAG	CCTCTTCAGG	180
GTGAGTGAAT	GGCAAAGCGG	TTGCTTCTGG	CTCCTCCTTC	CCCTGTGGTC	TTGGAAGTGT	240
GTGGAAGGCA	GGGACAGAGA	TGGAGGCCGA	GCCAATAGAC	TGAAGAGACC	ACAGCAATTG	300
GCTCCTCCAT	CTAGAGATTT	TCTTGGCAGT	ATTCCATGGG	ATGTTAAGCA	AAGGAAACCA	360
AAGGAATCGT	TTCAAATGGA	CTCATGGCTT	AGAAATCTTT	ATTCTTAGGG	CAGTCAGTAG	420
TATTCTAAAG	CTTTCTGACA	AGATAAAGGA	AGTCACCAAA	ATTTCTTTTT	TTAAATTGTA	480
TCTAATCCTC	AACAACAAAC	CAAAACTCTC	GAG			513

- (2) INFORMATION FOR SEQ ID NO:236:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GAATTCGGCC	TTCATGGCCT	ACTTGGAAAT	GTTTGATGCT	ACTCTGAAAG	ATCGAGAACT	60
GAGCTTTCAG	TCGGCTCCAG	GTACTACCAT	GTTTCTGCAT	TGGCTAGTGG	GAATGGTATA	120
TGTCTTCTAC						180
GTGGTTTCTA	AGGAATTTGA	ATGATCCAGA	TTTCAATCCA	GTACAGGAAA	TGATCCATTT	240
GCCAATATAT	AGGCATCTCC	GAAGATTTAT	TTTGTCAGTG	ATTGTCTTTG	GCTCCATTGT	300
CCTCCTGATG	CTTTGGCTTC	CTATACGTAT	AATTAAGAGT	GTGCTGCCTA	ATTTTCTTCC	360
ATACAATGTC	ATGCTCTACA	GTGATGCTCC	AGTGAGTGAA	CTGTCCCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:237:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TTCATGGCCT	AGAGATATGC	TTCTTTGTAC	CAATATGGAA	AATCTAAAAG	AAAAAACCCA	60
CACTCAGCAC						120
GGGTCCAAAC						180
CTATGATCAA						240
					TCGAGCATCT	300

TAAAATGATT CAACAGGAGG AGATAAGGAA GCTCGAG

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GAATTCGCGC	ATTCGGTACA	ACAAGAGAGA	TAAACGATGA	AACCGTTACA	TTATACAGCT	60
TCAGCACTGG	CGCTCGGACT	GGCGTTAATG	GGGAATGCAC	AGGCAGTGAC	GACCATTCCG	120
TTCTGGCATT	CTATGGAAGG	GGAACTGGGT	AAAGAGGTGG	ATTCTCTGGC	CCAACGTTTT	180
AACGCCGAAA	ACCCGGATTA	CAAAATTGTA	CCGACCTATA	AAGGCAACTA	CGAACAGAAT	240
TTAAGCGCGG	GGATTGCCGC	ATTTCGTACC	GGCAACGCGC	CGGCTATTTT	GCAGGTTTAT	300
GAAGTTGGCA	CCGCCACCAT	GATGGCGTCG	AAAGCCATTA	AACCGGTGTA	TGACGTGTTT	360
AAAGAGGCAG	GGATTCAGTT	CGATGAGTCG	CAGTTTGTGC	CGACGGTTTC	AGGTTACTAC	420
TCCGACAGCA	AAACGGGCCA	CTTACTCTCC	CAGCCATTCA	ACAGCTCGAC	CCCCGTTCTC	480
TATTACAACA	AAGACGCCTT	CAAGAAAGCA	GGATTAGACC	CGGAACAGCC	GCCGAAAACC	540
TGGCAGGATC	TGGCGGACTA	TGCCGCGAAA	CTGAAAGCCT	CCGGCATGAA	GTGCGGCTAC	600
GCCAGCGGCT	GGCAGGGCTG	GATCCAACTG	GAAAACTTTA	GCGCCTGGAA	CGGTCTGCCG	660
TTTGCCAGCA	AAAACAACGG	CTTTGACGGC	ACGGACGCGG	TGCTGGAGTT	CAATAAGCCG	720
GAGCAGGTGA	AACACATCGC	CATGCTCGAG				750

337

- (2) INFORMATION FOR SEQ ID NO:239:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TCATGGCCT	ACTTACAGAA	CCTATTCACT	GGGAAGGAAG	CCCTCATTAT	60
ATTCTTATGT	GTGTTTCAGG	ACGACTGGGT	TTGGATTCAG	AAGAGGATTA	120
CAAAAGGTGG	ATGTTCCCAA	GGCCTTGATT	ATTGTTGCAG	TTCAATGTGG	180
CATTTCTGT	TGACCCAGTC	AGGCAAAGTG	CTGGCCTGTG	GACTCAATGA	240
TGGGTCTGA	ATCAGTGCAT	GTCGGGAATT	ATCAACCATG	AAGCATACCA	300
TACACAACGT	CCTTTACCTT	GGCCAAACAG	TTGTCCTTTT	ATAAGATCCG	360
CCAGGCAAGA	CTCACACAGC	TGCTATTGAT	GAGCGAGGCC	GGCTGCTGAC	420
AACAAGTGTG	GGCAGCTGGG	CGTTGGGAAC	TACAAGAAGC	GTCTGGGAAT	480
					490
	TTCTTATGT AAAAGGTGG CATTTCTGT TGGGTCTGA ACACAACGT	TTCTTATGT GTGTTTCAGG AAAAGGTGG ATGTTCCCAA CATTTCTGT TGACCCAGTC TGGGTCTGA ATCAGTGCAT ACACAACGT CCTTTACCTT CAGGCAAGA CTCACACAGC	TTCTTATGT GTGTTTCAGG ACGACTGGGT AAAAGGTGG ATGTTCCCAA GGCCTTGATT CATTTCTGT TGACCCAGTC AGGCAAAGTG TGGGTCTGA ATCAGTGCAT GTCGGGAATT ACACAACGT CCTTTACCTT GGCCAAACAG CCAGGCAAGA CTCACACAGC TGCTATTGAT	TTCTTATGT GTGTTTCAGG ACGACTGGGT TTGGATTCAG AAAAGGTGG ATGTTCCCAA GGCCTTGATT ATTGTTGCAG CATTTCTGT TGACCCAGTC AGGCAAAGTG CTGGCCTGTG TGGGTCTGA ATCAGTGCAT GTCGGGAATT ATCAACCATG ACACAACGT CCTTTACCTT GGCCAAACAG TTGTCCTTTT TCAGGCAAGA CTCACACAGC TGCTATTGAT GAGCGAGGCC	TCATGGCCT ACTTACAGAA CCTATTCACT GGGAAGGAAG CCCTCATTAT TTCTTATGT GTGTTTCAGG ACGACTGGGT TTGGATTCAG AAGAGGATTA AAAAGGTGG ATGTTCCCAA GGCCTGATT ATTGTTGCAG TTCAATGTGG CATTTCTGT TGACCCAGTC AGGCAAAGTG CTGGCCTGTG GACTCAATGA ACACACACGT CCTTTACCTT GGCCAAACAG TTGTCCTTTT ATAAGATCCG CAGGCAAGA CTCACACAGC TGCTATTGAT GAGCGAGGCC ACAAGTGTG GGCAGCTGGGAAC TACAAGAAGC GTCTGGGAAT ACAAAGTGTG GGCAGCTGGG CGTTGGGAAC TACAAAGAAGC GTCTGGGAAT

- (2) INFORMATION FOR SEQ ID NO:240:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

the second secon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GAATTCGGCC T	TCATGGCCT	ACTTCTGGAC	${\tt TCTATAGAAC}$	CCACTGCCTC	CTGATGAAGT	60
CCCTACTGTT C	CACCCTTGCA	GTTTTTATGC	TCCTGGCCCA	ATTGGTCTCA	GGTAATTGGT	120
ATGTGAAAAA G	STGTCTAAAC	GACGTTGGAA	TTTGCAAGAA	GAAGTGCAAA	CCTGAAGAGA	180
TGCATGTAAA G	SAATGGTTGG	GCAATGTGCG	GCAAACAAAG	GGACTGCTGT	GTTCCAGCTG	240
ACAGACGTGC 1	TAATTATCCT	GTTTTCTGTG	TCCAGACAAA	GACTACAAGA	ATTTCAACAG	300
TAACAGCAAC A	AACAGCAACA	ACAACTTTGA	TGATGACTAC	TGCTTCGATG	TCTTCGATGG	360
CTCCTACCCG T	TTTCTCCCAC	TGGTTGAACA	TTCCAGCCTC	TGTCTCCTGC	TCTAGGATCC	420
TCGAG						425

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GAATTCGGCC TT	CATGGCCT AAG	CAGAACT .	AATTTGCTAA	GTCTTTTGTT	TAGTCCTGCA	60
AGACTGATGC TT	TAATACACA GTO	CTGTTCTC	CTGTGTCTAG	GTCAGGAACT	CCAGTTTGCT	120
TTTCTGTTTT G	GTCCTGGT AGO	CAGCTGTT	GAGTAACTTT	CATTGGAGGT	TGGGAAGGAA	180
GTGAGGAGAA AG	STGTTCTTG TT	PAGTGTTT	TATTTCCTAT	AATAGGATGC	TGCCTAACCC	240
AGTTCATCTC T	ATGTCCTGT TC	ACTGAATA	TTCCGGGTAA	TTGAAAGAAA	ATATAATGGA	300
TGGGCTCCAT TX	AAAACCAGC TC	AAAAAAA.	ATTCTTGTCA	GTAAAGATTT	CTTGTCAAGA	360
TGTCTTGGAT TO	CACTTTTG TTC	GAGGAAAG .	ACAGTGTAAA	TAGTTAAAGA	ATGTTGATAA	420
AATTGAAACA TI	TTGGTTGTG GA	ATTGTGTG	TGGTACTCGA	G		461

- (2) INFORMATION FOR SEQ ID NO:242:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GAATTCGGCC	TTCATGGCTT	ATGGACAAGG	AAGCATTCAG	AGCATGGTGT	CATCTGACTC	60
CACATCACCA	GATTCTTCTT	TAACAGAAGA	ATCACGTTCT	GAGACAGCCA	GTAGTTTATC	120
CCAGAAGATT	TGTAATGGGG	GATTATCTCC	TGGTAACCCA	GGAGATTCTA	AGGACATGAA	180
GGAAATTGAG	CCCAATTATG	AAAGTCCCTC	TAGTAATAAT	CAGGATAAAG	ATTCATCACA	240
GGCTTCCAAA	AGCTCAATAA	AAGTTCCAGA	GACCCACAAA	GCAGTCCTTG	CTCTCCGATT	300
AGAAGAGAAA	GATGGCAAGA	TTGCTGTACA	AACTGAGAAG	GAAGAAAGTA	AAGCCTCTAC	360
AGATGTTGCT	${\tt GGGCAAGCAG}$	TAACCATAAA	CCTTGTCCCC	ACAGAAGAGC	AAGCAAAACC	420
TTACCGAGTT	GTGAACCTGG	AACAGCCATT	GTGCAAGCCA	TATACTGTCG	TGGATGTGTC	480
AGCAGCCATG	GCCAGTGAGC	ACCTCGAG				508

- (2) INFORMATION FOR SEQ ID NO:243:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GAATTCGGCT	TCATGGCCTA	GGTTTTCTGT	ACATGGAGAT	TAAACTGTCT	TCCAAAGTGA	60
AGAGTTTATT	${\tt GTTCTAGATC}$	TTGAGCACAA	AGGTTGGTAT	ACGTTAATAA	AAAAAATAGC	120
AAGGGAAGAA	AATCATTTCC	TTCATACCAA	GTAAGAGAGC	ACTTATCATG	GTAGGCACTG	180
GCTTTGCAAT	TATGAGACCA	GTAGTAGAAA	TAGCTTTAGT	TTCCTCAATT	TTCCTGGAGT	240
ATTCTTCAGA	CTTTCTTTAC	ACTGCTCAAG	GTGGGGCGAG	TGGCAGGGCG	GACCCTGGCG	300
ACCTGACGCT	GCGGAGGCTC	GAG				323

- (2) INFORMATION FOR SEQ ID NO:244:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

GAATTCGGCC	TTCATGGCCT	AGCTTCAGTA	GCAAATAAGG	ACATCATCTG	CTATAACCTA	60
CAAGCAGTTG	GACAGATATT	CTACATTTCC	TCATTTCTCT	ACACCGTCAA	TTACATCTGG	120
${\tt TATTTGTACA}$	CAGAGCTGAG	GATGAAACAC	ACCCAGAGTG	GACAGAGCAC	ATCTCCACTG	180
GTGATAGATT	ATACTTGTCG	AGTTGGTCAA	ATGGCCTTTG	TTTTCTCAAG	CCTGATACCT	240
CTGCTATTGA	TGACACCTGT	ATTCTGTCTG	GGAAATACTA	GTGAATGTTT	CCAAAACTTC	300
AGTCAGAGCC	ACAAGTGTAT	CTTGATGCAC	TCACCACCAT	CAGCCATGGC	TGAACTTCCA	360
CCTTCTGCCA	ACACATCTGT	CTGTAGCACA	CTCGAG			396

- (2) INFORMATION FOR SEQ ID NO:245:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GAATTCGGCC	TTCATGCTTA	GCCTCAGCTC	TTTCTTCTGG	GTTGTTTGTA	TTTTCTTTTC	60
TGTCCCAAAC	AGTTTCCCCC	ACAAAAAGAA	CTTTATGTCT	TTCTCTGTCT	TCCCTCAGTC	120
CTTCCAGTCA	GCAGCCTGTG	ATTGGGCTTT	TCCCCTCAGA	AACGAACAAT	CCAGAACCCA	180
CTGTTTAAAA	CAACTGTATT	TTGCCTTGGG	AAGTCCCATT	GCCTTCCCTG	AAAACATTAA	240
ACATTCCTCC	GATCCCCAGC	CTGAGTCTCT	CTGTCTCTGG	GCCCCATCCT	GCTCCACAGC	300
AGGGCTGGTG	TGTCCAGCAC	AGAGTGACCC	TCCGATGCCC	TTTCCCACCC	GCCGCCCTGC	360
CTCCCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:246:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAATTCGGCC	TTCATGCCTA	GAGAACTTGA	AGCTTTGCGG	CAGGAATTTA	AAAAGAAAGA	60
CAAGACGTTG	AAAGAGAATT	CCAGAAAGTT	GGAGGAAGAA	AATGAGAATC	TCCGAGCAGA	120
GCTACAGTGT	TGTTCTACAC	AACTGGAATC	CTCTCTCAAC	AAATACAACA	CCAGCCAGCA	180
AGTCATCCAA	GACTTGAATA	AAGAGATAGC	CCTTCAGAAG	GAGTCCTTAA	TGAGCCTGCA	240
GGCCCAGCTG	GACAAAGCTC	TGCAGAAGGA	GAAGCACTAT	CTCCAGACTA	CCATCACCAA	300
AGAAGCCTAT	GATGCATTAT	CCCGGAAGTC	AGCCGCCTGC	CAGGATGACC	TGACACAAGC	360
CCTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:247:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GAATTCGGCC	TTCATGGCCT	ACGGCTTCAT	AGTAACTCTT	TGCCATATCT	CTAGCCAGCT	60
GCATAAAACG	TTCGCCATCA	GATGGAGACA	AAAGGTTTAA	AATACGCCTA	TAACCATCCA	120
TGGCCATTTT	ATGATCACCC	ATCTGTTCAT	AAAGGCTTGA	TCGCTCCCAC	AGATAACGGA	180
CATTAGTAGG	TTCATATTTA	AGAGCTTTTG	TATAGCAAAA	AATAGCCTGC	TTAATATTGT	240
CTTGTTCCAG	AGACATTTCT	GCCAGTCTAA	CCCATTCTTC	TGTGTCACTG	GGATTTAAAT	300
GCGCAGCAAT	CAACTCAAAC	TGCAATGATT	TTTCCATGTC	ACCTTGGTCC	TCATATATCA	360
TGGCTAGAGT	AGAGAATGGC	TCATAAGCCA	GAGGAGCTTG	TCTTATGATT	TCCATGCACA	420
TCAATATCGC	CTCTTCACGT	TCTCCTCGAG				450

- (2) INFORMATION FOR SEQ ID NO:248:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAATTCGGCC	TTCATGGCCT	AACGAAACTG	ACGTCTACCT	CATGGGGCTG	CTGTGTGGGT	60
TTGGGAGGCA	AAAATCTATG	AAGGGTTTTT	TGAAATCCCA	TAGGTGCCAC	ATCTATGAGA	120
TGTTTGATAA	ATGTGAATAT	GCTTTTACAT	TTGGGCTTAT	CTAATTTGCA	ATAAGAGAGC	180
CTCTCTCTAT	CAACACCAGC	TTCTCTCTCG	GGCTGTTTGC	TCAGGGAAGG	CAAGAAAGCC	240
ACGTGCTGGC	CCTCTGCCTT	CTCTAAAGTG	CTGTTGGAGC	ATGGAGGAGC	TGGAGGAGAT	300
GGGGATGGAC	TGACAGCTAA	GAGGGCGGCT	GCTGGGACTA	GATAGTGGAT	GAAGAAAGAA	360
GGACGAGGAA	GCCGTGGGGC	AGCCTCTTCA	CATGGGGACG	AACTCGAG		408

- (2) INFORMATION FOR SEQ ID NO:249:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GCCCATGACA (GAGAGCAGTG	CCAAAGACAT	GGCGTACGAA	CATCTGATAG	ATGACTTATT	60
GGCTGCTCAG	AAGGAAATTC	TGTCTCAGCA	GGAAGTCATC	ATGAAGTTAA	GGAAAGACCT	120
TACCGAAGCC (CACAGCAGAA	TGTCGGATTT	GAGAGGGGAG	CTAAACGAGA	AGCAGAAGAT	180
GGAACTGGAG (CAGAACGTGG	TGCTGGTCCA	GCAGCAGAGC	AAGGAGCTGA	GTGTGCTCAA	240
GGAGAAGATG (GCCCAGATGA	GCAGCCTGGT	AGAAAAGAAA	${\tt GATCGGGAGC}$	TGAAGGCCCT	300
TGAGGAGGCA (CTCAGGGCTT	CCCAAGAGAA	ACACAGACTC	CAGCTGAACA	CAGAGAAGGA	360
ACAGAAGCCC (CGGAAGAAGA	CCCAGACGTG	TGACACCTCT	GTGCAGATAG	AACCCGTCCA	420
CACTGAGGCC :	TTCTCCAGCA	GCCAAGAGCA	GCAATCCTTC	AGCGATCTAG	GGGTCAGGTG	480
CAAAGGGTCC (CGGCACGAGG	AGGTCATTCA	GCGTCAGAAA	AAGGCCTTAT	CTGAACTTCG	540
AGCGCGAATT A	AAAGAACTCG	AG				562

- (2) INFORMATION FOR SEQ ID NO:250:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GAATTCGGCC	TTCATGGCCT	ACCCAAACAG	ACAGAAAACG	CCACGAGGCA	AGTGTAGTCT	60
CTCACAGCCT	GGACCCTCTG	TCAGCAGTCC	ACATAGCAGG	TCCACAAAAG	GTGGCTCCGA	120
TTCCTCCCTT	TCTGAGCCAG	GGCCAGGTCG	GTCCGGCCGC	GGCTTCCTGT	TCAGAGTCCT	180
CCGAGCAGCT	CTTCCCCTTC	AGCTTCTCCT	GCTCCTCCTC	ATCGGGCTTG	CCTGCCTTGT	240
ACCAATGTCA	GAGGAAGACT	ACAGCTGTGC	CCTCTCCAAC	AACTTTGCCC	GGTCATTCCA	300
CCCTATGCTC	GNG .					313

- (2) INFORMATION FOR SEQ ID NO:251:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GTCTTGACAA	AACCTAACTT	GCGCAGAAAA	CAAGATGAGA	TTGGCATGGC	TTTATTTGTT	60
${\tt TTTTTTGTTT}$	TGTTTTGGTT	TTTTTTTTT	${\tt TTTTGGCTTG}$	ACTCAGGAGA	TCCCTCCCCG	120
GGGCTCCCGC	CGGCTTCTCC	GGGATCGGTC	GCGTTACCGC	ACTGGACGCC	TCGCGGCGCC	180
CATTTCCGCC	ACTCCGGATT	CGGGGATCTG	AACCCGACTC	CCTTTCGATC	GGCCGAGGGC	240
AACGGAGGCC	ATCGCCCGTC	CCTTCGGAAC	GGCGCTCGCC	CAACTCTCGA	G	291

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

CGGGAAA	TGA	AGCGGAAGCA	GGCGGAGTCC	GAGAGGCCCA	TCTTGCCAGC	CAATCAGAAG	60
CTCATTA	CTT	TATCAGTGCA	AGATGCACCC	ACAAAGAAAG	AGTTTGTTAT	TAACCCCAAC	120
GGGAAAT	CCG	AGGTCTGCAT	CCTGCACGAG	TACATGCAGC	GTGTCCTCAA	GGTCCGCCCT	180
GTCTATA	ATT	TCTTTGAATG	TGAGAACCCA	AGTGAGCCTT	TTGGTGCCTC	GGTGACCATT	240
			TGGAACTGCA				300
GCCCGAG	CTA	CACTGGAAAT	CCTCATCCCT	GACTTTGTTA	AACAGACCTC	TGAAGAGAAG	360
CCCAAAG	ACA	GTGAAGAACT	CGAG				384

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GGGACGTTGG	TGTTGAGGTT	GGCATACGTA	TCAAGGACAG	TAACTACCAT	GGCTCCCGAA	60
GTTTTGCCAA	AACCTCGGAT	GCGTGGCCTT	CTGGCCAGGC	GTCTGCGAAA	TCATATGGCT	120
GTAGCATTCG	TGCTATCCCT	GGGGGTTGCA	GCTTTGTATA	AGTTTCGTGT	GGCTGATCAA	180
AGAAAGAAGG	CATACGCAGA	TTTCTACAGA	AACTATGATG	TCATGAAAGA	TTTTGAGGAG	240
ATGAGGAAGG	CTGGTATCTT	TCAGAGTGTA	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:254:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

GAGTTTGTTG	GGCTTACCTT	ATTTTAATTA	AAAAGAAGTC	GGGGCTACCA	GGGGTTTCAG	60
ACGTGCTCGA	TGGACACGTG	ATTTGTAAAC	AGCCAAGATT	CTGGGGGACG	GGGGGGTGCC	120
TCGGTGGGGT	TGACATTTGA	GTTACAGGGA	CTTAATAATG	GCCAGCCTTT	CACATCCCAT	180
GGGAAACCGC	CCCCCCGGGC	CTTGGAGAAT	GGGGGTCCAA	GTGCCTATCC	CCCTTTGGAT	240
GTAAAATTCA	TCGTTAGTAA	ACATCATCCG	CCCAGCAACA	AGCAAAGCAC	ATCGCAAGAT	300
TAAAACAAAG	AATCCGCCGT	GAACAGAAGG	CCTCCATCTC	TGCTCTCAGG	CAGGTGTCCT	360
TCAGGGAGGA	GCCTCAGGCA	GCTGTTCTAA	CCCTGCTGCC	AACGCCTGGG	CTGTTTCTGC	420
CGACAATCTT	CTATTTCTCT	AAAAGAGTAC	GCTGAACAGC	TGGCTCTGCG	TTGATTGAAT	480
TCTAGACCTG	CCTCGAG					497

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GAATTCGGCC	TTCATGGCCT	AGAGAACCGT	TGCTTTTCCG	AGTTGCTCTT	CTTCCAGGCT	60
CCGTTGGTGG	TCGGCATGGC	CCGTGGAAAT	CAACGAGAAC	TTGCCCGCCA	GAAAAACATG	120
AAGAAAACCC	AGGAAATTAG	CAAGGGAAAG	AGGAAAGAGG	ATAGCTTGAC	TGCCTCTCAG	180
AGAAAGCAGA	GGGACTCTGA	GATCATGCAA	GAAAAGCAGA	AGGCAGCTAA	TGAGAAGAAG	240
TCTATGCAGA	CAAGAGAAAA	GTGATGACTG	GCTATTTGGA	AAACCTGGGT	GCTACTGCCA	300
ACTGGGTGTA	TCATAAGCTC	TAAGATCAAG	ATTTTGTAGA	GTGGACAGTC	ATTACATATG	360
TTATAACTTA	TCCTTTAAAA	ACTATTTTAA	ACTTTATCCT	TTCAGCTTTA	CTTAGTGCGA	420
TGTTTTAGAA	GCAGTCTTCA	AAGAATAAAA	CACTAACCAT	GCTGCTCGAG		470

- (2) INFORMATION FOR SEQ ID NO:256:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GAATTCGGCC	TTCATGGCCT	AATTTTGTAT	TTTTAGTGGA	GACGGGGTTT	CTCCATGTTG	60
GTCAAGCTGG	TCTTGAACTC	CCAACCTCGG	GTGATCCGCC	CGCCTTGGCC	TCCCAAAGTG	120
CTGGGATTAC	AGGCGTGAGC	CACCGCGCCT	GGCCAGTAGT	TTCTTAACAT	TAAATTATCC	180
GCAAAATGGA	AGAAATACTA	GAGGTCTGTG	AGGATGTTTC	TTCTCTTTCA	GTCTGTTGTG	240
GTGGTTTGTA	GTTTACAGGG	GCTTGGGTAA	CTGGATTTTT	AGGTTTATTA	TTTTAAATAG	300
TAGACTCAAC	ACTATTTTGT	ATTGCAGTAG	AGATCACTTA	TGCAGATCTT	TTTAATACCA	360
TTTCATAGAG	ATTAAGGGTC	ACCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:257:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GAAACAGGGC	TCAAAGAAGT	GGTAACTGCT	GTGGAGGAAA	TGACAAGTAA	ACCAAAACCA	60
GGACAAGAAG	TCTTGGAAGA	CGACCAGGAA	AATACTTTAA	AATATGAGTA	TGAAGAAGAC	120
TTTGAAGTAG	ATGAGGAGAA	ACAAGGTGAA	AAATCTAATG	AAGAAGGACA	GGCTGATGTT	180
CAAATGAATG	GAATACCGCA	GTCACCTTTG	GATGATAAAA	AAGATAATTT	AGACCCTGAA	240
AAAGAGAGTG	AAACCTCATC	ACAGAAGGCA	CCAGATGCCC	CTCACAATCT	CANACATGAG	300
				GIGACAAIGI	GAMAGAIGAG	
AATGATGGAT	GCTCTGAGAG	TGAACGTCTC	GAG			333

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

CACAGTGCTG	GNTCACAACA	AGATGNTCNA	GGTGTCAGCC	GTACTGTGTG	TGTGTGCAGC	60
CGCTTGGTGC	AGTCAGTCTC	TCGCAGCTGC	CGCGGCGGTG	GCTGCAGCCG	GGGGGCGGTC	120
GGACGGCGGT	AATTTTCTGG	ATGATAAACA	ATGGCTCACC	ACAATCTCTC	AGTATGACAA	180
GGAAGTCGGA	CAGTGGAACA	AATTCCGAGA	CGATGATTAT	TTCCGCACTT	GGAGTCCAGG	240
AAAACCCTTC	GATCAGGCTT	TAGATCCAGC	TAAGGATCCA	TGCTTAAAGA	TGAAATGTAG	300
TCGCCATAAA	GTATGCATTG	CTCAAGATTC	TCAGACTGCA	GTCTGCATTA	GTCACCGGAG	360
GCTTACACAC	AGGATGAAAG	AAGCAGGAGT	AGACCATAGG	CAGTGGAGGG	GTCCCATATT	420
ATCCACCTGC	AAGCAGTGCC	CAGTGGTCTA	TCCCAGCCCT	GTTTGTGGTT	CAGATGGTCA	480
TACCTACTCT	TTTCAGTGCA	AACTAGAATA	TCAGGCATGT	GTCTTAGGAA	AACAGAATCT	540
CGAG						544

- (2) INFORMATION FOR SEQ ID NO:259:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GAATTCGGCC TTCATGGCCT ACATCAGCAT CCCTGGGAGC ATCAGAAATG CAGAGCTCAG	60
GCCCGCCCCG GAGCTACCGA ATCAGAACCT ACATTTTACA CACCCCTCAG CTCAGAGCTT	120
GTTTCTCCCT GGATTCCATG GCCCTGTGCT GCTGGCAGCC CGGGGTTAGG GCATTTCGTT	180
GTCACCTGGC GACGGTGAAG CCTAGTTTCC TCCAGAGAGA TTATGCTGCT CTCCATCCAA	240
GTGAAGTGGC AATGGTGCCA GCCTGAGATT TCTGCCCTGA GTTTTAAGTA CGAGAGTGTG	300
GGCTGACAAT AAACTCCTTT ATTCTACCCT CTTCTGTTCT CATAAGGAGA AATTTAAATT	360
CTGGAAGAGA TGAAGCTTGC ATTTACCCAA GAC	393

- (2) INFORMATION FOR SEQ ID NO:260:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

60	AATACCAAAG	AAAAAAAACC	TATTCCTTTA	AAGGGATTGT	AAAGAGGCCT	GAATTCGGCC
120	TTATTCACTT	CAACGTTGTT	CTGTTGATTT	AGCCAAAATT	TGTTGGCCTT	AAGCCTACAA
180	CATTGCAGAA	CAACACAGAA	GACATAAACA	AGAAAATCAA	GCCATGGAAA	CTATCGGGGA
240	CTTAAACTCA	GTGAAGCAAA	TCTTTGGAAA	TAAACCTATT	CAATGGAAAA	GTTTTTAAAA
300	TTTGAATCTA	ATTCCCCTCC	AAGGCGAGTC	CTCAAATCTC	ATATAACCAC	GATAAAGAAA
360	GCATTCTTTG	CATCAGCAGA	TCCAGTAACT	AACAGATTTC	GCCACGGAAT	CCCAACAACA

```
GGCAGTCTAA AACCCACATC TACCATTTCC ACAAGCCCTC CCTTGATCCA TAGCTTTGTT 420
TCTAAAGTGC CTTGGAATGC ACCTATAGCA GATGAAGATC TTTTGCCCAT CTCAGCACAT 480
CCCAATGCTA CACCTGCTCT GTCTTCAGAA AACTTCACTT GGTCTTTGGT CAATGACACC 540
GTGAAAACTC GTGATAACAG TTCCATTACA GTTAGCATCC TCTCTTCAGA ACCAACTTCT 600
CCATCTGTGA CCCCCTTGAT AGTGGAACCA AGTGGATGGC TTACCACAAA CAGTGATAGC 660
TTCACTGGGT TTACCCCTTA TCAAGAAAAA ACAACTCTAC CTACC 705
```

- (2) INFORMATION FOR SEQ ID NO:261:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GAATTCGGCC	AAAGAGGCCT	ACCTTACTTG	AGTCCACAGG	CAAGGCCCAA	TAATGCATAT	60
ACTGCCATGT	CAGATTCCTA	CTTACCCAGT	TACTACAGTC	CCTCCATTGG	CTTCTCCTAT	120
TCTTTGGGTG	AAGCTGCTTG	GTCTACGGGG	GGTGACACAG	CCATGCCCTA	CTTAACTTCT	180
TATGGACAGC	TGAGCAACGG	AGAGCCCCAC	TTCCTACCAG	ATGCAATGTT	TGGGCAACCA	240
GGAGCCCTAG	GTAGCACTCC	ATTTCTTGGT	CAGCATGGTT	${\tt TTAATTTCTT}$	TCCCAGTGGG	300
ATTGACTTCT	CAGCATGGGG	AAATAACAGT	TCTCAGGGAC	AGTCTACTCA	GAGCTCTGGA	360
TATAGTAGCA	ATTATGCTTA	TGCACCTAGC	TCCTTAGGTG	GAGCCATGAT	TGATGGACAG	420
TCAGCTTTTG	CCAATGAGAC	CCTCAATAAG	GCTCCTGGCA	TGAATACTAT	AGACCAAGGG	480
ATGGCAGCAC	TGAAGTTGGG	TAGCACAGAA	GTTGCAAGCA	ATGTTCCAAA	AGTTGTAGGT	540
TCTGCTGTTG	GTAGCGGGTC	CATTACTAGT	AACATCGTGG	CTTCCAATAG	TTTGCCTCCA	600
GCCACCATTG	CTCCTCCAAA	ACCAGCATCT	TGGGCTGATA	TTGCTAGCAA	GCCTGCAAAA	660
CAGCAACCTA	AACTGAAGAC	CAAGAATGGC	ATTGCAGGGT	CAAGTCTTCC	GCCACCCCCA	720
ACACTCGAG						729

- (2) INFORMATION FOR SEQ ID NO:262: .
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 686 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

```
60
GAATTCGGCC AAAGAGGCCT ACTACCATGT CCTCTTGGAG CAGACAGCGA CCAAAAAGCC
                                                                      120
CAGGGGGCAT TCAACCCCAT GTTTCTAGAA CTCTGTTCCT GCTGCTGCTG TTGGCAGCCT
CAGCCTGGGG GGTCACCCTG AGCCCCAAAG ACTGCCAGGT GTTCCGCTCA GACCATGGCA
                                                                       180
                                                                      240
GCTCCATCTC CTGTCAACCA CCTGCCGAAA TCCCCGGCTA CCTGCCAGCC GACACCGTGC
ACCTGGCCGT GGAATTCTTC AACCTGACCC ACCTGCCAGC CAACCTCCTC CAGGGCGCCT
                                                                      300
CTAAGCTCCA AGAATTGCAC CTCTCCAGCA ATGGGCTGGA AAGCCTCTCG CCCGAATTCC
                                                                      360
TGCGGCCAGT GCCGCAGCTG AGGGTGCTGG ATCTAACCCG AAACGCCCTG ACCGGGCTGC
                                                                       420
                                                                       480
CCTCGGGCCT CTTCCAGGCC TCAGCCACCC TGGACACCCT GGTATTGAAA GAAAACCAGC
TGGAGGTCCT GGAGGTCTCG TGGCTACACG GCCTGAAAGC TCTGGGGCAT CTGGACCTGT
                                                                       540
                                                                       600
CTGGGAACCG CCTCCGGAAA CTGCCCCCCG GGCTGCTGGC CAACTTCACC CTCCTGCGCA
CCCTTGACCT TGGGGAGAAC CAGTTGGAGA CCTTGCCACC TGACCTCCTG AGGGGTCCGC
                                                                       660
                                                                       686
TGCAATTAGA ACGGCACATT CTCGAG
```

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 571 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GAATTCGGCC	AAAGAGGCCT	AGGAGAGAGG	AGGTGCTGCA	AGACTCTCTG	GTAGAAAAAT	60
GAAGAGGGTC	CTGGTACTAC	TGCTTGCTGT	GGCATTTGGA	CATGCTTTAG	AGAGAGGCCG	120
GGATTATGAA	AAGAATAAAG	TCTGCAAGGA	ATTCTCCCAT	CTGGGAAAGG	AGGACTTCAC	180
ATCTCTGTCA	CTAGTCCTGT	ACAGTAGAAA	ATTTCCCAGT	GGCACGTTTG	AACAGGTCAG	240
CCAACTTGTG	AAGGAAGTTG	TCTCCTTGAC	CGAAGCCTGC	TGTGCGGAAG	GGGCTGACCC	300
TGACTGTTAT	GACACCAGGA	CCTCAGCACT	GTCTGCCAAG	TCCTGTGAAA	GTAATTCTCC	360
ATTCCCCGTT	CACCCAGGCA	CTGCTGAGTG	CTGCACCAAA	GAGGGCCTGG	AACGAAAGCT	420
CTGCATGGCT	${\tt GCTCTGAAAC}$	ACCAGCCACA	GGAATTCCCT	ACCTACGTGG	AACCCACAAA	480
TGATGAAATC	TGTGAGGCGT	TCAGGAAAGA	TCCAAAGGAA	TATGCTAATC	AATTTATGTG	540
GGAATATTCC	ACTAATTACG	GACAGCTCGA	G .			571

- (2) INFORMATION FOR SEQ ID NO:264:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GAATTCGGCC	AAAGAGGCCT	ACCAAGCAAG	AACAGCTAAA	ATGAAAGCCA	TCATTCATCT	60
TACTCTTCTT	GCTCTCCTTT	CTGTAAACAC	AGTCACCAAC	CAAGGCAACT	CAGCTGATGC	120
TGTAACAACC	ACAGAAACTG	CGACTAGTGG	TCCTACAGTA	GCTGCAGCTG	ATACCACTGA	180
AACTAATTTC	CCTGAAACTG	CTAGCACCAC	AGCAAATACA	CCTTCTTTCC	CAACAGCTAC	240
TTCACCTGCT	CCCCCCATAA	TTAGTACACA	TAGTTCCTCC	ACAATTCCTA	CACCTGCTCC	300
CCCCATACTC	GAG					313

- (2) INFORMATION FOR SEQ ID NO:265:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs.
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

GAATTCGGCC	TTCATGCCTA	GCCTCTGAGT	TCAGCTCAGA	ACACAGATGA	TCTCATTGAT	60
TCCTCACGTC	AACCTTGGGA	AATCTGGGTA	CCCTGGGACG	TCCACACATG	AGGACCGAGG	120
CTCAGGGACA	TCAAGGGACT	GGCCTGGTCC	CAGAAACAGG	GAGTAAAATG	GGAAGTAAAC	180
TCAGTCCCAC	GTCTGCCTGA	CTCCAGAGTT	TGGGCCACTG	AACCATGCGG	CTGCCATCTT	240
GGAGTTCTTT	GAGCTGTGAA	GTGCTGTGCA	TCGTGTGATT	CTGTGTCCCT	TTTGTGCAGG	300
TACCAGGATT	TCTATGCATT	CGACCTGTCA	GGAGCCACTC	GAG		343

- (2) INFORMATION FOR SEQ ID NO:266:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GAATTCGGCC	TTCATGGCCT	ACAGGAAGCA	CAGAAAGACA	AAATTGGAAA	TGTCTAGTTC	60
CATGTTGATG	CCTTCAGAAG	ATGCAGGTGA	ACAAAGAGAG	GCCGGGAAAT	CAGAGCTAGT	120
TGAAACCCAA	CATGTTACCT	TAGAGCCAGA	GCTACCACTG	AGTTCTCTAA	GCACAGTCAA	180
ATCCCAGGAT	TATGCTGAAA	CAGAGCAGGA	${\tt GGTCATTTTA}$	CAAGCTATAG	AGGCCATGGA	240
GGCCACAGAA	GCCCTGGAGG	CCACAGACGC	CATGGAAGCC	ATAGATCAAG	GTAGCATGAA	300
AGATTATGGA	${\tt GATG^TGATCT}$	CTAAGCTGGA	AAGACTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:267:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GAATTCGGCC	TTCATGGCCT	AGGCACCCCT	AGGCGACTCA	GGGTTCGGGG	AGGAGGAGAC	60
CAGACGGGGC	CTTGGCTGGC	ATGGCCTCTT	CACAGGGCTG	CCGTGAAGAA	ACTTCGTGAC	120
AGCGGCGGAG	AGGTGGCCCA	GGAGTGAGAC	AAGCAGGCCC	CGGGCCTTGG	ACTCAGACAT	180
GCTGGGTCCG	GTCAGGCCCG	TGTGGGAACC	AGTGTTTTAG	GGACTGGGTA	CTCTCTTAGA	240
GAAGAACTGA	TGCTAAAGAG	TCAGGAAGAC	ACGAGCGGGC	CAAATAAAAG	AGGAAGAGAG	300
GCCCTCAGGA	CATCATGGCA	CTTACTGCTT	GGATTTGTCT	CCCCGTCCAG	AATTCTGTGG	360
ACTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:268:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GAATTCGGCC	TTCATGGCCT	ACTTGGGAAT	TAACATCTTC	GATAAATCCC	AGAAGTCTTT	60
AAGTGACAGT	AGAGAGCCTA	CAGAGAAGCC	TGGGAAAGCA	GAAAAATCTA	AGAGCCCAGA	120
AAAAGTGTCA	TCGTTCTCAA	ACTCCTCCTC	CAACAAGGAA	TCAAAAGTAA	ACAATGAGAA	180
GTTTCGTACT	AAGAGCCCCA	AGCCTGCCGA	AAGCCCCCAG	TCAGCCACTA	AGCAGTTGGA	240
TCAGCCCACT	GCTGCTTATG	AGTATTATGA	TGCTGGCAAT	CACTGGTGCA	AAGACTGCAA	300
CACCATCTGT	GGGACTCGAG					320

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 542 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GAATTCGGCC	AAAGAGGCCT	${\tt AGGGATATTT}$	ACTGAGGGCC	TACAGGGTGC	CCAATACTGA	60
GCTAGCTAGG	CTCAGGGACC	TGTACACACA	TGCATTCTCC	ATTAGGGTTC	TGCAATCCTG	120
ACACTATTAC	TATCCTCAAG	GACTCTGCGC	ATCCAGACCC	GTCTATTAGT	TAGCAATGAG	180
AACCCCTGCC	ATGGCCAAGT	TACACAAGAA	CACCCTTGCC	CTACCTCTGC	CCCCTGCNGA	240
TCTGAAAGTA	ACCTGGTCTG	AAAGAGAAGT	AAAGATGTGG	CTGTCCCTGG	GTGCTAGGGA	300
GAGAGGCCTG	TTGACAAAGC	CACCAGCTGT	CTCCAGTCAG	AGCCAGGGAG	ACAGGCTTCT	360
CCCTGCACCA	TCCGCACTGC	CATAGACACA	GCAGCCAGCA	ACAGCACTTG	GACCATTACG	420
GAGTTCCAGG	CCCAGTCTCC	AACTGACCTC	CCTCCTGCTC	CAGCTGCCCA	TGCTAACAAG	480
AGCCAGGGCA	CAAGACCTCA	CTTGGAACAA	GTACCAGGCA	GAAGAGAGCA	TNACCNGCCG	540
GT						542

- (2) INFORMATION FOR SEQ ID NO:270:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 613 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GAATTCGGCC	AAAGAGCCTA	GTCGATTGAA	TTCTAGACCT	GCCTCCTTTT	CCACTTGAAT	60
TGTTAAATTG	TTTACTCCAG	CATCTTTAAG	TATTCCTGTA	ACCTGCTGTA	CTATTCTTTG	120
TTCTAGCACA	TCAGATGTCA	CCTGTATATG	AATTGTTCCT	GCCACAATAC	TAGCAGAATG	180
ACGCCAAAAA	TGTGGGTCTC	GGTATGATAT	TAATCCTTCA	ATTTTCTGTA	TCTTTTCTAA	240
AGCAATATGT	AGTTCTTTTT	CATATTCTGG	TGGCAATCTC	AGGAGTAGAA	CCTGGCAGGC	300
ATCTTTAATC	AGTGGAACAA	CACTGAGAAA	TATTAATATA	GCAATAAAAA	GAGAACAGAG	360
TGGGTCAGCG	ATGAACCATC	CAAACTGCTC	TATAAGAACT	GTGGATACGA	TCACACCAAT	420
GCTGCCAAGA	GTATCTGCCA	AAACATGTAG	AAATACACCC	CTCATGTTAG	CATTCATGCC	480
TCCACCCGCA	GATCCGTGGC	TGTGACCATG	CCCATGGTCA	CTGTGTCCAT	GCATATGATG	540
TGAATGGCTG	TGATCAGATG	AGTGACAGCT	TCCTTGAGCC	TAAACCGTCG	ATTGAATTCT	600
AGACTGCCTC	GAG					613

- (2) INFORMATION FOR SEQ ID NO:271:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 763 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GAATTCGGCC	AAAGAGGCCT	AGTCTGGTTC	TTGCTTGATC	TGAGAGCTTC	CATCAGTCTC	60
TTTTATTTCT	TCTGTGGCTG	GAACTTCCAA	CTGGCTTGGT	TCAGCTGATT	CTTGTATCAC	120

```
GGGGCCTTCT GACTCACTCT GATCAACCAG CTGGTTATTA ATCACAAGTC CTGGAAATGG
                                                                      180
TCTAATGACC GTGAATTTGA TAAACTCGGC AGAGTCTAAG ATCCTTCTCA TGGAGCTGAT
                                                                      240
TTCCAGGTAG CTGGGGGCTT TGAAAGGACA CCCCCGGGGG CATGCCATCA ACTACCACAC
                                                                      300
AGCCAGGGTT AATTGTGATT TCCCTGTAGG GAACTTTCAC AGGAAAACCC ATACCAATAG
                                                                      360
CTTCACCAAA TTTCCGACTA AAGAGGTCAT TCACTTGTTC TCTTAGCTGT CTAGCTTTTT
                                                                      420
CAACTITCGA GAGTCTTTCA TTATCATCAT CTGGAATTGT CACCTGAATG ATGTTAAGGT
                                                                      480
CTTCAACACC TGATGCAGTA GTATTAACAT TGGGTGATGA ATTTATTTT CTGGGAGGGC
                                                                      540
TCTTAGAGGA GGTGCTCTCC TTAATCGCCG TCTCAAACAT TTCGGGCTTT TTAATGATGA
                                                                      600
ACTTAATTTT GGCTTTGTTT CTGAGTATCT TCTCCAGCCT CGGAATGCCA AAAGTCGATG
                                                                      660
GTCTTCGGAA TGGCACACCC TCAGGTAAGC CTTCCACATA AAAGTCTTCC GGGAAAGACT
                                                                      720
CAAATAACGC GAACGGCACC TTCACAGCTT GTTTAAGGCC AAG
                                                                      763
```

- (2) INFORMATION FOR SEQ ID NO:272:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GAATTCGGCC AAAGAGGCCT AATTAAGGAA ATACTTTGCA TAAATTAATC AGCCCCACAG
TATTTCCTTA ATAAGAATAA AATGAATTTA ACACTGATTC TG 102

- (2) INFORMATION FOR SEQ ID NO:273:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 565 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GAATTCGGCC AAANAGGCCT	ACNCCAGTCA	AGGAAAGTCA	AGTNGCAAGA	AGGAANTGTC	60
TAAAAGAGAT GGCAAGGAGA	AAAAAGACAG	AGGAGTGACG	AGGTTTCAGG	AAAATGCCAG	120
TGAAGGGAAG GCCCCTGCAG	AANACGTCTT	TAAGAAGCCC	CTGCCTCCTA	CTGTGAAGAA	180
GGAAGAGAT CCCCCTCCAC	CTAAAGTGGT	AAACCCACTG	ATCGGCCTCT	TGGGTGAATA	240
TGGAGGAGAC AGTGACTATG	AGGAGGAAGA	AGAGGAGGAA	CAGACCCCTC	CCCCACAGCC	300
CCGCACAGCA CAGCCCCAGA	AGCGAGAGGA	GCAAACCAAG	AAGGAGAATG	AAGAAGACAA	360
ACTCACTGAC TGGAATAAAC	TGGCTTGTCT	GCTTTGCAGA	AGGCAGTTTC	CCAATAAAGA	420
AGTTCTGATC AAACACCAGC	AGCTGTCAGA	CCTGCACAAG	CAAAACCTGG	AAATCCACCG	480
GAAGATAAAA CAGTCTGAGC	AGGAGCTAGC	CTATCTGGAA	AGGAGAGAAC	GAGAGGGAAA	540
GTTTAAAGGA ATAGGAAATC	TCGAG				565

- (2) INFORMATION FOR SEQ ID NO: 274:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 188 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

GAATTCGGCC AAAGAGGCC	T ACTTAAATCA	AGGCCAAAAC	TAAGGATTTA	GGTAGAGTGT	60
ATTAGCCTTT CAATACCTC	C TTATTAAACA	GTTGTTTTCA	TACTTTTCAA	AGGTGTGTAG	120
AAGTTTTGTA AATAAATTT	T CTGATAGGAT	AAACTAGATT	CCCTATGATC	TCTTATTTAT	180
TTATCATT					188

- (2) INFORMATION FOR SEQ ID NO:275:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GAATTC	GCC	AAAGAGGCCT	AGTCCGTGAT	GCGTACACAC	CTGTCGAGCA	CGAGCTCCTC	60
TAGGCGC	TGC	${\tt AGGTCGCAGG}$	CCACGTACTC	CAGCGCCATG	TCGGTGATNC	GTGGGCACCA	120
CGAGAGC	STCA	AGGNTGCGCA	GCTTGCGCAG	GTTCTCGGCC	ACGAGCTCCA	CGCCGTCGTC	180
GGTGAC	TTG	GAGCAGCCCG	AGAGGCTGAA	CGCGGTGAGG	TTGGGCAGGN	TGTGCACCAC	240
GTTGAC	CACG	CCGTGGTTGG	TGATCTCCCA	GCAGGAGAGC	AGGCGCAGCG	TGTGCGTGCT	300
GTGGCC	TGG	CGCGCCGTGA	AGTAGGCCAG	CGCCGTGTCC	GTCACGTGGT	AGGCCTGCAG	360
GCTCAG	TCC	GCCAGGTTGG	GCAGCAGCTG	CGAGATGGCC	GCGATGGCGT	CGTCGGCCAC	420
GTTGAT	CAG	TCACTCACGC	TCAGCGAGGT	GATGCGCGCG	${\tt CTCAGGCTGG}$	ACCACAGCCC	480
GGCCTCC	GTG	AAGTCGTTGC	AGCCCGACAG	CTCCAGACGC	ACCACGCCCT	GCATCTGTTC	540
AAGCATA	AACC	TCGAG					555

- (2) INFORMATION FOR SEQ ID NO:276:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

GAATTCGGCC AA	AGAGGCCT ACAGTGAA	TA ATCAGAAGTC	AGTTTGGGAG	AAGTCAAAAT	60
GGACACAATC TT	CTTGTGGA GTCTTCTA	TT GCTGTTTTT	GGAAGTCAAG	CCTCAAGATG	120
CTCAGCTCAA AA	AAATACCG AATTTGCA	GT GGATCTTTAT	CAAGAGGTTT	CCTTATCTCA	180
TAAGGACAAC AT	TATATTTT CACCCCTI	GG AATAACTTTG	GTTCTTGAGA	TGGTACAACT	240
GGGAGCCAAA GG	AAAAGCAC AGCAGCAG	AT AAGACAAACT	TTAAAACAAC	AGGAAACCTC	300
AGCTGGGGAA GA	ATTTTTTG TACTGAAG	TC ATTTTTCTCT	GCCATCTCAG	AGAAAAAACA	360
AGAATTTACA TT	TAATCTTG CCAATGCC	CT CTACCTTCAA	GAAGGATTCA	CTGTGAAAGA	420
ACAGTATCTC - CA	TGGCAACA AGGAATTI	TT TCAGAGTGCT	ATAAAACTGG	TGGATTTTCA	480
AGATACAAGG CT	CGAG				496

- (2) INFORMATION FOR SEQ ID NO:277:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

GAATTCGGCC	AAAGAGGCCT	ACACCCAGAG	ACTGTAATTT	GTGTAGTTTT	TCTTTTTAA	60
CTTAAAGACA	ACTTTAAAAA	ATACTTACAT	TAATGTTTTT	TATATTCATA	GGTGGGTATA	120
TTCGCCTCAT	TCAAATGGCA	GTAGCCTTGG	CTCACATAAG	ACATGTTTCA	TGTGATCTGT	180
ATCCTGGCAT	ACCAGTTATA	TTTTGTGGGG	ACTTTAATAG	TACACCATCA	ACAGGAATGT	240
ATCATTTTGT	CATCAATGGC	AGCATTCCAG	AGGATCATGA	AGACTGGGCT	TCCAATGGGG	300
AGGAGGAAAG	ATGCAATATG	TCTCTTACAC	ATTTCTTCAA	GCTGAAAAGT	GCTTGTGGTG	360
AACCTGCTTA	CACAAATTAT	GTTGGTGGCT	TTCATGGATG	TCTAGATTAC	ATTTTCATTG	420
ACTTAAATGC	${\tt TTTAGAGGTT}$	GAACAGGTGA	TTCCATTACC	TAGTCATGAA	GAAGTTACCA	480
CTCCACTCGA	G					491

- (2) INFORMATION FOR SEQ ID NO:278:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GAATTCGGCC	AAAGAGGCCT	ACAGAGAACA	GATAAAAATA	AGCCTGTGGA	ATGACCACTT	60
TGTGGAATAC	GGCAGAACCG	TGTGTATGTT	TCGCACAGAG	AAGATTCGGA	AGCTCGTAGC	120
CATGGGCATC	CCTGAATCTT	TGCGAGGGAG	ACTCTGGCTT	CTCTTCTCAG	ATGCGGTGAC	180
GGATCTTGCC	TCACACCCTG	GTTACTACGG	GAATCTGGTG	GAGGAGTCCC	TGGGGAAATG	240
CTGCCTGGTA	ACCGAGGAGA	TAGAACGAGA	CCTGCACCGC	TCCCTGCCAG	AGCACCCCGC	300
CTTCCAGAAC	GAAACGGGAA	TTGCTGCTTT	GAGGAGAGTC	TTGACGGCCT	ATGCCCACCG	360
GAGCTCGAG						369

- (2) INFORMATION FOR SEQ ID NO:279:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GAATTCGGCC	AAAGAGGCCT	ACTCTCCCTT	TCCACTCCCT	${\tt GGTGTTCCCA}$	GGAGTGAGAT	60
GAGGGTGGAG	GGGCCCAGCA	CAGCACCTTC	AACCTCAGGA	TGAGAGAGGC	CCTTTCACAA	120
AACTCTAAGG	CAGGGGAACA	GGAAACAGAG	AAAGCCGGAG	AACCCCAGGA	GGGCCCCAAG	180
AGCGGATTCT	GGTGATTATT	AATGTGCTTG	CCCAATGAAG	AAAGAATACT	GGCACTCTCT	240
AGGTATGATG	AGAGCAGACA	GCAAACGTGG	GGCCTGTCTA	CAGTGATTCG	CTACCCCAAT	300
GTATGGTCAT	CCACGTTAGA	AGCAGCAGTG	AAAGGCGTGT	TGCTTTTCAT	TATTAACTTC	360
AAATCCCAGT	CCCTAAACCA	GCTCTTGACG	CCCCTCTGTC	AGGTGCTAAT	CCTGGAAACT	420
GGAGGCCACC	TGGTCTCCAC	TTTAGGTGAG	GAAAACCTGG	GAGAAGCCAT	CAGACTGCAC	480
CTGTGGCATG	AGATGCTTTG	AGACAGGTCA	AGAGGAGGAG	CTCTCGAG		528

- (2) INFORMATION FOR SEQ ID NO:280:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:	
GAATTCGGCC AAAGAGGCCT ACAGTGTCGG AGTAGATTTG AAACTGGAGG TGAAGGTAGG AGTAAGTGAT AGATTTTAGA ATTAGTGCTC AGAGCTGAAA TATCCAGTCC GTGAACTTAG AGGCCAGCCT TCATACCACT GTGATGACAG GAACTACCCT AATCTTTTCT GTCCTTTTCT CTCTGCTGTC CCTCGGGCTG CCAGGCCAGC AGCAACACCC ACAGGTAATC TCCCCGCTGA CTCCATCCAC TTGCTCTGCC CTCTGCCCTC TCTGTGCCCC GTTGCACCTG AGCGTACACC CCAGCAGTGG CATCCAACTC GAG	60 120 180 240 300 323
(2) INFORMATION FOR SEQ ID NO:281:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 337 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:	
GAATTCGGCC AAAGAGGCCT ACTCAGTCAG TACCATGCCA GTTACCTTTT TTCCTTGTGA CTTAATGAAT TGGATTTTCC TCAATCTGTT ATTTGTAGGA GGTTTGTATG GGGCCAGGGT AGATTTCCAG ATTTCTGCCT CAGAGGTAGT CTTTTTCACA TATGACACCT GGGTGTTT CTCTGTGTGG CCACAAGTCT TCTGCCTCC TAAAAAAATG TCTAGACCTT CTAGAAGGTC TTTTGCCGCT AATTCTGAAC TTTCCACTCC TTCCTTTGCA GCTGTGATTG GAGGGACATG GCTCCAGCAT GCCAATGTAA ACCACCGCCC CCTCGAG	60 120 180 240 300 337
(2) INFORMATION FOR SEQ ID NO:282:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 194 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:	
GAATTCGGCC AAAGAGGCCT AGGCTCTTCC ACTTAATTTC ATACTTTCAG GTCTGGATGC CCATTTTAAT TCTTCTGAAA GCATGCCTCC TTCTGGCTTC AGGACTCCAT CTCCAGCCTT ATGATCTAAA AATAATGGAA AATTACCCGG TATCGTTAGA GCTACACCAA AATTGCATTG AGCCAAAACT CGAG	60 120 180 194
(2) INFORMATION FOR SEQ ID NO:283:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 296 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GAATTCGGCC	AAAGAGGCCT	AAAATCATCA	TATTCATAGA	GATATTAAAA	GTGCAAATAT	60
CTTACTGGAT	GAAGCTTTTA	CTGCTAAAAT	ATCTGACTTT	GGCCTTGCAC	GGGCTTCTGA	120
GAAGTTTTGC	CCAGACAGTC	ATGACTAGCA	${\tt GAATTGTGGG}$	AACAACAGCT	TATATGGCAC	180
CAGAAGCTTT	GCGTGGAGAA	ATAACACCCA	AATCTGATAT	TTACAGCTTT	GGTGTGGTTT	240
TACTAGAAAT	AATAACTGGA	CTTCCAGCTG	TGGATGAACA	CCGTGAACCA	CTCGAG	296

- (2) INFORMATION FOR SEQ ID NO:284:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GAATTCGGCC	AAAGAGGCCT	AGCAACATCC	ACGCAGCTGC	TCATCAGGTA	CGAGTGCTTC	60
CATATCCATT	TACCCACCAT	TGGCAATTTG	AAAGGACCAT	CCAGACCCCC	ATAGGATCCA	120
CATGGAACAC	CCAGAGGGCT	TTCCAAAAGC	TGACTACTCC	CAAGGTCGTC	ACCAAGCCAG	180
GCCATATCAT	TAACCCCATA	AAAGCAGAAG	ACGTGGGCTA	CCGGTCTTCC	TCAAGGTCGG	240
ACCTGTCTGT	CATACAGAGG	AATCCAAAAC	GAATCACCAC	ACGTCACAAA	AAACAGCTGA	300
AGAAATGCTC	TGTAGATTGA	GTTGCTGGAG	GAGTGACAGC	CAGGAGCCCT	GACTTCACTT	360
CCTTTGGTCC	AGTTTTACTC	TGATACAGGG	TGGATTCCAA	AACTGGCTCA	GTACATTGCA	420
TGTAGTTAAG	CCACATTTTA	AAAATAAAGG	CTCGAG			456

- (2) INFORMATION FOR SEQ ID NO:285:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GAATTCGGCC	AAAGAGGCCT	AAGGTCGGCC	TGTTCATCTT	GATTAGCATC	CAGGCCTTGG	60
AATATTTCAT	CAATGACAGC	TTTATCTTTG	ATATTCTTGA	TGGTGTTTGC	AAGCTCCTTT	120
GTAAGCAGCT	GCTTCAGCTC	ACCCCTCGAG				150

- (2) INFORMATION FOR SEQ ID NO:286:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

AATCCAAGCA ATAACCCAAG CAAAACTTCA GATGCACCTT ATGATTCTGC AGATGACTGG TCTGAGCATA TTAGCTCTTC TGGGAAAAAG TACTACTACA ATTGTCGAAC TCGAG

(2) INFORM	ATION FOR SEQ ID NO:287:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 278 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:287:	
AGATAAATGC CAGTAGAGGA CCTTTTATAT	GCTAGGAGAA GACTCAGATG AAGAAGAGGA AATGGATACC TCTGAAAGGA TGGTAGCCAA GATGATGAGA TGGGTTGCAC CTGGGGAATG GGAGAAGATG TGATGCTGAA GAGAACCCTA TTGTCTTAGA GTTTCAGCAG GAAAGGGAGG AAAGGATCCC AAAAAGGCTC TCCAAGGCTT TTTTGACCGA GAAGGAGAAG TGAATTTGAT GAACAGGGAC AACTCGAG	60 120 180 240 278
(2) INFORMA	ATION FOR SEQ ID NO:288:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 364 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:288:	
ATTTAACCTT CATCCAGTAT TTTAAAATTT AACATTGATA	GGCCAACTGC CCAATAGTTT CCAGTAGAAA CATGGCCATA CCAGTCTAGA CTCATTTAAT CAATAGCACA ATCTAACCTA CACAAGAATA AGCAATCAAA AACATGTTTT TCATTTTAC TTTCTTGCGG TCAATTTTTT TAATGATCTA TTTCAAAAATG ACAACTACTA TGGAATACTG AATACAAAGT TCAGTAACAC ACAACAACAG CAGCAACAAT ACCACAACCA CCACCACTGA ATGGTCTGGG ATGGCTGTTG TACTTAGTTA CGAAGAAGAG TGGGGACAGA AAATGAAGCT	60 120 180 240 300 360 364
(2) INFORMA	ATION FOR SEQ ID NO:289:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 471 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:289:	
TCAGAGACGG CCCTGTTTGC ACGGGGGAGC CCGGTGGTGA	GTATGTCCCA CCTAAAGGTC GGCTCTGCTG CCGACATCCC CATCAACATC ATCTCAGCCT GCTGACGGCC ACTGTGGTC CGCCCTCGGG CCGGAGGAG TGAAGCGGCT GCGTAATGGC CACGTGGGGA TTTCATTCGT GCCCAAGGAG ACCTGGTGCA TGTGAAGAAA AATGGCCAGC CAGCCCCATC TCAGCCAGTC GGAAATTGGG GATGCCAGTC GTGTTCGGGT CTCTGGTCAG AAGGCCACAC CTTTGAGCCT GCAGAGTTTA TCATTGATAC CCGCGATGCA	60 120 180 240 300 360
	187	

GGCTATGGTG GGCTCAGCCT GTCCATTGAG GGCCCCAGCA AGGTGGACAT GACCTGGAGG ACGGGACGTG CAGGGTCACC TACTGCCCCA CAGAGCTCGA	
(2) INFORMATION FOR SEQ ID NO:290:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 281 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:	
GAATTCGGCC TTCATGGCCT AGATTGAGTC ACATTGTTCT CTTTGATCCA GACAACATCA CTCAAACAAC CCTATTACTT CAGTAGCAAT GAACTGTTCT TAAGCATCTC ACT.GTTCCT TTTCTTCAGC TGTATGGCAC CCTGTCTTCC AGGCTCCTCA GCTGGGTAAG GTGAGCCAAC GTTACCAGGA GTATATGCTG TCAAAGTCTT TCATAGAAGG CTGTGCTTGG GCAAACTCGA G	TGGATTTTAT 120 TGTACACCAG 180
(2) INFORMATION FOR SEQ ID NO:291:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 250 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:	
GAAACTCTGC CCCTGAAGGT TTGTTTTCTA ATTCAGAGGT TTAAATTAAT (TAATAAAACC AGAGATCCTA TGGGAAATTT AGCCTAAGAC AGTGCTGGAA A GTTGATACAA AGAAGTGTTT GGCCACATTA CAGGTCTCAG ACTCAACTGC T TGCCGCTCTG TGCCTATGTC TTGCTTTTTT GCTGAGTTCC CTATTTCCAT A GATCCTCGAG	ATTGCCATAT 120 TATGTGTGAC 180
(2) INFORMATION FOR SEQ ID NO:292:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 264 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:	
GAAATGTCAG AGGCACATAA GCTTTTACAA AAATTGTTGG TTCATTGTCA (AACACAGAAA TGGTGATCAG TGTCCTACTG TCCGTGGCAG AGCTGTACTG TCCCCTACCA TCGCGCTGCC CATGCTCCTG CAGGCTCTGG CCCTCTCCAA (TTACAGTACT TGGCCTCTGA AACAGTGCTG AACTTGGCTT TTGCGCAGCT ATCCCAGAAC AGGCCCAACT CGAG	GCGATCTTCC 120 GGAGTACCGG 180
(2) INFORMATION FOR SEQ ID NO:293:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GAATTCGGCC	CTTCATGGCC	TAGGTTTCTC	CGTGTTGGTC	AGGCTGGTCT	CGAACTCCTG	60
ACCTCAGGTG	ATCCACCTGC	CTCAGCCTCC	CAAAGTGCTG	GGATTACAGG	CATGAGCCAC	120
CATGTCCTGC	TATAAATAAC	TTTTAATAGG	CTCTTTTTCT	GGCTTTTTTT	TTTAGTAACT	180
CAGCCCATTT	TCTTCTTCTC	AATCTGGTCT	TTGTTAATGT	TGATAACGCT	GTCTTACTTT	240
TAAATTGCCG	TGATTAGAAA	TTACTAGAGA	TATATAAACC	TAGTCTTTTG	GGGGATTTTG	300
AAAGGGTCAT	AGTATTCTTA	CTGTCTTTCA	AAATGTACCT	TATATTTGAA	CATTGGAAGA	360
TACGTGTTGC	TGAATACAAG	TTAGTTTCAT	ACACACACAT	ACACATGACA	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:294:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GAATTCGGCC	TTCATGGCCT	ACTCCATTCC	CAGATAGAAA	GCTTGAATGA	AGAGTTGGTC	60
CAGCTGCTTC	TCATCCGAGA	TGAGCTGCAC	ACAGAGCAGG	ATGCCATGCT	GGTGGACATT	120
GAAGACTTGA	CCAGACATGC	TGAAAGTCAG	CAGAAGCACA	TGGCAGAGAA	AATGCCTGCA	180
AAGTGAAAAG	AAGCCATTCA	ACCAGAGAAC	AAGCTAGAAT	TTATTTTGCT	TCTGTGGTTG	240
TAAAAATGCT	GTTGCTAAAG	GTGGCGCAGA	AACAAATATC	AGTGTTAGTC	ATTGATAATG	300
TCTGAAGCTT	AATGTCCAGT	GATTGGCCTT	TGCTTCTTAA	TTTATTTTAA	TTTTTTACTT	360
GTGCCACTTA	ATATCAGGCA	TTTTAATAAA	ATATTGTTAC	AAAAAATGTA	CAGTACTGAC	420
ACCACCACAA	ATCATGGTTA	ATAAAAGAGA	GTCTCGAG			458

- (2) INFORMATION FOR SEQ ID NO:295:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GTGTAAAACC	AATGCCAGGA	AAACCAAATA	CACAAAACCC	TCCACGGAGA	GGTCCTCTGA	60
GCCAGAATGG	GTCTTTTGGC	CCATCCCCTG	TGAGTGGTGG	AGAATGCTCC	CCTCCATTGA	120
CAGTGGAGCC	ACCCGTGAGA	CCTCTCTCTG	CTACTCTCAA	TCGAAGAGAT	ATGCCTAGAA	180
GTGAATTTGG	ATCAGTGGAC	GGGCCTCTAC	CTCATCCTCG	ATGGTCAGCT	GAGGCATCTG	240
GGAAACCCTC	TCCTTCTGAT	CCAGGATCTG	GTACAGCTAC	CATGATGAAC	AGCAGTCTCG	300
AG						302

(2) INFORMATION FOR SEQ ID NO:296:

1	PCT/US98/06956	
	PC 1/US90/U0950	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:		
CATGGATCTG CCTCCTGAGA GGGATGGAGA GAAGGGGAGG AGCACAAA CATGCCAAAA CTTGCACTTC CCAAAATGAA GGCTTCTAAG AGTGGGGT GAGAGACGTG GATCCTTCCC TTTCTAGTGC CACAGCAGGG GGTAGCTT AAAGGCCAGC AGTGACGGTG GTAGGGGAGG ACTTGGTGCA ACAGCAAG TGAGGGTGTG AACACTCACC GGCCACAGGT CCACATTCCC AGTTTGGGTCATCCCAAACAT GATCTCCAAGG CCAAGGTGA CAGCAGAGGA TGTGGGCTGCCAAACAT GATCTGTCTA CCGAAGGTGA CAGCAGAGGA TGTGGGCTGCAAACAT GATCTGTCTA CCGAAGGTGA CAGCAGAGGA TGTGGGCTGCAAACAT GATCTGTCTA CCGAAGGTGA CAGCAGAGGA TGTGGGCTGCAAACAT GATCTGTCTA CCGAAGGTGA CAGCAGAGAGA TGTGGGCTGCAAACAT GATCTGTCTA CCGAAGGTGA CAGCAGAGGA TGTGGGCTGCAAACAT GATCTGTCTA CCGAAGGTGA CAGCAGAGGA TGTGGGCTGCAAACAT GATCTGTCTA CCGAAGGTGA CAGCAGAGGA TGTGGGCTGCAAACAT GATCTGTCTA CCGAAGGTGA CAGCAGAGGA TGTGGGCTGCAAAAAAAAAA	CA GCCTGCCACA 1 TC AAGACACAGA 1 TG CCACAGGAAG 2 CT TTGCCAAACC 3 TG ACCTGCCTCT 3	60 20 80 40 00 60
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 308 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:		
GTGCTGGTGG CGCGGGGAGT GCGCGTCAAG GTGAACGAGG CCTACCGGCTGCCTGCGT ACCCAGCGTC GCTCACCGAC GTCTCCCTGG CGCTGAGCCACGACTCACGACTCACGACTCACGACTCACGACTCACGACTCACGACTCACGACTCACACGACTCACACGACTCACACACA	GA GCTGCGCCCC 1 AG CAGCGACGCT 1 GC CCGCTATGCT 2 AT CGCCACCCCA 3	60 20 80 40 00
(2) INFORMATION FOR SEQ ID NO:298:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 269 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:		

GAATAAGTAA	ATTCATGGAA	AGGAAGAAAT	TAAAAGAAAG	TGAGGAAAAG	GAAGTGCTTC	60
TGAAAACAAA	CCTTTCTGGA	CGGCAGAGCC	CAAGTTTCAA	GCTTTCCCTG	TCCAGTGGAA	120
CGAAGACTAA	CCTCACCAGC	CAGTCATCTA	CAACAAATCT	GCCTGGTTCT	CCGGGATCAC	180
CTGGATCCCC	AGGATCTCCA	GGCTCTCCTG	GATCCGTACC	TAAAAATACA	TCTCAGACGG	240
CAGCTATTAC	TACAAAGGGA	GGTCTCGAG				269

- (2) INFORMATION FOR SEQ ID NO:299:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GAGCGACCTT	TGGAATAGTT	AAGCACAGGT	CATTGTGGAC	ATGAATTCAG	GCCTCTGTAC	60
TAAAATCTAT	TTCAGGGAAT	GTTCTGTCTA	GTGATTTGCT	CACCATTTGA	TATATAATGA	120
ATTATAGGAC	AAGTATAAGC	TGATCTGCTA	TAGCTGTCCA	TCAGAGAGAA	TACACGTGGC	180
TATAACATCT	ATAACAAAAC	GACGATTCCT	CTACAAGAGG	CTGTTTCTCA	CTGCTAACGT	240
TGGTGTTTCT	GGCGTGGGAA	GAAATGCACA	GGCGTGCATG	GCATGCACGT	TCAGACAGCT	300
GCATTGTAAG	AGTTCTGTCA	TGCAGTCTGA	AAAGGGAAGA	AACAGGATGG	CTTTCTGTAG	360
CCACACCTGT	GAGGCGTGAT	GATTGTTGTA	TTATTAGATT	ACTGATTTTT	CTTTTCTGAA	420
AATACATTTG	AGTTTTAATC	ACATCTGTGG	AACTCGAG			458

- (2) INFORMATION FOR SEQ ID NO:300:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GGGATGCCTG	TTCTTGGGGT	AGAGAAGTCA	GGTAGCCCAG	GGCCCGCACT	CTCAATAGAC	60
CTTCAGAGAA	AAGGCATCGA	GGTAAATGCC	GCACTCGAG			99

- (2) INFORMATION FOR SEQ ID NO:301:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 569 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GGTCTAACAG	TAACACTACT	CAAGAGACCC	TGGAAATAAT	GAAAGAATCA	GAAAAAAAAC	60
TGGTGGAAGA	ATCTGTAAAC	AAAAACAAGT	TTATATCTAA	GACTCCAAGT	AAGGAAGAAA	120
TTGAGAAAGA	ATGTGAAGAT	ACCAGTTTGC	GTCAGGAGAC	ACAGAGGCGG	ACATCTAACC	180
ATGGTCATGC	CAGGAAAAGA	GCCAAGTCTA	ATTCCAAGCT	AAAGTTGGTG	CGTAGCCTGG	240
CAGTGTGTGA (GGAGTCCTCC	ACCCCATTTG	CTGATGGGCC	ATTAGAAACC	CAGGATATAA	300
TTCAATTGCA	CATCAGTTGC	CCTTCTGACA	AGGAGGAAGA	AAAGTCCACA	AAAGATGTCT	360
CTGAAAAGGA	AGACAAGGAC	AAAAACAAAG	AAAAGATCCC	AAGGAAGATG	CTGTCCAGAG	420
ACTCCAGCCA (GGAATATACG	GACTCCACTG	GAATAGACCT	ACATGAATTT	CTTGTAAATA	480
CACTGAAAAA (GAACCCAAGG	GACAGAATGA	TGCTGCTAAA	ATTAGAACAG	GAGATTCTGG	540
AATTTATTAA	TGACAACAAC	CCACTCGAG				569

- (2) INFORMATION FOR SEQ ID NO:302:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GCGATTGAAT	TCTAGACCTG	CCACCCAAAC	CCCAACTCTC	AGACTTACCT	CCCAAACCAC	60
AGATGAAGGA	CCTGCCCCCC	AAACCACAGC	TGGGAGACCT	GCTAGCAAAA	TCCCAGACTG	120
GAGATGTCTC	ACCCAAGGCT	CAGCAACCCT	CTGAGGTCAC	ACTGAAGTCA	CACCCATTGG	180
ATCTATCCCC	AAATGTGCAG	TCCAGAGACG	CCATCCAAAA	GCAAGCATCT	GAAGACTCCA	240
ACGACCTCAC	GCCTACTCTG	CCAGAGACGC	CCGTACCACT	GCCCAGAAAA	ATCAATACGG	300
GGGCACTCGA	G					311

- (2) INFORMATION FOR SEQ ID NO:303:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 683 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

ACAGCATGAA	GGCAGAAGCC	AATGCCCTGC	ATCACAAACA	CGACAAGAGG	AAGCGTCCGG	60
GGAAGAATGC	ACCCCCAGGA	GGTGATGAGC	CACTGGCAGA	GACAGAGAGT	GAAAGCGAGG	120
CAGAGCTGGC	TGGCTTCTCC	CCAGTGGTGG	ATGTGAAGAA	AACAGCATTG	GCCTTGGCCA	180
TTACAGACTC	AGAGCTGTCA	GATGAGGAGG	CTTCTATCTT	GGAGAGTGGT	GGCTTCTCCG	240
TATCCCGGGC	CACAACTCCG	CAGCTGACTG	ATGTCTCCGA	GGATTTGGAC	CAGCAGAGCC	300
TGCCAAGTGA	ACCAGAGGAG	ACCTAAGCCG	GGACCTAGGG	GAGGGAGAGG	AGGGAGAGCT	360
GGCCCCTCCC	CGAAGACCTA	CTAGGCCGTC	CTCAAGCTCT	GTCAAGGCAA	GCCCTGGACT	420
CGGAGGAAGA	GGAAGAGGAT	GTGGCAGCTA	AGGAAACCTT	GTTGCGGCTC	TCATCCCCCC	480
TCCACTTTGT	GAACACGCAC	TTCAATGGGG	CAGGGTCCCC	CCCAGATGGA	GTGAAATGCT	540
CCCCTGGAGG	ACCAGTGGAG	ACACTGAGCC	CCGAGACAGT	GAGTGGTGGC	CTCACTGCTC	600
TGCCCGGCAC	CCTGTCACCT	CCACTTTGCC	TTGTTGGAAG	TGACCCAGCC	CCCTCCCCTT	660
CCATTCTCCC	ACCTGATCTC	GAG				683

- (2) INFORMATION FOR SEQ ID NO:304:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 653 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAATTCGGCC	AAAGAGGCCT	AGAGATGTCT	ACTCTCAGCT	CACGCCTGTA	ATCCCAGCAT	60
TGTGGGGAGG	TCAAGTTGGG	TGGATTGCTT	GAGCCCAGGA	GTTTGAGACC	AGCCTAAGCA	120
ATAGGCAAAA	CCCTGTCTCT	ACAAAAATCA	GCCAGGTATG	GTAGTGTGTA	CCTGTAGTCC	180
TAGCTACTCA	GGAGGCTGAG	GTGGGAGGAT	CGCTTGAGCC	TGGGAGGTGA	AGGCTGAAAT	240
TAGCCATGAT	CATGCCACTG	CACCCCAAGC	CTGGGCAACA	GAGCAAGACC	TTGTCTCAAA	300
AAAAAAAGGA	TGAGCTAGGT	TTGTATCTGT	AGACAGAGAT	TTATGATTAA	TTGGTAGGTG	360
AAAAAGTGTA	TTAAAGTACA	GTTATAGATT	AGAGTACAAA	ATGAATGAGT	ATATATGCGT	420

TTAAAAGTAT	GTATACATAT	CAGGAAAGGT	TACATGAGGA	TTTTCACTTT	CCACTTTATA	480
TCTCCCAGTA	TTTGAATTTT	TAATAACAAT	CTTTTTATCA	TAAAACTATA	TTAAATTAAA	540
CTTTTAGATT	TTTTAGTGGT	ATAAGTAGAA	CAGGAACCCT	AATACATTGT	TTTCTACTTT	600
TGTGATAAAG	ATAATTCATG	ATAGATGAAG	TTGCAAACCG	AAAGATCCTC	GAG	653

- (2) INFORMATION FOR SEQ ID NO:305:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GAATTCGGCC	TTCATGGCCT	AAGGTATTCC	AAAATGTCTA	ATTTATTTA	TCCGATGGTA	60
AATGTAATAA	TTAAAGAAAG	AGGAAAGAAT	CATGAAAGGT	GGCCCTTAAA	GAGGGCTTCT	120
GGCAGAGTTA	GGTCAGAGGC	ACACTTTCTT	ACAGACTAAG	AGTTTTTAAG	TACTCAAGGT	180
GATGTTTATC	AGAAGCTTGG	ACTGCTTCTG	TGTCTTTTTA	TTGTGCTTAT	CTGGGAGGGA	240
GAGTTCTGTG	TCTGCTCCTA	TACATCTTTC	TGCAGCTGCA	GACATACTCC	CTGAGTCTGC	300
TTTTAGCTTT	CCTATCTTAG	TGCACCTGAA	GGGAAAGGAA	TGAGCTTATT	AAGGCCCACT	360
GTTTTACTGG	GGCCCATTGT	ATGAGAGTGA	AGTTTGGCAG	TTACCCAAGA	GACGTTCCCC	420
TCACCTCCCT	CCGGCGCTCG	AG				442

- (2) INFORMATION FOR SEQ ID NO:306:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GAATTCGGCC	TTCATGGCCT	ACCAATATGC	AAATCAGTAC	CTCTTCTCTT	AGAGGTGTTC	60
ATGCCCAAGC	TCCTCAGACA	AGTCCATCCC	ACTGTGTGGG	AGGAAGTTGA	AGGGTGAGGA	120
TTTTTAAGAT	TTTTATCTTG	CTTGAAGTTG	TGAAGACTCA	ATGACAAATG	GCTAGGTTTT	180
GAAGGGGTCT	TGGAAGTCAT	TACTGGGGAT	AGACCCCTCT	TGATACTTGT	CACATTAATA	240
TCTGCCCAGA	CTCTCACACA	TTCAGATGTT	TAACGTCACA	TGCATTAAGT	TCTTTTGGTT	300
GCATGAGACA	GTGATGCACA	GAAACTCACT	TAGGAAAGGA	GATAGGTGGC	AATAAAGAAA	360
ACAGGGATTT	CATAGGAATG	CAGTAAAAAA	AAAACCATGG	CCTAATCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:307:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GGGGTTGTCT GAGGCCCAGA GGTCGTATAA GGGCCGCTCT ACGGTGTCCT GGGGCCCGGG

ing the second s

	PC17US98/06956
CTTGGCCCTT GTTGCAGAAG GGTTGAGGAG CCGGGCTGGG CCCTGCGC AGCTCGCCCT GCTTGGCCAG CTTCTCCCAT AGCTGCTCCT TCCGCCTG TTGGGGACCT GGTGGGCGAG GACGTCTTTG GGGGCAGGGA CTTTGGAT	AG CTTCTTGGCG 180
(2) INFORMATION FOR SEQ ID NO:308:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 533 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:	
GCGCACCATC CTGGGAAGTG CATGTCTCAG ACCAACTCCA CCTTCACC CGCATCCTGC ATCCTTCAGA TGAGCTCACT CGGGTCACAC CAAGCCTT ACTCCAGCTT GTGGCAGCAC CAGCCACTTG AAATCCACGC CGGTGGCC CCACGGAGAC TGAGCCTGC TGAGTCCTTC ACTAACACCC GTGAGTCC AGCACATCCC TGGGGCTCGT GTGGCTGTTG AAGGAGCGGG GCATTTCT GACCCCCAGA GCTGGGACAG GGCCGGCCGG GGCTCCCTCC TGCACTCC ATGGCTGTGA TCCCCTCTAC TCCGCCGAAC TCGCCTATGC AGACACCC CCCTCCTTTG AGTTCAAGTG CACGAGCCCT CCCTACGACA ATTTCCTG GCCAGCTCCA TCCTGAGGGA AGTGAGAGAA AAGAACGTCC GCAGGACC	AA CTCAGCCCA 120 AC ACCATGCACT 180 AC GACCACCATG 240 GC TGCCGTGTAC 300 TA CACGCCCAAG 360 AC ATCCTCCCA 420 GC TTCCAAGCCA 480
(2) INFORMATION FOR SEQ ID NO:309:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 297 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:	
GAATTCGGCC AAAGAGGCCT ACCCTAAAAC ATTTATTTCA AGGAGAAA GGCGCAAAAAA TGGCTGGGGC AAATTATAGAA AACATGAGCA CCAAGAAG GGTGGGATTC TGCTCGTGTT CCAAATCATC GCCTTTCTGG TGGAGGC GGGCCCACAA CGGCAGTGTC CTACATGTCG GTGAAATGTG TGGATGCC CACAAGACAA AATGGTTCGT GCCTTGGGGA CCCAATCATT GTGGCAAG	CT GTGCATTGTT 120 TT GATTGCTCCA 180 CG TAAGAACCAT 240
(2) INFORMATION FOR SEQ ID NO:310:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 248 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:	

GGTCAGTTTT AGGACACTTG AACACTTCTT TTCCCCCCTC CCCAGTTCTC CAGGTGCGTT ACCTCGAG	240 248
(2) INFORMATION FOR SEQ ID NO:311:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 343 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:	
GAATTCGGCC AAAGAGGCCT AGGTAAATAA CTAATATTGA TGTATTTTA TATTTTAATA TAGACTAGTA AACTATGCAG AGTTAAGTGT TACATTAGAA TCTTGAACTC TCCTAACATT TCTCTTCCTC AGTTTCCTAT TGTTTTGGTA GAGTATGTAG ACATTTGCGA GATTAATTTA GAGTTGGTAG ATACATTCTG GATTTCATTT TACTTTAGAT AGCAGGTTTG GCACTTTAAA TATATTTAAT TCAGTAAGAG AATAACTGAG TATGAGCTGT ATCCTCATCT TACTGTTGAA GACATCCCAA ATAGTTGGGT GTGCACTGTG GCGGGATCTC GAG	60 120 180 240 300 343
(2) INFORMATION FOR SEQ ID NO:312:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 268 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:	
GAATTCGGCC AAAGAGGCCT ACGGGGAGGC GCGCCCGCGC TGAGTCGGCG GCGGGTAGCC ACTCCATGCC CTTGTCCGAT GGTTTGCAAC TCCGATTTTG CACACCGCTC CACCGTGCCC CCCAGCGCAC ACCCATTCAC ACTCACGCCA ACACTCTCGC TGAACACTTT TATAATTGTT AGGCGTGGCC GTTGGGACTT TGGGCGCAGC GCGGCTGATA CTGCGTCTGG AGGATTGATA TTTACTTTTG CATTGCGGTT ACCTCGAG	60 120 180 240 268
(2) INFORMATION FOR SEQ ID NO:313:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 354 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:	
GTCTCTCGCC GCCGGAGGAA GATGANGCTG AAGATTGGAT TCATCTTACG CAGTTTGCTG GTGGTGGGAA GCTTCCTGGG GCTAGTGGTC CTCTGGTCTT CCCTGACCCC GCGGCCGGAC GACCCAAGCC CGCTGAGCAG GATGAGGGAA GACAGAGATG TCAATGACCC CATGCCCAAC CGAGGCGGCA ATGGACTAGC TCCTGGGGAG GACAGATTCA AACCTGTGGT ACCATGGCCT	60 120 180 240
CATGTTGAAG GAGTAGAAGT GGACTTAGAG TCTATTAGAA GAATAAACAA GGCCAAAAAT	300

- (2) INFORMATION FOR SEQ ID NO:314:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 514 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GAATTCGGCC	AAAGAGGCCT	AGTGCAAGAA	CATGAAGCAC	CTGTGGTTTT	TCCTCCTGCT	60
${\tt GGTGGCAGCT}$	CCCAGATGTG	${\tt TCCTGTCCCA}$	GGTGCACCTG	CAGGAATCGG	GCCCGGGACT	120
GTTGAAACCT	TCGGACACCC	TGTCCCTCAC	CTGCTTTGTC	TCGGGTTACT	CCCTCAGTAG	180
TGTTCACTAT	TGGGGCTGGA	TCCGCCAGTC	CCCAGGGAAA	${\tt GGACTGGAGT}$	GGATTGGGAA	240
CATCCATCAC	AATGGTAGAA	CCAATTACAA	CCCGTCCCTC	GCCAGCCGCG	GTTCCATCTC	300
AGCCGACACG	TCCAAGAACT	CCCTCTCCCT	GAATCTGACC	TCTGTGACCG	CCGCAGACTC	360
GGCCGTCTAT	TTCTGTGCGA	GCGGCCCTAT	TGCCTCCTTT	GAATCGACGA	CTCTAAAGGT	420
GGGCGGAGAC	TTTCACTCCT	GGGGCCAGGG	AATCCTGGTC	ACCGTCTCCT	CAGCATCCCC	480
GACCAGCCCC	AAGGTCTTCC	CGCACAGCCT	CGAG			514

- (2) INFORMATION FOR SEQ ID NO:315:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 215 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GAATTCGGCC	AAAGAGGCCT	AGGACACTAG	AATTATTAGT	GTTCATTTTC	ATCTAAGATC	60
TTTATTCTCT	AACGTTCTTG	GTCCTATTGA	AACATTGCAG	TATGCAAAAC	TACTGCAATG	120
TTAAACCCAA	GAGAAAAGCC	ATTATCATGT	GTATGCTGGT	CATCATGATC	AGTGTGGTAC	180
AATTTTTAAA	AATAAACTAT	CATGCCCTTC	TCGAG		•	215

- (2) INFORMATION FOR SEQ ID NO:316:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 788 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

		CTCCTCCC	COCHOCHOCO	aa	aaaaaaaaaa	60
GAATTATGTA	CGCCCTCTTC	CTCCTGGCCA	GCCTCCTGGG	CGCGGCTCTA	GCCGGCCCGG	60
TCCTTGGACT	GAAAGAATGC	ACCAGGGGCT	CGGCAGTGTG	GTGCCAGAAT	GTGAAGACGG	120
CGTCCGACTG	CGGGGCAGTG	AAGCACTGCC	TGCAGACCGT	TTGGAACAAG	CCAACAGTGA	180
AATCCCTTCC	CTGCGACATA	TGCAAAGACG	TTGTCACCGC	AGCTGGTGAT	ATGCTGAAGG	240
ACAATGCCAC	TGAGGAGGAG	ATCCTTGTTT	ACTTGGAGAA	GACCTGTGAC	TGGCTTCCGA	300
AACCGAACAT	GTCTGCTTCA	TGCAAGGAGA	TAGTGGACTC	CTACCTCCCT	GTCATCCTGG	360
ACATCATTAA	AGGAGAAATG	AGCCGTCCTG	GGGAGGTGTG	CTCTGCTCTC	AACCTCTGCG	420
AGTCTCTCCA	GAAGCACCTA	GCAGAGCTGA	ATCACCAGAA	GCAGCTGGAG	TCCAATAAGA	480

TCCCAGAGCT GGACATGACT GAGGTGGTGG CCCCCTTCAT GGCCAACATC CCTCTCCC TCTACCCTCA GGACGCCCC CGCAGCAAGC CCCAGCCAAA GGATAATGGG GACGTTTGCC AGGACTGCAT TCAGATGGTG ACTGACATC AGACTGCTGT ACGGACCAAC TCCACCTTTG TCCAGGCCTT GGTGGAACAT GTCAAGGAGG AGTGTGACCG CCTGGGCCCT GGCATGGCCG ACATATGCAA GAACTATATC AGCCAGTATT CTGAAATTGC TATCCAGATG ATGATGCACA TGCTCGAG	540 600 660 720 780 788
(2) INFORMATION FOR SEQ ID NO:317:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 214 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:	
GAATTCGGCC AAAGAGGCCT AAATCATCCT GATGATGGTT TTCTTACATA AACATGAGCT TCTGACCATG TACCATGGAT GGGTTCTCAC TTCCTGCTAT ATCCTGATCA TCACTATTGC AAATATTGCA AATTTGGCCA GTACTGCTAC TGCAATCACA ATCCAAAGGG ATTGGATTGT TGTTGTTGCA GGAGAAGACA GAAGCAAACT CGAG	60 120 180 214
(2) INFORMATION FOR SEQ ID NO:318:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:	
GTTGTCTTTT TTCCCCTTTA TAGCTGCTGG AGTGAATTTT AGAAAGCCTA AGTCATACAT CACATTGCTT CATGGGCATC CCAGTACACT TTGGATTTTA TTTTACATCC TTACTGATCT GATTCTCATC TCTGTCTCTT CATGGTTCTC TGCCTTCTAG TTACACTGGT GACCTTTCAA AACCTTTACC ACATTGAGTT CATTCCTTAC TTTTCACTCT TTCTCTGCCT GGAGTGTTCT GCCCCCATCTT TACGTGGCAC GCTCGAG	60 120 180 240 267
(2) INFORMATION FOR SEQ ID NO:319:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:	
GAAGCTTTCA GGCTATCTTC TAGTCAAGAT GAGTGATAAG CCAGACTTGT CGGAAGTGGA GAAGTTTGAC AGGTCAAAAC TGAAGAAAAC TAATACTGAA GAAAAAAAAT ACTCTTCCCT CAAAGGAAAC TATCCAGCAA GAGAAAGAGT GTGTTCAAAC ATCATAAAAT GGGGATCGCC TCCCAACAGC AGATTTCGAC ATTACCTGAG AGTCTTGATT TTAGGCTTGT TTTTTGTAAA CCCATGTGTT CTCGAG	60 120 180 240 256

- (2) INFORMATION FOR SEQ ID NO:320:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GCTGCGTGTG	ATGGAGACCA	AACCCGACAA	GGCAGTGTCC	ATCATTGAGT	GTGACATGAA	60
${\tt CGTGGACTTT}$	GATGCTCCCC	TGGGCTACAA	AGAACCCGAA	AGACAAGTCC	AGCATGAGGA	120
GTCGACAGAA	GGTGAAGCCG	ACCACAGTGG	CTATGCTGGA	GAGCTGGGCT	TCCGCGCTTT	180
CTCTGGATCT	GGCAATAGAC	TGGATGGAAA	GAAGAAAGGG	GTAGAGCCCA	GCCCCTCCCC	240
AATCAAGCCT	GGAGATATTA	AAAGAGGAAT	TCCCAATTAT	GAATTTAAAC	TTGGCGCGCT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:321:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GAATTCGGCC	AAAGAGGCCT	ACTCTTACAC	CTTCCGCTCC	GTGGGCACCT	TCAATATCAT	60
CGTCACGGCT	GAGAACGAGG	TGGGCTCCGC	CCAGGACAGC	ATCTTCGTCT	ATGTCCTGCA	120
GCTCATAGAG	GGGCTGCAGG	TGGTGGGCGG	TGGCCGCTAC	TTCCCCACCA	ACCACACGGT	180
ACAGCTGCAG	GCCGTGGTTA	GGGATGGCAC	CAACGTCTCC	TACAGCTGGA	CTGCCTGGAG	240
GGACAGGGGC	CCGGCCCTGG	CCGGCAGCGG	CAAAGGCTTC	TCGCTCACCG	TGCTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:322:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GCGCCGTGTC	CTTTTGCGTT	GGTACCAGCG	GCGACATGAC	GGGGTACACT	CCGGATGAGA	60
AACTGCGGCT	GCAGCAGCTG	CGAGAGCTGA	GAAGGCGATG	GCTGAAGGAC	CAGGAGCTGA	120
GCCCTCGGGA	GCCGGTGCTG	CCCCCACAGA	AGATGGGGCC	TATGGAGAAA	TTCTGGAATA	180
AATTTTTGGA	GAATAAATCC	CCTTGGAGGA	AAATGGTCCA	TGGGGTATAC	AAAAAGAGTA	240
TCTTTGTTTT	CACTCATGTA	CTTGTACCTG	TCTGGATTAT	TCATTATTAC	ATGAAGTATC	300
ATGTTTCTGA	AAAACTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:323:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

GCAAAAATCT	CAGGCCCCAG	AAAAGCCTCT	TGTCATCTCT	CAGATGGGTT	CCAAAAAGAA	60
GCCCAAAATT	ATCCAGCAAA	ACAAAAAAGA	GACCTCGCCT	CAAGTGAAGG	GAGAGGAGAT	120
GCCGGCAGGA	AAAGACCAGG	AGGCCAGCAG	GGGCTCTGTT	CCTTCAGGTT	CCAAGATGGA	180
CAGGAGGGCG	CCAGTACCTC	GCACCAAGGC	CAGTGGAACA	GAGCACAATA	AGAAAGGAAC	240
CAAGGAAAGG	ACAAATGGTG	ATATTGTTCC	AGAACGAGGG	GACATCGAGC	ATAAGAAGGA	300
ACTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:324:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GCACTTCTGA	GAGGATGCTG	GGAATCTGCA	GGGGGAGACG	GAAATTCTTG	GCTGCCTCGT	60
TGAGTCTTCT	CTGCATCCCA	GCCATCACCT	GGATTTACCT	GTTTTCTGGG	AGCTTCGAAG	120
ATGGAAAGCC	CGTGTCTCTG	TCACCGCTGG	AGTCCCAGGC	ACACAGCCCC	AGGTACACGG	180
CCTCCAGCCA	GCGGGAGCGC	GAGAGCCTGG	AGGTGCGCAT	GCGCGAGGTG	GAGGAGGAGA	240
ACCGCGCCCT	CCGCAGGCAG	CTCAGCCTGG	CCCAGGGCCG	AGCCCCACCC	ATCCTCGAG	299

- (2) INFORMATION FOR SEQ ID NO:325:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GAATTCGGCC	TTCATGGCCT	ACTCCAAACT	CATGCCCTTG	TTTTTATCTC	TGCCCTTGGA	60
TGGCTGTCTT	CTATTTTCAC	TCACAATTTC	AACACATTTT	GACTTGCTCG	TGTCACCTAG	120
GGTTTCCGCC	TCAGGTATGT	CTTCTTCCTT	AATTTCTTTG	CCGTCTTTGG	TGCTGTTGAC	180
CTCACCCTTT	CTGGGGTCTT	CCTATTGGTC	TCAGCTTCAG	GTTTGCAGCC	GCCCCTGGTT	240
TOTOTOTOT	TOCTTOTOTO	CCCTCTTCCC	CTCCTTCTCA	CCCACCCTCC	ΣC	292

- (2) INFORMATION FOR SEQ ID NO:326:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GAATTCGGCC	TTCAGACTTG	AAGTGGAGAA	GGCTACGATT	TTTTTGATGT	CATTTTGTGT	60
AAGGGCGCAG	ACTGCTGCGA	ACAGAGTGGT	GATAGCGCCT	AAGCATAGTG	TTAGAGTTTG	120
GATTAGTGGG	CTATTTTCTG	CTAGGGGGTG	GAAGCGGATG	AGTAAGAAGA	TTCCTGCTAC	180
AACTATAGTG	CTTGAGTGGA	GTAGGGCTGA	GACTGGGGTG	GGGCCTTCTA	TGGCTGAGGG	240
GAGTCAGGGG	TGGAGACCTA	ATTGGGCTGA	TTTGCCTGCT	GCTGCTAGGA	GGAGGCCTAG	300
TAGTGGGGTG	AGGCTTGGAT	TAGCGTTTAG	AAGGGCAAAC	TCGAG		345

- (2) INFORMATION FOR SEQ ID NO:327:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GAATTCGGCC	TTCATGNCCT	ACCTTTCCGT	CCGTTCTTTC	ACGCCTTCCT	CCTCATTTTC	60
CTTCCTTCTA	TTTTCCCTTC	CCTCTTTCCG	CTTTCCTGCC	CCGTTTCCTT	CCTCCCTCCC	120
TTCCTCCTTC	CTTCCTTCCT	CTGCGTTCTT	CCTCTCTCCT	TTGTTCCTTC	CTCCTCCTCC	180
CCACTCCCTT	TTCCTCTCCT	CTTCCCACCC	CAGTCTCCTA	CTCCCCAGTC	CTCCCATCCC	240
CATGGAACAT	ACACCTGCTT	TGTCTGGGAG	CCACGTTATT	CCTGCCAGCC	AGACCCTGGC	300
CAGGAGGATC	AGGGTCACGG	TCAGCTTGGG	CCGAGAACCC	TTCACATGAG	ACAAGCTCCT	360
CTGCCAGGGT	TTCCTGTGGG	AAAGGCCCCA	CTTCCCGACC	CTCCTGGGCC	ACTGCATGGG	420
GTCCCCTCTT	CGGCTTCTTC	TCCCCTCTCC	ACCCGGCAGC	CCCCCCAGCT	CGAG	474

- (2) INFORMATION FOR SEQ ID NO:328:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 556 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GAATTCGGCC	AAAGAGGCCT	AATTTACTCC	CCAATATAAA	ACATTTTACC	TGCGATCTAT	60
GTGTACATAT	TGAATGATGT	GTAACAATAT	CATAATTTTT	ATGTTCTGCA	TTTTTTCACT	120
TATATATCTT	TATTTAAATG	GACTTAACTT	TACTAATGGA	GTAATTTTTA	GCTTTCAGAA	180
GGAGTTCTCA	CTCGAAGATA	AAGAACAGCT	CGCTAACCAC	GAAAGAGGAA	TCGATGCTCA	240
GCTTTTAGTT	GCACTTCCTA	AAGTTGCAGA	ATTAAGACAA	ATCTTTGAAC	CAAAGAAGAA	300
AGAATTCTTA	GAAATGAAAA	GAAAAGAAAG	AATTGCCAGG	CGCCTGGAAG	GGATTGAAAA	360
TGACACTCAG	CCCATCCTCT	TGCAGAGCTG	CACAGGATTG	GTGACTCACC	GCCTGCTGGA	420
GGAAGACACC	CCTCGATACA	TGAGAGCCAG	CGACCCTGCC	AGCCCCCACA	TCGGCCGATC	480
AAATGAAGAG	GAGGAAACTT	CTGATTCTTC	TCTAGAAAAG	CAAACTCGAT	CCAAATACTG	540
CACAGAAACC	CTCGAG					556

- (2) INFORMATION FOR SEQ ID NO:329:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 385 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GAATTCGGCC	AAAGAGGCCT	ACAAAACCAT	CCATAAATAA	ACAAAGCTAA	GAAAGCTAAG	60
AAACAAAGCT	AAGAAACAAA	GACTGAGGTG	${\tt AGGGAGATTT}$	GAGTATTTT	TTTTCCTCTA	120
CCAACAAGTG	AAGAATTGAA	CACCTTAATC	CATCTGATCT	CCCAGGTGGA	AGCCACAAAT	180
CTTTTTTTT	GTTTTGCTCA	GCATATTGGC	ACAGTGAGAA	ATTCATTTTA	TACTCTCTGG	240
CATCTCTCTT	GTAAACTCAC	CAAGTCTCAA	TAAGTTCACA	AAGAAGGCAG	AGACAAATAA	300
CCCTAGAATG	CAGGTGATTG	TTTATTTATG	TATTTTCCTT	GTTACATACC	CACCTATACC	360
CAAGGCCTTT	GCAGAAAAGC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:330:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 696 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

GAATTCGGCC AAAGAGGCCT AGGAAGCAGG AGTTTATTTT TATCCTTTTG TAAGTATTAA	60
CTCGGTAATC ACAACAACA CGGAGCAATC TCAATGCTGT TTATCCGGAG GACAGTCTGC	120
GGGGTCGTGA CGATTCTTTT CTTCTTGAAG TTTTTCCTTT TCCTGAATCT CATAATGATT	180
CTTGGCCATG ATTCTGTCTT TTCAATGACT GTGGCTTCTA CTCGAACAAG ATCCTTTCCG	240
AGGAGTGGCT TGCCAAGCAG CGTGAAGTTG TCTGCCCCAA CCAGCAGGAC CTTCTCCAGT	300
CGAATTCTCT CTCCACACGC AAGGTCTAGT TCATTTCCAA TTAAGATCAG GTCTTCAGAG	360
GTCACCTTCC ACTGGCGGCT GGCAAAGTGC ACCACGGCAA AGAGCCTGCC ATACTGCCCC	420
GTGACGATCA TCTCATTCAC TTTCTTCACG ACCTCTGCAT GGTGTCTGGT CTCCTCAACT	480
GGGTCTGGCA GAACAACTTC TGGCCAAGGT GGTGAACTCA GGGATGTTTT AGGAACATAT	540
CCTGGTAGAT ATGAAGTGCT CTGTGAATTG AACCTTCGAG AAGCAGACCA AAGGGAGGCT	600
GCTCCGGGCC CCGAAGGTCT CAGGATGCTG TGGCTGCACG CGGACGCCAG CCGCCCTAAG	660
GTGACCGTCA GGGAAGATGC TGCCATGGCC GCCGCC	696

- (2) INFORMATION FOR SEQ ID NO:331:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GAATTCGGCC	AAAGAGGCCT	AATTTTTGT	ACATCTGGGC	CCTTAGTTTT	TATTCTGTTT	60
ATTATATGTC	TCTGTCTCTC	TCTATTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	120
GTGTGTGTGT	GTGGTGCAGG	AGTGCCACCC	CCAGGGCCCT	GTCAACCTCT	CTTTTCTCCT	180
CCATGGCTGT	CTGCCTGCGT	ATCTGTCTCT	GAGAATCCTC	GGGGCGGTCA	GGGGATGTCA	240
GGAGGGGAAG	GAGCCGCCCT	CCCTATCTTG	CTGCTCCTCT	TGGCACTCAG	GGGCACCTTC	300
CATGGAGCCA	GACCGGGTGG	AGGGGCTTCT	GGGATTTGGT	GTCTGCTGCT	GCCAGAGCAG	360

GAACCCCCAG TACTCGAG 378

- (2) INFORMATION FOR SEQ ID NO:332:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GAATTCGGCC	TTCATGGCCT	ACATTGGGAT	TATTGGTGCT	GTGACCATGG	CTGGCATCAT	60
GGCGGCAGAC	AGAAGTGAAT	CACCTAGTTT	GACCCAAGAG	AGAGCCAACC	TGAGCGATGA	120
GCAGTGCACA	CAGGTGACCT	CCTTGTTGCA	GTTGGTTCAT	TCCTGCAGTG	AGCAGTCTCC	180
TCAGGCCTCT	GCACTTTACT	ATGATGAATT	TGCCAACCTG	ATCCAACATG	AAAAGCTGGA	240
TCCAAAAGCC	CTGGAATGGG	TTGGGCATAC	CATCTGTAAT	GATTTCCAGG	ATGCCTTCGT	300
AGTGGACTCC	TGTGTTGTTC	CGGAAGGTGA	CTTTCCATTT	CCTGTGAAAG	CACTGTACGG	360
ACTGGAAGAA	TACGACACTC	AGGATGGACT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:333:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 547 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GAATTCGGCC	AAAGAGGCCT	ACTTATTTTC	CTGTGAAAAT	GCCTACCACA	AAGAAGACAT	60
TGATGTTCTT	ATCAAGCTTT	TTCACCAGCC	TTGGGTCCTT	CATTGTAATT	TGCTCTATTC	120
TTGGGACACA	AGCATGGATC	ACCAGTACAA	TTGCTGTTAG	AGACTCTGCT	TCAAATGGGA	180
GCATTTTCAT	CACTTACGGA	CTTTTTCGTG	GGGAGAGTAG	TGAAGAATTG	AGTCACGGAC	240
TTGCAGAACC	AAAGAAAAAG	TTTGCAGTTT	TAGAGATACT	GAATAATTCT	TCCCAAAAAA	300
ACTCTGCATT	CGGTGACTAT	CCTGTTCCTG	GTCCTGAGTT	TGATCACGTC	GCTGCTGAGC	360
TCTGGGTTTA	CCTTCTACAA	CAGCATCAGC	AACCCTTACC	AGACATTCCT	GGGGCCGACG	420
GGGGTGTACA	CCTGGAACGG	GCTCGGTGCA	TCCTTCGTTT	TTGTGACCAT	GATACTGTTT	480
GTGGCGAACA	CGCAGTCCAA	CCAACTCTCC	GAAGAGTTGT	TCCAAATGCT	TTACCCGACT	540
CCTCGAG						547

- (2) INFORMATION FOR SEQ ID NO:334:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GAATTCGGCC	TTCATGGCCT	AGGGGAAATT	GAGTCAAGAA	AAGGTTCAAT	ATTTTTTAAT	60
GGTAGAATTG	ACCGTATGTG	TATGTGCTTC	TAGAAGTGAT	TCAGGAGAGA	GGGTGGAATG	120

GATGGTGTGG	GACGGAGGGA	AGAATTGGTG	GAATGATGTT	GGCAAAAAGG	AATAGGCTTT	180
TGTGCATAAG	TTGAGGGATT	GGCCTTGCCT	AGAAACATGG	ACAATTCGTC	TATAGTAAGA	240
AGAGAAAAGG	TAGATCTATG	ACCACAGACA	TAGTCAGATA	ATCATTTTAA	AATTCTTTAA	300
TCAATAGATG	TTTCTGATGT	ATGGCAGGCA	GTAAGCTAAG	CAGTTTACAT	ACCTGATTTC	360
ATTTAGTTAT	TATAACAATC	CCAGTCTAAA	ACTCGAG			397

- (2) INFORMATION FOR SEQ ID NO:335:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GAATTCGGCC	TTCATGGCCT	ACTCCATCCT	TAAGGTCACC	ATTGGTATGT	TCCTGCTCTC	60
TGGAGATCCC	TGCTTCAAGA	CGCCACCATC	GACTGCCAAG	TCCATCTCCA	TCCCAGGCCA	120
GGATTCCTCC	CTGCAGCTGA	CGTGTAAGGG	TGGTGGGACC	AGCAGTGGGG	GCAGCAGCAC	180
CAACTCCCTG	ACTGGGTCCC	GGCCCCCAA	GGCTCGGCCC	ACTATTCTCA	GCTCAGGGCT	240
GCCAGAGGAA	CCCGACCAGA	ACCTGTCCAG	CCCTGAGGAG	GTGTTCCACT	CTGGCCACTC	300
CTCGCAACTC	GAG					313

- (2) INFORMATION FOR SEQ ID NO:336:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GAATTCGGCC	AAAGAGGCCT	AGATTGAATT	CTAGACCTGC	CTCGGCCTCC	CAAAGTGCTG	60
GGATTACAGG	CTTGAGCCAC	CACACCTGGC	CTAGTGATTT	GTAATTTCAT	GAGCTGTTGC	120
TGTATTGCCT	TCCACAGACA	GTCAATTTAT	AATCCCTCAG	TATTATATAA	TCAGGAAGAT	180
TCAGTGAATG	GAATTTTGGG	TTGGTGGAGG	ACATATTTTT	TAATTGGTAG	ACCACTGAGT	240
GCTTTTGCAA	ATCTCCTTAA	ATCACATTAC	AGCAGGAACA	ACTATAGAAA	ATACAATTAT	300
TTAGGAGCAA	CCTGATCTGT	GAGCTAATTT	AATGAGTGGA	GCCCAGCCTA	CATGCTGAAG	360
AGCTCACATG	CCTCCTACCT	AGTTCCTTAA	CTAGGTTTTC	ACTCATGCCC	ATTTTGTCAT	420
ACTCTTGAAA	CCTTCCTATC	TTTGCATAGA	ACATTATTCT	TTCCACT		467

- (2) INFORMATION FOR SEQ ID NO:337:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GAATTCGGCC AAAGAGGCCT ACTTCTTTGA AGAACCATGA AGTCACACTA TATTGTGCTA

GCTCTAGCCT CCCTGACGTT CCTGCTGTGT CTCCCCGTGT CCCAGAGCTG TAACAAAGCA	120
CTCTGTGCCA GCGATGTGAG CAAATGCCTC ATTCAGGAGC TCTGCCAGTG CCGGCCTGGA	180
GAAGGGAACT GCCCCTGCTG TAAGGAGTGC ATGCTGTGCC TCGGGGCCCT GTGGGACGAG	240
TGCTGCGACT GTGTCGGTAT GTGCAACCCT CGGAATTACA GCGACACCCC GCCCACATCC AAGAGCACCG TGGAGGAGCT GCACGAGCCC ATTCCGTCCG CTGTCGAG	300
	348
(2) INFORMATION FOR SEQ ID NO:338:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 259 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:	
CARMINGGOOG THEOLOGICAL ACCORDING CARMINGS AND ACCORDING TO ACCORDING	
GAATTCGGCC TTCATGGCCT AGCCAGTCTT CAGTTATAAC CACTCCACCC TCCTCACTTT CTCTCTCTCT CTCTCTTTTT TTTTTTTTT TTTTTTTGCTA TGGGATTTAA TGGGAAAAAT	60 120
ATGTAAAAAC TGTCACTAGT CAGCTGGCTC TTTTTCCTAT GAAATCTATC AGTACCTTTC	180
TCCATCCGTT GTTCTCAATA ATGACCACAG AGCCTGAGTA TACCAAGAAA ACCAATATTC	240
GCATTACAGG TCACTCGAG	259
(2) INFORMATION FOR SEQ ID NO:339:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 183 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) Torologi: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:	
GAATTCGGCC AAAGAGGCCT AGCCTTCTGC AAGATGCTTC TGATTCTGCT GTCAGTGGCC	60
CTGCTGGCCT TCAGCTCAGC TCAGGACTTA GATGAAGATG TCAGCCAAGA AGACGTTCCC	120
TTGGTAATAT CAGATGGAGG AGACTCTGAG CAGTTCATAG ATGAGGAGCG TCAGGGACCA	180
CCT	183
(2) INFORMATION FOR SEQ ID NO:340:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 264 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:	
GAATTCGGCC TTCATGGCCT AGTTTTAACT GAGTGCAACA AGTATTTTCG TTAAGAGATT	60
TTTTTTCGTA ATTTACCATT CTGCTGAATC AATTTTTAAT CCAGTTGGAA GCTCTAAAAT	120
TCTAACATAA TTCAGAAGCA TTAAAAAAGA AGACTAAGGA AGAGAAAGCT ACATTTTAT	180
TTCAGCTTGT ATTGCATTGT GCAGAAAGGA AAATAGTCTA GCTAATTTAC TTTTCCTATG	240

264

AAAAACCTTA GAAGGCTCCT CGAG

- (2) INFORMATION FOR SEQ ID NO:341:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GAATTCGGCC	TTCATGGCCT	AGCCTTTCTA	GTCTTCCCTC	TTCTGTAGGA	ATANCATGTT	60
CCTCAAATGG	TCCTGAACTT	TTTCACCATT	TTGGTGAACC	CTTTTAAAGT	AAATTTACTC	120
AATGCTTTAA	AATTCATAGT	CTTAAAATAA	ATGTGAATTT	TGTTTCCAGG	TATTTATTCT	180
GGGGTACAAA	AACTTCCCAG	AATTTACAGT	AGGAAAGGAA	ACCCCTTTAT	GATGTGGCTT	240
ATTATTACAA	GCATTCAGAA	ATGATGCTGG	CTAAGTCAAA	TCATTCCTTG	AGACAGTGAT	300
TCCTAAATGT	AATGCCGCCT	TCCTGAACTC	TCACATATTC	TATATCATGG	TTATTTTAAA	360
AAATATATTT	TTAGCCTTTT	GTAACCTTAG	TCTTGTTTTG	AGCAATCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:342:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 466 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GAATTCGGCC	TTCATGGCCT	AGGGATTATA	GGTGTGAGCC	ACCGCGCCCG	GCCAGGAATC	60
ATTTTTATCC	${\tt AGGTAAGGCA}$	TACAGAACCG	GAGGGTTCTT	${\tt GTCTAAGTTG}$	TACCATGAAT	120
GTGTGCTCAG	TGGCTACTTT	GAAATAGACT	TACTGTACAA	TCCCTGAGCA	GGAATGAAAA	180
TAAAAGCTGG	AAATCACGGG	TTGCTCTGGG	GTTTTCAGGA	AGGTGTCGTC	CGTCTGGGGT	240
GAGTGTCCTC	CTTTCTCANG	GGATTTCATG	TGGCATTATT	TTGTTTTCAT	CTGAGAGGCA	300
ACATAAGCTG	GGAGGGAAGG	GCTGCAAAGA	GGGGGCCAGG	ACAAATGTGT	ACCTGGGGGC	360
CCCCATTTTG	ACTCCACCCT	GAGCTGGGGC	TGGGCCACAG	GAGGGCAGAG	GGAACACTTT	420
GGGACGGGGA	GGGAGCCCCT	GGACTGAAAG	AATGGGGTGA	CTCGAG		466

- (2) INFORMATION FOR SEQ ID NO:343:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GAATTCGGCC	TTCATGGCCT	AGAATTTTGG	AGTCTTTATC	ATAGGTAACC	TGGACCACAG	60
TTACTATTTA	TTGACAATGT	GATTGAGTGT	ATGGAGGAAA	GCACAGTGGA	TGCTAGGCTT	120
TGTAAATATG	GGGATGTAGA	AAAGCAGATA	GTTCAGTGTC	TACCTTTTTC	TAGAACTACC	180
TTGAACCTTA	AATTTTAAGT	CATGTTCATT	GCTAGAAAAT	TAAATGTACT	TATTAAAACC	240
AATGAAAAAG	CACATTTCTG	AAATGAAGTT	AGAGATAATC	TCTGTGTCTT	ATAAAAAGAC	300
AAAAAAAAAA	ATCTGGTAAG	GACTCGAG				328

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GAATTCGGCC	TTCATGGCCT	AGTGACCAGA	CATAAGAACT	CATTTTTAGT	TAAAGCATTT	60
TAAAAAAGTA	TACAAGGCAG	AGTTGCAAAC	AATCTCAGCC	TATGAAAAGG	ACAGCTGCAG	120
TCAATGTTCC	CACTAATATT	TTCCATCCGT	GTACTGAGTG	AATTTGTAAT	GTGCAACTCA	180
TGTCAAGAAA	ATAAACAGAT	GTGCÁCCACA	AGCGGAACAA	CAATGAAAGA	ACTTACATAG	240
ATTTTTATTA	AGATTGAACT	TTTGATGTTG	ATTCCACTGG	TAAGAGAGCA	CTGTAGGCAA	300
AGGTCTTGTA	TTTATAAAGT	TATCTCCTAT	TGAGGAAGAT	GAAGATGTCA	ATACTCCCCA	360
ACAGAATGCT	TTGAGCTCTT	TCTAGTAGAT	CTGTGCCAAC	TCTGAAACAC	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:345:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GAATTCGGCC	TTCATGGCCT	AGTAAATACA	AAATACAAAA	ATACTGGTGA	GAGAATGGGA	60
TGATGATTAT	ATTCCTGGTT	CAGTTTTTCT	TCCTGAGAAA	TTTGATAATA	CATCTTTTGA	120
TTTTTAATAA	GTGAAATAAC	TGGTGACTGT	GTTGTATGTG	TGTGTGTGTG	TTTTTTTTT	180
TTTTTTTAAA	TAGAAGTGTG	AAAAGAAACT	TCATCCACGG	AAACTTÇAGG	ATAATTTTGA	240
AACAGGCAAG	TCATTTCCTA	TCTTTTTATA	ATCTCTGCCT	TGTGGGATTT	GGTTTGGTTT	300
ACCTAACTTT	GATTTTAGTG	GGAGTATGTG	AGCTGTGACT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:346:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GAATTCGGCC	TTCATGGCCT	AGCCTTCGGA	ACCCCACCAG	AGTCACAGCC	AGGAAGGGCA	60
GCGGGGCGCA	CCAGGCCGAA	GGCTCACGCC	ACAGGGAGGG	CAGCTAGGAC	ATGGGGGGAA	120
GCGCGTTAAA	CCAGGGAGTC	CTGGAAGGGG	ACGACGCCCC	CGGCCAGTCC	CTGTACGAGC	180
GGTTAAGTCA	GAGGATGCTG	GACATCTCGG	GGGACCGGGG	CGTGCTGAAG	GACGTCATCC	240
GAGAAGGAGC	TGGAGACCTA	GTGGCGCCTG	ATGCTTCGGT	GCTAGATGCT	TCGTCTTGGG	300
TAAACTCCTC	GACTCCCAAG	GCCCCAGCTC	CATCTTTACC	TCAGAGCCTC	CTGAACCTCC	360
TCCTCCAGCC	TCACCTTCCT	CCAGCCTCAC	CACTCCTCCC	TGGACCTGCA	GCTCCGCACC	420
CCCGGGGGCC	TCAGAACTAC	CCCTTCCAGG	GCCTCAGAAC	TACCCCTACG	GTTTCTCCTG	480

The second secon

CGTAACCTTC TGCCTACCTT CCTGAGAGTG GTTGGTGACA CGAG	GCAGCCGGGG	CTAGAAACCT	540 544
(2) INFORMATION FOR SEQ ID NO:347:			
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 570 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear			
(ii) MOLECULE TYPE: cDNA			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	347:		
GCCTTCATGG CCTACCCAGT GATTGTCACC ATGGCCAGCA TGCATGATCC CAGTGAAGAC TGTGGTGTTG CAAGATGCCA GAGACCTTGC CTGAAGGACC CCAGCAGGAT CTGCCCCCAG GAGGCAGCAC AGAACCCCAG CAGTACTGAT GGCTCTACAC ACTTTAGATG GCTATTATA TTCCTGTAAA TACTGCGATT CAATTTGTGG GACATATGAA CTCAGAGCAC ACAGACTTTA TGCAGTGGGT GCAGTTTCT GGCAAAAACC CCTGAGGGGC TGTCACTCCG GGGAAGCCAG CTTTGTGTGG AACGTGGCCA GTGGAGCAGA GCATCCCTGA GAGCACCAGC ACTCCTGACC GAAGGGGCTG ATGGACAGGC AGAGCTCGAG (2) INFORMATION FOR SEQ ID NO:348: (1) SEQUENCE CHARACTERISTICS:	GCATGGAGGC AAGCATCTGC TGGCCAATGG TCAGATCCCA ATAAAGACCC TTTCCTTGCA AGCCAGACAA	CCAGCCCGCT TGCCAGCAGT GCATCGGAGC TGACATGACC AACCTTTGTA CAATGCCACA TCATGTGGTT	60 120 180 240 300 420 480 540 570
(A) LENGTH: 300 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear			
(ii) MOLECULE TYPE: cDNA			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	348:		
GAATTCGGCC TTCATGGCCT AGAAAAAAGT TTTCAAAGGG ACTATTTTCT ATGATGGAAA TTCTGTGAAG AAACAATAAC CTGTCCTAAT AGTAAGGTGG TCTTTCTTCT AATCTCCCCA CAACAGGGTA CCTTGTGTGA GTAACTGTAG ATTTCTGACT GAGCACCTGT TGTAAGATGT GCTGCCGGAG GTTCTCCTGG	AAATTCTCCC TCCATCCACC TCTTCTCGCA	TGACTCCTGT CATCAGGAAG CCTTCAGCTG	60 120 180 240 300
(2) INFORMATION FOR SEQ ID NO:349:			
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 424 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear			
(ii) MOLECULE TYPE: cDNA			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	349:		
GAATTCGCCC TTCATGGCCT AACAACCACC ACCACCTGGA ATAGCCGGCC TCAGGGTCAC AGAAAGCAAA GGGCACTCAG			60 120

GACACTGCCA TCAGGGTTGC ATTGGCTGTC GCTGTGCTCA AAACTGTCAT TTTGGGACTG

WO 98/45437

	PCT/US98/06956	
TGACCAACAG CCGCTTGTGA	TCCTGTGGTG GAGGAGAAGG AAAGGTAGCA GGGCGCCAAG CAGTGACTTC AGTGTGGGGA GAAGGGATGT GTATTAGCCC CGGAGGACGT GATGTGAGAC GTCCTCCACA CTCGTTCCCC ATTGGCAAGA TACATGGAGA GCACCCTGAG AGGCAAAGCC GCAAGGCAGA AGGAGGCTGG GTCCCTGAAT CACCGACGCT	240 300 360 420 424
(2) INFORM	ATION FOR SEQ ID NO:350:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 445 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:350:	
CCCCGGGACA GCTTTGCAGA CAGATATCTG GGGGTGTAAA TGTAGACAAC GAGTTATTTC	TTCATGGCCT AATTAGATTA TTTTGAGCTT GGGAACACTT GTACATGGTT TAAATGTAGA AGTTCTGTAG AGCAGTATCT TCACATTGAG GGATGTGAAG GTATAGATAG TTTAATGTAA TTTAGAGTTC TTCATTATCT TTCCTAGGAT CCGATGATGA CCTTCTAACCC ATTCAGAATC TTTCTATGGT ATATTGCCCT ATCCTCCAGG ACCCTAAACA GATGGACAGT TGATGCATTT CAGGGTAAGC AATATATTTG ACCCCTGAAA CAATTCAGTA TGCTTGTCAT TTGTTAACTA AAACATAATT TTGAATAAAA AATAAATTTT AATAAATACA TGTTCCCAAT AAAGCAATCC TCGAG	60 120 180 240 300 360 420
(2) INFORM	ATION FOR SEQ ID NO:351:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 278 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:351:	
AATAGCTGTT AGAAGCAAAA AAAATTCACT	ATGGCCTAAT TTTGGAACTA AGAGACAGAT TTTTTGTTTT TGTTTTTTA AACTAGTCTC ATAAGGACAA AATACAGAAA GACAGTTCTT ACAGAGAAAT AAAGGAACCA ATGGAAAATT TAAAACTGAA AAATAGAATA TCTGAAATAA AGATGACATA ACTGTTGAGG AAAGAGTATG TGAATTGAA GAAAGAGCAA CCATTGTAAA GAACAAAGAG AACTCGAG	60 120 180 240 278
(2) INFORMA	ATION FOR SEQ ID NO:352:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 457 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:352:	

60

120

GAATTCGCCT TCATGGCCTA CAGATTATCT TACACTGAAC TGATCAAGTA CTTTGAAAAT

GACTTCGAAA TTTATCTTGG TGTCCTTCAT ACTTGCTGCA CTGAGTCTTT CAACCACCTT

TTCTCTCCAA	CCAGACCAGC	AAAAGGTTCT	ACTAGTTTCT	TTTGATGGAT	TCCGTTGGGA	180
TTACTTATAT	AAAGTTCCAA	CGCCCCATTT	TCATTATATT	ATGAAATATG	GTGTTCACGT	240
GAAGCAAGTT	ACTAATGTTT	TTATTACAAA	AACCTACCCT	AACCATTATA	CTTTGGTAAC	300
TGGCCTCTTT	GCAGAGAATC	ATGGGATTGT	TGCAAATGAT	ATGTTTGATC	CTATTCGGAA	360
CAAATCTTTC	TCCTTGGATC	ACATGAATAT	TTATGATTCC	AAGTTTTGGG	AAGAAGCGAC	420
ACCAATATGG	ATCACAAACC	AGATGGCAGG	ACTCGAG			457

- (2) INFORMATION FOR SEQ ID NO:353:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

GAATTCGGCC	TTATGGCCTA	GCAGGCGCCA	AGGTAACATG	AACAAACAGC	TGCTTGCTGC	60
CCCCAAGCTT	TAGTTTCTAG	TGGGCCTGGA	GCAATTGTGA	AGGACAACTC	CACCCAAGGC	120
CCAGTATTGA	AGAGGGGTAG	GGTGGGAGGA	TTGTACATAT	CGCGAACGCT	TGGCAAATCT	180
${\tt CTAGATTTTT}$	TTTCCTCCTA	GGAAATAATA	ATTTTTAAAA	AGGCTTGTAA	AAAATAATAA	240
AATGTTTCAT	GACAGCAGCA	GATGTAAAAC	TCCCAGTACT	CCGGGCGACC	TCGAG	295

- (2) INFORMATION FOR SEQ ID NO:354:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

GCCTAGACAT	GATGGTGGCC	ACGTGCCAGG	GGACCACACC	CTATGTACAA	AGCAGGAGAA	60
TGATGCTCCC	AGCTGAGCTG	CAGGATGGGC	GCTGGGCTGA	CTGGAGGGGT	AGACGGGGTG	120
GGGTCTGACC	CCATTAGCCT	TTCCCCATCC	AACCTGGGCC	CCCATAAGCC	ATTCTCTGGC	180
CCTCTGCACA	AGACAGACTC	AGCAAATCTG	CGAGGTATGG	GGATTCTGCC	AACTCCCCAC	240
CTCGCCTCAC	CTTCCCTAGG	TCTGCGCGTT	AGGAGATTCT	GGAGCCAGAG	GGAGAGACCC	300
CAGAAACTCC	CCGGTCGGCG	ACCCAGCCCG	AGACGCCTGG	GGTCCCAAGG	GAAGCTGAAC	360
GCCCGCAGAA	TGGGGAAATG	GAGAGAGAAC	CTGAAAGAGC	CCCTGTAACT	CGAG	414

- (2) INFORMATION FOR SEQ ID NO:355:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GAATTCGGCC	ATCATGGCCT	ACTCCCGAGT	AGCTGGGACT	ACAGGCATGT	GCCACCACGC	60
CCAGCTAATT	արդում Հարարարար	ተተተተተ የተ	AGATGGGGGTT	CCACCATCTT	አርርምአርርአ ም ር	120

ATTTCGATTT	CCTGACCTTG	TGATCCGCCC	GCCTCGGCCT	CCCAAAATGC	TGGGATTATA	180
GGTGTGAGCC	ACCACGTGGC	CTCATTTCAT	TCTTTCATGT	GGATAGGCAG	TTGTTCCAGA	240
AGTATATAGT	GAGGAGCTTC	TTCTTTCTCT	AATGATCTGC	AATGTCACCT	TCATCATTTA	300
TGAAGGTTGC	ACATATACAT	GGGAATTTTT	TAGTCTGGCA	TTAAATGTTC	TTCAAAAGAG	360
TTCCTGCAAA	CGTTTTTGTT	TTTATTTCCT	ACTGTTCCCT	TCACGTACTC	TCTACTGAAC	420
TAAACTCTCT	AATGTGTCTC	GAG			•	443

- (2) INFORMATION FOR SEQ ID NO:356:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GCGATTGAAT	TCTAGACCTG	CCTCGAGCTC	AAGAGCAGCC	CACCTGTTCA	GTATTCATAC	60
CCACATATCC	ATAATAGAGC	TCTTCTCTTC	CCCCGGGTTC	CTCTGCCTCA	GCCTTTTCCT	120
CTTAGCAGAT	GCCATCTGCA	${\tt GGGCCACTTG}$	GCTGCCCGTA	GCAGTAACCG	CACAGTCTTC	180
CACATTTACT	CCCTCAGCCT	CAGCTGCTCC	TGCAGCCCAG	GCACTGTCTC	TGTCTCTGCA	240
TTGCTCAAGC	CTCCACCATC	TCGGTTACAC	CCCACAGCCA	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:357:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

GAATTCGGCC	TTCATGGCCT	ACTGCCTTAG	CCTCCCAAAG	TGCTGGGATT	ACAGGCGTGA	60
GCCACCATGC	CCAGCCCTAT	AGTAGTTCTT	CTTTTGCCCC	TTAATATCCT	CACCCACATG	120
TCCTGTACCC	TGCCTGAACC	CTCCTCCTCT	TTTTGTTCTG	ATCTTTGAGC	TCCCTAGAGC	180
CCATAATTCT	TTAGAGCAGG	TATGTCCCGA	GTCTGAAACA	TGCCCTTATT	TGTCCCAAGC	240
TCTGGACATT	TCTCACCCCA	TCTCTCGAG				269

- (2) INFORMATION FOR SEQ ID NO:358:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

GAATTCGGCC	TTCATGGCCT	ACCAAGGAAG	CCTTTCTGTT	TTTGGCCCAA	GGAGCGTCAA	60
TAAGATCTTT	GAAAATACTT	TGAAGTCATT	TTGTGTGTGT	GTATGTGCAT	ACACACCTGA	120
TTTGTTTTAT	TTTTTATTTT	TATTTTTTGA	GTTAGGGTCT	GGCTCTGTCG	TCCAGGCTAG	180
AGTGCAGTGG	TGTGGTCTCA	GCTCACTGCA	ACCTCTGCCT	CCCAGGCTCA	AGCCGCCCCC	240

CCACCTCGAG	250
Cariot Cara	250
(2) INFORMATION FOR SEQ ID NO:359:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 258 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID	NO:359:
GAATTCGGCC TTCATGGCCT AATGGGAGAT TGGTGGG GAAAAGAAGA TAGGTTGTAT TTTGGTCATA CTGACAC GTGAAAAAAG CTAGCAGACA GTTGAACTGC GGCTGTG ACTCATCGTT GTAGTCATTC GTAAAGAGTA AATACTT CACCACGGAA CACTCGAG	CAA CATGCCTAAA GGATAGCCCT 120 SAAA CAGGAAGCCG TGAGGGCTAG 180
(2) INFORMATION FOR SEQ ID NO:360:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 259 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID	NO:360:
GAATTCGGCC TTCATGGCCT AGGAAGCCAC AGGTCGG CCCTCGCTGG CCGGGGGCTC CTGGGGTTTG TCCAGCT CTTTTCTCCT GGACATTCTC CATTCCGGGT AGAGCCG TTCACGTTGT AGCCAGTCTT CGCACTGGTC TCAATGA CGCTGCCCCC CCCCTCGAG	TGA TGTCGATCAT CCCTTCTTTG 120 ACG CCACACGTCG AAAAAGCTGC 180
(2) INFORMATION FOR SEQ ID NO:361:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 422 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID	NO:361:
GAATTCGGCC TTCATGGCCT AAAGATTAGC CTGGGTA TAAAAAATAA TAATAAAAAT AACATTCACA TTGGTAT AAGGCATTCA TTAAGGTATT GTTAAAACTT GTGTTAA TGGGATAGAA ATAAAATGTG ATAAAAAGCT GAAAGAA TTGAAAATATT AGAGACATAA TGCTGTCTAA TAAAAAA ACAGTGACTG	TGT TCACTAAGGT ATTGGTTGTT 120 AGCA TGTTAAAGTC TCAGTAACTT 180 ACC ACCACAAGGG AGAGTCCTTT 240 ACGA CATCAAAGAA AAACTACACT 300

AG

TTGATTTACT AATCTTTTAT TTAGGAAATT TACATTTTTA CATTAGTGAG ATTGGCCTCG

420

(2)	INFORMATION	FOR	SEO	ΙD	NO.362.
121	THEORETTON	ron	250	20	40.302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: GDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GAATTCGGCC	TTCATGGCCT	AGTTATTCTT	CTAATAGCTC	AGCTACTTTT	CCTTAAAATA	60
TCTTTTTCTC	TGCAAAGCCT	TCATATAATT	GTTGTTATTA	TAACAGTGAT	GATGACTGCC	120
ACTCATTACA	ACTGCTGTTG	TTAATCTTTG	TTGTTATTTT	AAACCATATG	TTATTTAAAC	180
CATAAACTGC	ATCATAAAAG	CAGTTTCTTT	CTAATCCATG	ATGACACCTG	CTAGCCAGGT	240
ATCGTATCAA	TTCTTCACAG	GTCTATTGAA	TTCTAGACCT	GCCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:363:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

AAAAATTTCA	ACAAATCCTG	AAGTCTTTCT	GTGAAGTGAC	CAGTTCTGAA	CTTTGAAGAT	60
AAATAATTGC	TGTAAATTCC	TTTTGATTTT	CTTTTTCCAG	GTTCATGGTC	CTTGGTAATT	120
TCATTCATGG	AAAAAAATCT	TATTATAATA	ACAACAAAGA	TTTGTATATT	TTTGACTTTA	180
TATTTCCTGA	GCTCTCCTGA	CTTTGTGAAA	AAGGGTGATG	AAAATGCATT	CCGAATCTGT	240
GAGGGCCCAA	AACAGAGACT	CGAG				264

- (2) INFORMATION FOR SEQ ID NO:364:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GAATTCGGCC	TTCATGGCCT	AGACCCTCAT	CAATAGATGG	AGACATACAG	AAATAGTCAA	60
ACCACATCTA	CAAAATGCCA	GTATCAGGCG	GCGGCTTCGA	AGCCAAAGTG	ATGTTTGGAT	120
GTAAAGTGAA	ATATTAGTTG	GCGGATGAAG	CAGATAGTGA	GGAAAGTTGA	GCCAATAATG	180
ACGTGAAGTC	CGTGGAAGCC	TGTGGCTACA	AAAAATGTTG	AGCCGTAGAT	GCCGTCGGAA	240
ATGGTGAAGG	GAGACTCGAG					260

- (2) INFORMATION FOR SEQ ID NO:365:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GCGCCTATCA	CAAGCAGATC	ATGGGTGGCT	TCAAGGAGAC	GAAGGAGGCT	GAAGATGGCT	60
TCCGCAAGGC	CCAGAAGCCT	TGGGCCAAGA	AGATGAAGGA	GCTGGAGGCA	GCCAAGAAGG	120
CCTACCATTT	GGCTTGCAAA	GAGGAAAAGC	TGGCCATGAC	ACGGGAGATG	AACAGCAAGA	180
CGGAGCAATC	GGTCACACCT	GAGCAGCAAA	AGAAGCTGCA	GGACAAAGTG	GACAAGTGCA	240
AGCAGGATGT	GCAGAAGACA	CAGGAGAAGT	ATGAGAAAGT	GCTGGAAGAT	GTGGGCAAGA	300
CCACACCCCA	GTACATGGAG	AACAAACTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO:366:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GAATTAACAG	AGTTTTCAGA	ATTAGAATAC	TCAGAAATGG	GATCATCGTT	CAGTGTCTCT	60
CCAAAAGCAG	AATCTGCCGT	AATAGTAGCA	AATCCTAGGG	AAGAAATAAT	CGTGAAAAAT	120
AAAGATGAAG	AAGAGAAGTT	AGTTAGTAAT	AACATCCTTC	ATAATCAACA	AGAGTTACCT	180
ACAGCTCTTA	CTAAATTGGT	TAAAGAGGTT	GAAGTTGTGT	CTTCAGAAAA	AGCAAAAGAC	240
AGTTTTAATG	AAAAGAGAGT	TGCAGTGGAA	GCTCCTATGA	GGGAGGAATA	TGCAGACTTC	300
AAACCATTTG	AGCGAGTATG	GGATCTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:367:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GCGATTGAAT	TCTAGACCTG	CCTCGAGTAC	GGAGCGAAAC	TCTGTCTCAA	AAAAAAAAA	60
AAAAAAAA	ACCGAGTATA	AAAGGCATTT	TTTTCCTTTA	AACTAAGTAA	AATATAATGT	120
TGAATAGTTC	TATTTTGCTT	AACGGGCTTT	TGTTATTTGT	TTTGTGTAGA	AATTGGCATT	180
TTTCACATAG	AAATCTCGAG					200

- (2) INFORMATION FOR SEQ ID NO:368:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GAATTCGGCC	TTCATGGCCT	AGAGAAATGA	GGAAAAAGAA	GGAAGAATAT	TTAACTTTTA	60
${\tt GTCCTCTTAC}$	AGTTGTAATA	TTTGTGGTCA	TCTGCTGTGT	TATGATGGTC	TTACTTTATT	120
TCTTCTACAA	ATGGTTGGTT	TATGTTATGA	TAGCAATTTT	CTGCATAGCA	TCAGCAATGA	180
${\tt GTCTGTACAA}$	CTGTCTTGCT	${\tt GCACTAATTC}$	ATAAGATACC	ATATGGACAA	TGCACGATTG	240
CATGTCGTGG	CAAAAACATG	GAAGTGAGAC	TTATTTTTCT	CTCTGGACTG	TGCATAGCAG	300
TAGCTGTTGT	TTGGGCTGTG	TTTCGAAATG	AAGACAGGTG	GGCTTGGATT	TTACAGGATA	360
TTCTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:369:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GAATTCGGCC	TTCATGGCCT	ACATTCGGAG	AAGTTGAAAG	AATTACACCC	AGAACACCCA	60
TGTCTACCAT	GTTACTACAT	TTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GCGTGTGCAA	120
TTTTAATTAC	AATGGTCGAG	GAAGCTCTTG	CTGAGAAGGT	GATGTTGAAT	AAAGACTCTA	180
AAGACCCTAA	AGAGTTGAGA	GAGAGCTGTG	TGGAGTTCTG	GGGCCCAGGC	ACAGCAAGTA	240
CAAAGATCCT	GAAGCAGGAG	CATTCTTGGT	GTGTTCAAGG	AAAGCAGGAC	AACCTCGAG	299

- (2) INFORMATION FOR SEQ ID NO:370:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

GAATTCGGCC	TTCATGGCCT	ACCGCCTTTC	CATTATGCAA	CTGTGGTGGC	TTTTCTTTTG	60
TTATACGACG	ATTATTTGTC	AACCCCACTA	TCTTTGCACT	CAACCATGGG	CCCCCTGGGC	120
TCAGAGACCT	CGTGACAGTC	ATCTTCTCAT	CACCACATCT	GCAAATGTGT	GGGTGGATGG	180
GGCAGCAACA	GTCCACCTCC	TCCAAGAAGC	AGTCCCTGAT	TTTTCCTCCC	CAGACAAATC	240
שייייבייייייייי	TCTTTCTTCCA	AACTCAAACA	ACTAACCACC	TCCCTCGAG		289

- (2) INFORMATION FOR SEQ ID NO:371:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

60	CCATCTGCCA	CTGTGAGTTA	CATTATCCTT	CAAGCTCGAT	TCATGGCCTA	AATTCGGCCT
120	AGTTATAGAA	TTCTGGGAAA	AAGTCGCTCT	CAATTCTCCC	ACACCCTCTT	AGTTCATCCG
180	TGGTTGCCTC	CAGGATTCAC	TACAACACCC	GATTCACAAA	TTGACCAAGA	ACAGGGAAAA
240	GACAAACGCC	CCTTGAGGCA	CTCAAGGCCG	GATCGCCCCT	AGTTCAACCA	TCCAGAGTCC
300	CTCGCCGCTG	ACTGCGGGGC	GTGGAGTCCA	GGGCGAGCTG	TCCACATCCA	TCGGCTCACG
360	GGATTCAGCC	TGGATCACCT	CCCTGGCACC	CGCCACCGAC	CCATGTCGTC	ACCCTCTCCC
420	AGTCAACAGA	TAAGAAATGG	GGCCAAGCTA	TCCAGGACAA	TTCCATATAA	AGTGCGGATT
480	GTGCACCCTG	TCACCATCCT	GTGGTGATTT	CGTCATTGCT	TCATTGGAGG	AACTCGGCTA
540	CGTTCTCGAG	ACCATACCAA	AAGGGCACCT	GTTCCGCCAC	TCCGGTACAT	GTCTTCCTGA

- (2) INFORMATION FOR SEQ ID NO:372:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

TCGACCCCTG	GCTAATGACA	AACTATGTGA	CCTTCATGGT	GGGGGAGATT	CTGCTCCTCA	60
TCCTGACCAT	CTGCTCCCTG	GCTGCCATCT	TTCCCCGGGC	CTTTCCTAAG	AAGCTTGTGG	120
CCTTCTCAAC	TTGGATTGAC	CGGACCCGCT	GGGCCAGGAA	CACCTGGGCC	ATGCTCGCCA	180
TCTTCATCCT	GGTGATGGCA	AATGTCGTGG	ACATGCTCAG	CTGTCTCCAG	TACTACACGG	240
GACCCAGCAA	TGCAACGGCA	GGGATGGAAA	CGGAGGGCAG	CTGCCTGGAG	AACCCCAAGT	300
ATTACAACTA	TGTGGCCGTG	CTGTCCCTCA	TCGCCACCAT	CATGCTGGTG	CAGGTCAGCC	360
ACATGGTGAA	GCTCACGCTC	ATGCTGCTCG	TCGCAGGCGC	CGTGGCCACC	ATCAACCTCT	420
ATGCCTGGCG	TCCCGTCTTT	GATGAATACG	ACCACAAGCG	TTTTCGGGAG	CACGACTTAC	480
CTATGGTGGC	CTTAGAGCAG	ATGCAAGGAT	TCAACCCAGG	GCTCGAG		527

- (2) INFORMATION FOR SEQ ID NO:373:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GGCAAGAAAG GATGTCCGCA	CAGCTGGCTG	CTGCTGAGAG	CAGACAAAAG	AAGCTGGAAA	60
TGGAGAAGCT TCAGCTACAA					120
AGGAAGAGCG TGGCAAGAAC					180
TCTCAGGCAA AGTCATAGAG					240
AGGAAAGAA AAAGACGAAT					300
CAGAAATGGA AGCTCAGATG					360
TTCGTGCCAA GCTGAACCGG				COCOAACACC	407

- (2) INFORMATION FOR SEQ ID NO:374:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GAATTCGGCC	TTCATGGCCT	ACTCTGTTTT	CTCCCTGGAC	TTATGTGCTT	CGTCTGGAAT	60
GTTACATCTC	TTCCTCTCTT	TCTTTTTTT	TGGTCCCCAT	GTTGACTGTT	TTATTGGGGT	120
TTCTGGATAT	CTCGGGGCCA	CCTCACAGGA	AGCGGTTTGC	AATGAGATCA	TAAACATTGC	180
CGAAAAATCT	GTTCATTACT	GCAGCACTGT	TTCTCATCCC	CTTGACTTTC	ATCACAAGGT	240
ATCCCCTTCT	GACAATAAAT	CATCTTTAAT	CATTTCTCAG	CAACCTCAAG	CCCAGCAGCG	300
AAGAGTCACC	CCCTATCTCG	AG				322

- (2) INFORMATION FOR SEQ ID NO:375:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

AAAGAGGCCT	ACCTAAACCG	TCGATTGAAT	TCTAGACCTG	CCCCAAAACC	60
ACAAGCTCAG	TCTTCTGTGT	CTTAATTTTT	GGCTTTACTC	TTAGCCCTGC	120
AGGCTCTCCA	CAGTCCAGCC	GCTTTGAGCT	ACTTTTCCTT	CCCTGATATG	180
TCACCTCTGA	GCCTCCGCAC	CTGCTGTTCC	ACAGCACTCT	CCGCATTGCC	240
GTGGCTCACT	GCTGAGCTGT	GTTCAGGCCC	TTTGGGAAAC	CCTCTCTTTC	300
CCTGGTCTGG	CTTGGGAGCC	CATGCTTACC	CCTGTCAGGA	CACCTTGAAA	360
AAAACATGAC	ACTTCCTTGT	CTGGCTGATT	TTCTTAGTGA	AGCGAGTAGG	420
GTCAGGACTT	CAGCAAGCAA	AATTCAGGAG	AGGTCATAAA	ATGTCTCGAG	480
	ACAAGCTCAG AGGCTCTCCA TCACCTCTGA GTGGCTCACT CCTGGTCTGG AAAACATGAC	ACAAGCTCAG TCTTCTGTGT AGGCTCTCCA CAGTCCAGCC TCACCTCTGA GCCTCCGCAC GTGGCTCACT GCTGAGCTGT CCTGGTCTGG CTTGGGAGCC AAAACATGAC ACTTCCTTGT	ACAAGCTCAG TCTTCTGTGT CTTAATTTT AGGCTCTCCA CAGTCCAGCC GCTTTGAGCT TCACCTCTGA GCCTCCGCAC CTGCTGTTCC GTGGCTCACT GCTGAGCTGT GTTCAGGCCC CCTGGTCTGG CTTGGGAGCC CATGCTTACC AAAACATGAC ACTTCCTTGT CTGGCTGATT	ACAAGCTCAG TCTTCTGTGT CTTAATTTTT GGCTTTACTC AGGCTCTCCA CAGTCCAGCC GCTTTGAGCT ACTTTTCCTT TCACCTCTGA GCCTCCGCAC CTGCTGTTCC ACAGCACTCT GTGGCTCACT GCTGAGCTGT GTTCAGGCCC TTTGGGAAAC CCTGGTCTGG CTTGGGAGCC CATGCTTACC CCTGTCAGGA AAAACATGAC ACTTCCTTGT CTGGCTGATT TTCTTAGTGA	AAAGAGGCCT ACCTAAACCG TCGATTGAAT TCTAGACCTG CCCCAAAACC ACAAGCTCACAGCTCACAGCCTGC TTAGTTTTT GGCTTTACTC TTAGCCCTGC AGGCTCTCCACCC CTGCTGTTCC ACACCACTCT CCCTGATATG TCACCTCTGACTCTCTTCCTTCCTTCCTTCCTTGAGCTCACTCT GCTGAGCTGT GTTCAGGCCC TTTGGGAAAC CCTCTCTTTCCTTGCTGTCTGCTTTCCTTTGCTTGTCTTTCCTTTGCTTTCCTTTGCTTTCCTTTGAAAACATGAC ACTTCCTTGT CTGGCTGATT TTCTTAGTGA AGCGAGTAGG GTCAGGACTT CAGCAAGCAA AATTCAGGAG AGGTCATAAA ATGTCTCGAG

- (2) INFORMATION FOR SEQ ID NO:376:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GAATTCTAGA	CCTGCCTCGA	GTAACCAGAG	AGTCTTGTCA	ACATTAACAC	TAGCAGTATT	60
TCCAACACTT	TATTTTTTTA	ACTTCCTTTA	TTATACAGAA	GCAGGATCTA	TGTTTTTTAC	120
TCTTTTTGCG	TATTTGATGT	GTCTTTATGG	AAATCATAAA	ACTTCAGCCT	TCCTTGGATT	180
TTGTGGCTTC	ATGTTTCGGC	AAACAAATAT	CATCTGGGCT	GTCTTCTGTG	CAGGAAATGT	240
CATTGCACAA	AAGTTAACGG	AGGCTTGGGA	AACTGAGCTC	GAG		283

- (2) INFORMATION FOR SEQ ID NO:377:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GAATTCGGCC	TTCATGGCCT	AAACAGCAAA	GAACAACTCA	TCACCGCTCA	CGTTCAGTAT	60
CTCCTCATCG	CGGCAATGAT	CAGGGAAAGC	CGCGTTCACG	TTTACCAAAT	GTGCCATTAC	120
AGAGGAGTTT	AGATGAAATT	CATCCAACAA	GAAGGTCACG	TTCTCCAACC	AGACACCATG	180
ATGCCTCCCG	AAGTCCAGTT	GATCATAGAA	CCAGAGATGT	GGATAGTCAG	TATTTATCAG	240
AACAAGACAG	TGAGCTTCTT	ATGCTGCCCA	GAGCAAAACG	AGGACGAAGT	GCAGAATGCC	300
TACATACTAC	CAGAATGTCT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:378:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

GAATTCGGCC	TTCATGGCCT	ACTGAAATTT	CAATAAAACC	AGCTTGAAAG	TTCCATTACT	60
AGAAAGATAA	GAGTGGTCAG	AAAACATTTT	TTATTAACCT	ATTTCATCTA	GTAAGAGTAT	120
CTTAAATGTT	TTTTCTCTTG	AGTACTGAAT	ACACATGCAG	GACAATGGAC	CTAAATACAG	180
${\tt TTAACTTTTG}$	TTTTTCACTC	CTTTGCTTTT	GCATTGTCAA	TAGTCCGGTA	AGGTTTAGGT	240
TCTATCAGAA	GTACTCAGAC	ATGCAGTGGG	CAATCGATAA	TTTCTACCTG	GGCCCTGGAT	300
GCTTGGACAA	CTGCAGGGGC	CATGGAGATT	GCTTAAGGGA	ACAGTACTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:379:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GAATTCGGCC	TTCATGGCCT	AGTCTGTGTG	TAGTGGAAAC	TCTATTGCCT	GCCCTGCACA	60
TCTGCTCCTT	TTCTTCTCTG	CACTCTGGGA	CAGCTTCTAA	AGTTTGTCCA	ACATGTCATT	120
GACTGAGTTT	TGTATCATTT	CAGTTCTGCT	CTTTACTGGT	TCCTATGTGG	ATGCTAATTA	180
TGCAAATGCA	TTTTCCACCT	CTTGCACTCC	TTTTTCTAAG	TCACCTCACT	TCTCATTTCC	240
TCATGTTTTT	CCNTTATCCT	CTTCTCTCGA	G			271

- (2) INFORMATION FOR SEQ ID NO:380:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GAATTCGGCC	TTCATGGCCT	AACGCGGCCA	GGCGATTCGG	TGAAGCGATT	CCTGCAGGCG	60
TTGGTTCCCC	TCTTTGACCT	GGTACAAAGA	ATTTTACGTG	AAAGATTTTG	TCGTCAGAGT	120
CCACATAGTA	ACCTATTTGG	AGTGCAAGTA	CAATACAAAC	ACTTAAGTGA	GCTGCTGAAA	180
AGAACTGCTC	TCCATGGAGA	GAGTAACTCT	GTCCTTATTA	TCGGACCCCG	AGGATCAGGA	240
AAAACTATGT	TAATAAATCA	TGCTTTGAAA	GAACTCATGG	AAATAGAAGA	AGTGAGTGAA	300
AATGTATTAC	AAGTTCACTT	AAATGGACTG	CTGCAGATCA	ATGACAAAAT	CGCCCTAAAG	360
GAAGTCTCGA	G					371
(2) INFORMA	ATION FOR SE	EQ ID NO:381	l:			
(i)	SEQUENCE CH	ARACTERISTI	CS:			

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GCAGAGTTAA	GCAAATTAAT	TATAGCTATC	TTTAAGCTAT	AAATGTGTTA	ACATGTATAT	60
ATACCATTTA	TTATGTTCTA	CTTTAGTGAT	ATACCTTAAT	TTAGTGGGCT	TTGGCAGGGC	120
GGGGGAGGGG	GAACGTTCAT	TAATCTCTGA	GGAAAACAAA	ACCTGTTTTC	TACTTGAGTC	180
TAACATATGG	TCCCAATTTA	TTAATACTTC	TGTTAAATTT	GATGTCAGGT	CAACATTTTT	240
CAGAAATGTA	TTTATTCTCA	GAAACAGAAC	ACTCGAG			277

- (2) INFORMATION FOR SEQ ID NO:382:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

GAATTCGGCC	TTCATGGCCT	AGTTGTTACT	GGAGTTAAAG	AGAGAACTGA	GAAAGACAAA	60
GGAGTAGAAC	GTTTACTCAA	ATAAGTAATA	ACAGAAAACT	TTCCAAACCA	GAATATACAG	120
GTACAGGAAG	GTCAAGGGTC	ACCAATCCGA	GTTAACTCAG	ACAAGAATAC	TCCAATTTAC	180
AAACTCATAA	GGGTCAAAGA	CAAAGAGAGA	ATTTAGAAAA	CAGCAGGAGA	ATAGAAGCAA	240
ATAACATATA	AGATAGATCC	AATATGCTTG	GTAGCAGATT	TCTCAGCAGG		290

- (2) INFORMATION FOR SEQ ID NO:383:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GAGAGTGTGG AGAGGGTACA	TTTCCCTTGT	ATNCTATGTT	CTTCTTTCTA	GTGGGTCTCA	60
TGTAGAGATA GAGATATTTT	TTTGTTTTAG	AGATTCCAAA	GTATATATTT	TTAGTGTAAG	120
AAATGTACCC TCTCCACACT	CCATGATGTA	AATAGAACCA	GGAATAAATG	TGTCNTTGTG	180

ATAATCCCAT AGCAATTTAT GGTAAGAACA AGACCCCTTT CCCTCACCAC CGAGTCTCGA	240 241
(2) INFORMATION FOR SEQ ID NO:384:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 299 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:	
GAATTCGGCC TTCATGGCCT AGAAACACAA TAAAGCCCCA CAACAGCAAA CTTTTTAAAC GACGAAAGAG AGCTCTAAAT AACAGCAAAA TGCTGCTCTT CTTGCTCCCA TTATGTTTAC TATTACTGTG CTCTAGTGAG AATAGCAAAG GGTCAAAGGA ATTTATAACA CTTCCTATAC CTTCAACTTA CCAAGTCCCC TACCAAGTAA CAGTTTTCTG TCAGAGAGAA AGTTCTGCCC TCCCTGCTCA AAGGTGTCCA TGCCAACTAG ACTTCCCCTG TAGCTACCTG GGTCTCGAG (2) INFORMATION FOR SEQ ID NO:385:	60 120 180 240 299
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 546 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: gDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:	
GAATTCGGCC TTCATGGCCT AGAAAGAGGT GGCAGAAGGA ATGGTAGGAA GGGGAGGATG TAAGCGATAT CATCAAGTCA GAATCATGAG TTCTTGGTGC CCGGATGTTA GAGGAGGAA AAGGTGAAGA TGGCTGAAGC TGTACACTTT CATGATGGTG GAATGGAGGG GTCCCTTGGG AATTAGGGGT GTCTCTAGGA AGAACCAGCT TAGGGTACAT TGAGAAAGAG GAGACAGGCT AGGCAGGTCT AGAATTCAAT CGCAGATCAC AGCATCACAGG ACCAGGCCTT TGATACTCTG AGCCTCGATA GCTCTGATAG CATGGAGACC AGCATCTCTG CTTGCTCACC AGACACACTC TCTAGTGCCA GCACTTCAAA TATTGCTAGA ATAGAAGAAA TGGAGAGACT TTTGAAGCAG GCTCATGCAG AAAAGACGCG GCTGCTCGAA TCCAGGGAAC GGGAAATGGA AGCCAAAAAAA CGAGCCCTGG AAGAAGAAAA ACGACCCGG GAAATCCTGG AAAAACGATT ACAGGGATAG CTCGAG	60 120 180 240 300 360 420 480 540
(2) INFORMATION FOR SEQ ID NO:386:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 317 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:	
GTTAGGATCA TACATCATAG GTGTATGTTT AACTGTTCAA GAAACTGCCA AACTGTTTCC CAAAGTGGTT GTATTGTTTT ACATTTCCAC GAGCAGTGTT TGAGAGCTCC AGTTCTTGCA CATCCTAGCC ACAAAAAGGT TCTGTTTTTT AAAGACAATT TTTTTTTCT TTGAGAGTTT	60 120 180

AAATGAGATT TCTCGAG

CGCCCTAGTC GCCCAGGCTG GAGTGCAGTG GTAAGCGAAT CCCTGCTACA GGCCAGAGAC

TGTTCTCAGT TGGTTTTTAC ACCAAGTATC GCACTTCATT CTAACACTCC ACCATTTTAC

240

300

(2) INFORMATION FOR SEQ ID NO:387:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 234 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:	
GAATTCGGCC TTCATGGCCT AGGTCAGGTT AGTCAGCTAA TCGATAAGAG ACTTGAAATT ACTCTTTTGG GATTAGCAAA TAGAAGGGAA AAACATGATA AGGGCACAGA GCGGTGGGTC TGGGGGAAAA AGCAGAGGCA CAGTTTGAAA AAAATGTGTA AGAGACTGAC TAGGTAAGAT ATGGTCACAG TTCATAAGTC CTTTGAATTC TAGGATTAAA AAGGTGAACT CGAG	60 120 180 234
(2) INFORMATION FOR SEQ ID NO:388:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 294 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:	
GAATTCGGCC TTCATGGCCT ACTAGATAAG TGTCAATTCC ATCTGCTTCT GATTTCCCAC GTCACTGCCC TGGTCCACAC ACTGTGATCT TCTGCCCCCA TCTGAGTGCC GCATACTCAG CCTTGTCCCT GCATCAGACC CCGGCCCAGC ACAGTAACGA GAATGGGCTT CCTAAACACA AATCTGATTT GTTCCGCCTT CCACTTCCTA GTGGCTTCAT TCTCGTGCCC TCACTCAGGG CCCTCACACACA TGCTGTTCCC TGCACCTCCG ACACCCTTCC CAGCGCCCCT CGAG	60 120 180 240 294
(2) INFORMATION FOR SEQ ID NO:389:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 215 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:	
GAATTCGGCC TTCATGGCCT AAGCAAAGCT AAGTGTAAAA CTAAAAAGCA GTTTGTTGCA ACTGGTCATA AAAGTGATTA AATCTAAAGC TGGCATTAAT AAGGAAGCAA GGTAATAAAA CAAAAATATA AACAGCTTTG AGAAAGTACA CCTAATAACA AAATCTTGTA ACACAACAAA TGAAAATCAC AAAAAATATA AGGAGACTCC TCGAG	60 120 180 215
(2) INFORMATION FOR SEQ ID NO:390:	
(i) SEQUENCE CHARACTERISTICS:	
220	

- (A) LENGTH: 477 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATTCGGCC TTCATGGC	CT AGAAAAACAC	TATAGTCACG	CAAGTAATGA	CCCTTCTTAT	60
CCTCAACCCC CAGCATATA	T GCACAAGGAC	AAACAGTATA	CATACAATCT	CACCTGAGAG	120
ACGTCCTCAG ACTTGTGT	G AAACCTTATC	ATGCTGCATT	ATCTCCCTTA	CAACATCCTT	180
CCTGCCTTGT TTCTCATT	T CACACTATAC	GGAGTAAAAA	AATATACAAT	TTCTATATAT	240
TATATATATA ACCTCCATA	T ATTTTATACT	ATTTCATATT	TTTATACTAT	CAGATTAATG	300
TTTTATATTT TATCTATCA	T TTTAAATATG	CTATGTAAAG	CATCTACAAA	ATTGGTCACC	360
ATTCCTATGG GAAGTATC	G CAGAACTCTA	GAAATGAATT	CATCTTTTGC	TTACCCCTCC	420
CTTTTTGAGG GGACAGGG	C TTTCTTCTTT	TCCCTCATCT	TCATCTTCCC	CCTCGAG	477

- (2) INFORMATION FOR SEQ ID NO:391:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GAATTCGGCC	TTCATGGCCT	AGTTAGTCAG	AGTGAAATAT	TCAATAATGA	GTGGTGCAGC	60
CTTGGGACTT	GAGATTGTTT	TTGTCTTTTT	TCTGGCATTA	TTTCTGCTTC	ATCGATATGG	120
AGACTTTAAG	AAACAGCATA	GACTTGTGAT	TATTGGAACA	CTGCTTGCTT	GGTATCTCTG	180
CTTTCTTATT	GTCTTCATAC	TGCCTCTGGA	TGTTAGTACG	ACAATATACA	ACCGGTGCAA	240
GCTCGAG						247

- (2) INFORMATION FOR SEQ ID NO:392:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GAATTCGGCC	AAAGAGGCCT	AGTCATCTGC	ATTTATTATG	AGCAGCAGGT	GGGACACTTC	60
CAGCAACAGT	AAAAAAAGT	AATTTACAAA	AGCAGGTTTC	AGTGAAGCCA	TCTGGTTGTT	120
ACCCTTGGGT	GCTCACACGT	AGATGCCAAC	CCAGAGCAGC	AGGAAGAGGA	CTCCAAAGCC	180
CATGAAGAGT	GAGGCCACTA	AGGAGATGAG	GAGCTCTTTA	TAGATATCAC	GAGTGTACTT	240
GGTAGAGGTG	ACCTCGTAAA	CGAAGAACCA	GGCGGTGAAG	AACATGCCAA	TGGCCAAAAG	300
CACCACGGTC	AGATGGGGGA	AGACAGCTGG	GTTCACTGGG	CTGGTATATC	TGCTCATGGC	360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:393:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GAATTCGGCC	AAAGAGGCCT	ACCCTGGGTT	AACATTCAAG	ATGGTACATG	CTGAAGCCTT	60
TTCTCGTCCT	TTGAGTCGGA	ATGAAGTTGT	TGGTTTAATT	TTCCGTTTGA	CAATATTTGG	120
${\tt TGCAGTGACA}$	TACTTTACTA	TCAAATGGAT	GGTAGATGCA	ATTGATCCAA	CCAGAAAGCA	180
AAAAGTAGAA	GCTCAAAAAC	TCGAG				205

- (2) INFORMATION FOR SEQ ID NO:394:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GAATTCTAGA	CCTGCCTCGA	GCCGGAGATG	GANAAGAAAG	TCAGCCTACT	CAAGGACAAT	60
AGCTCTCTGG	AATTTGACTC	TGAGATGGTG	GAGATGGCTC	AGAAGTTGGG	AGCTGCTCTC	120
CAGGTTGGGG	AGGCACTGGT	CTGGACCAAA	CCAGTTAAAG	ATCCCAAATC	AAAGCACCAG	180
ACCACTTCAA	CCAGCAAACC	TGCCAGTTTC	CAGCAGCCTC	TGGGCTCTAA	TCAAGCTCTA	240
GGACAGGCAA	TGTCTTCAGC	AGCTGCATAC	AGGACGCTCC	CCTCAGGTGC	TGGAGGAACA	300
TCCCAGTTCA	CAAAGCCCCC	ATCTCTTCCT	CTGGAGCCAG	AGCCTGCGGT	GGAATCAAGT	360
CCAACTGAAA	CATCAGAACT	TCTCGAG				387

- (2) INFORMATION FOR SEQ ID NO:395:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GAATTCGGCC	AAAGAGGCCT	ATCGAGAAGC	CTTGTTTATT	TAATGTGAGT	TTGTGCCTTT	60
TTGTCTCAAT	CTTCCAATAC	AGGTATATTG	AGAAAAAAAG	CAGTCTAATA	AAATCCTAGA	120
CAGAACTTTC	TGGAGTCCAG	TTTGGTGATG	TCCATTTTCC	AGCTGTATGT	ATCCTCAAAC	180
TTGCACTGAT	AACCGCCATT	TTACCAGGGC	AGGATTAGGA	AGAGGTACAA	AGGTGTGTCT	240
${\tt GAAAATTTTT}$	GCACGTGGAT	TTCTGCATAT	AATAGTCCCG	TGTCAGTTTA	CTTATGCAAA	300
CATTGCACAT	CTGAATTGTA	ATTCGGCCGT	TTCCTACTGA	CAGGATGTCC	TTTTGCTTTT	360
GTCTGCCTCC	TCTTCACATC	TTCCTCTTTA	TCCACCCTGC	AGCCGGGGGG	CGGGGGAGAC	420
CGGATCCCAG	GCAGGACAGT	GGCTAGGCTG	CGTGTCCCCA	CCCCCGACCC	TCGTTTGACC	480
CCTGGGAGCC	GGGGCGAAGA	CAGCACAAGG	ACGGAGCCCT	CGGATCCCTC	ACGAGTGGGG	540
CAGAGGCTGC	GGG					553

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAATTCGGCC	AAAGAGGCCT	ACAAGGTTAC	TTGACCAAGA	TGGTGACATT	GTAAGATTTG	60
AACAAAGGAA	ATGTGACTTC	AGAGTCATGG	TTGTTAACTA	${\tt TGCTATGAAG}$	TAGGAAAACT	120
${\tt TTATGAGGTC}$	TTTTTAACTC	AAACAGTCGA	GTTTTAAGTT	${\tt GAGGGTTAGC}$	AATGATGAAT	180
${\tt GAGTGGCCAA}$	AAAATGTATT	CATATTTTTA	GTCTTTCTTA	GAATTACTGG	TAGTTGTGCA	240
CAACTAGAGG	GTATTTATTT	GTGTGTGTAT	GTGTCGTGTG	TGTACGAGTG	CTGGAAATAC	300
TCTGCCAGTT	TACAGTAGAG	GCAGGCTTAC	ATAATTCAGT	CATGAAAGCT	GAGGCTTATA	360
GTTTAGAGGG	GATCGTCCTC	TTCTTAATGA	GTCTGTAAGT	TACAAAAATA	ACTTTTTTCT	420
TTATTTACTA	ACTGGTTGGT	TTTTAATATT	AAAATATTAG	GTGCTTCTCG	AG	472

- (2) INFORMATION FOR SEQ ID NO:397:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAATTCGGCC	AAAGAGGCCT	AGATTGGGGG	ACATTCTTCT	TTAGAAGGAA	AAGAGTCTAA	60
TTAGTGGATA	TTAAGTAATT	AAATAATACA	TACTATCAAA	TATTATGAGA	GTCACATGAA	120
CCATGAAGTC	TTCACTTAAT	TTAGGAGAAA	TGGGGAATAT	TTTCTATCAT	TCCTGATAAC	180
AGAACTAGAT	ATTTCAAGAT	CATAGTCATG	GAATGTAATC	CATAATACCA	AACAGGGTGC	240
TTTACTTTGA	AGCCATTGAC	CATTAAATTT	GATTGTTAGT	AGCACAGGCT	ACCAAAAAAT	300
AGCAAGGAAT	ATGGTATCCA	CACAGATCTC	GGCTGGCCTC	AAGTAATCAA	AAGTGAGAAT	360
GAAACATACA	TGACACAACT	GGGGACCTCT	GGGTTTCTGA	GACGTGGGCT	ACAAGATTAT	420
ATTAGGTAGA	AAACTAAAGG	AAATGTATTC	CAAGCAAAAG	TGGCAAGGGA	ATTTCACAGA	480
ACTAATTTTT	TAAGGGAGGT	AATAAAAGCA	GCAGTTAAAA	TGCATGTCCA	TGTATCAGAT	540
TCCTGGAG						548

- (2) INFORMATION FOR SEQ ID NO:398:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

60	TGAAGACAGC	ACCGATTTTC	CCGGCACGAG	AGGCTAAATA	AAAGAGGCCT	GAATTCGGCC
120	CCGCCCTGCT	GAATGATAAG	AACACCTCTG	AGCGGAAAAA	CTGTTAATCC	AGATTTATCA
180	CTTCGTGTGC	CAGCCTTGAC	ATTGTGGTAT	CATCCCTCTG	TGGAGTGGAT	CCAGGGAGGA
240	GCACAAGGGC	AGCTGGAGAA	AAGGAGCTGC	GGAGAACTGC	TCTCAAACTC	CTCATCCACT
300	CACGGTGATC	CCATCCTGCC	GGCTGGGGCT	GGTGGAGTCG	GCGTGGTGGT	GAGATCCTGG

CTGGCCAACA TGATGAATGG CGGCCCGGCT GCCCGCTCGG GGAAGCTGAG CATCGGGGAC CAGATCATGT CCATCAATGG CACCAGCCTG GTGGGGCTGC CCCTCGCCAC CTGCCAAGGC ATCATCAAGG GCCTGAAGAA CCAGACACAG GTAAAGCTCG AG	360 420 462
(2) INFORMATION FOR SEQ ID NO:399:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 428 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:	
GAATTCGGCC AAAGAGGCCT AGGCCGGGCA CACAGAAAAA TGCGAGGAAT AGAAATGCTT GCATACTCTT GATTTTTTT TTTTTTTTG GTGTAAAAAA CACACCCTCC CCTCCCACCC CAAAAAACAT CAAATTCCTT CCTTTTCCCC AAATCCCTGG ATCTTGGAAT GAAAGCCACC CTTCCCCAAT CTGTCCTCAC CTCCTTCAGC CCATCCAAGT TATGCACAAA AAACAAAAA TTAGTGAGAA ATTTGGGGAT TTGCACAACA AAAAATTAGA TAATGTTTTC CAAAACTAGG TCTTCTATGC TGTGTCAAAA AAAGTTTCCT ACAGACTGAG GATATTCACA CGACAGGAGC CTGGGGGTTA AATGAGCCTT TATTAGAATG TTGTAGCAGT TGTGTTTGAA GGCGGTGGCC CTACAAAA	60 120 180 240 300 360 420 428
(2) INFORMATION FOR SEQ ID NO:400:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 269 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:	
GAATTCGGCC TTCATGGCCT AAGTTGAAAC TTACGAGTAA CATACCTGGT GTCTGATTGG TTGTCATACT TTTCATTTTC CCTCCTTTCA GATCCAATCC ATTCTACACA TTATACTGAT TTTTTCCTAG TGTACTGATT TCTGTTATGT CACTTTGCTG CTTAGGCTTC TTAATGCTTA CTGTATCAGG TGTAAACACC TTTTGCTTAC CTTTCCAGGC CTTTTTAGAG TCTTATATAG CTTACTCCCA TGCTCCAACT CCCCTCGAG	60 120 180 240 269
(2) INFORMATION FOR SEQ ID NO:401:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 236 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:	
GAATTCGGCC TTCATGGCCT AGGCACTTTG AAGAGATATA GAACTCCGTG TATCACATTT TCCATTTTTA TTTCAATTTT TAATTGCCCA GAGCCTAATT TCTGTGGGCC TCTGCTGATT TGCACATTTG AGATTCGTGT GTAAATATGC GTGTGGCATG TGTACACGCC TGGGCCTCCT TATCACAAAG TGTGCTCTCT CAGTGTTTAA ATACACACAA TCCACATCGA CTCGAG	60 120 180 236

(2)	INFORMATION	FOR	SEO	ID	NO:402:
\ /	THE ORGENIA TON	7.01	~~~		11011021

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GAATTACCTT	ATACACATAG	CCTGAAGGTA	ATTTTATACA	ATATTTCCAA	TAGTTTTGTG	60
CTTCAAACAA	AGTTTGGGTA	CATTGAACCA	TCAGAAAGGA	AAGGTGTCAT	TGTCTCAGCC	120
ACCCATGTGG	ACAATCTCTG	GTTGTTTGGC	ATCACTGTTG	TTGCTGAGTC	TGAATGTGAG	180
GAACATGCCA	TTGGCATGTC	TTGCCCACAC	ACACACCATT	TTGTTATCTT	TTGTGGGTGT	240
GCTTATGTGG	GGGAATCTGG	GCGTGTGTGA	AAAAAATATA	TTGCAGCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:403:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GAATTCGGCC	TTCATGGCCT	ACTTGGGGTA	CTGAGATACA	TGGGGCCGAA	AAGGGGTAAT	60
ATGGCCATCT	TTTATCAGAA	AAAGTGACAA	AACGGGAATT	TAAAAAATGA	ATTTTCCATC	120
TGACTTTATT	TCCAAATACA	CTTTCTTTTT	TAAAAAACCA	ATACACTTTC	TTTGAGGATG	180
ACAGTATTAG	GAAATCCAAT	TATACAAAAA	ATACTACATC	TAGTCTGGGG	TAGATATATT	240
TATTTTTGGT	AACATACATT	AAGTGGCACT	AATTACACAG	TAACTATAAG	GTAACTAACA	300
TGAAACCACA	GAACTGTAAC	TCTGCCACAG	CTGCATGAAC	TCGAG		345

- (2) INFORMATION FOR SEQ ID NO:404:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GAATTCGGCC	TTCATGGCCT	AAAAAAAAA	AAGCCATTAA	TCTAATTAAT	TGTTTAATCC	60
TGCTTACAAG	ATTATCTTGA	AAAAATGTGC	TGGGGAGTAT	GGTATAATGA	ATTACGGGTC	120
CAAGAATTTG	GGTTCAGATA	CCACCTTCAG	TCTTTACTAA	GCTGCGTGAC	TTTAGCAAAG	180
TGCTTAGTCT	CTCTAAGCTT	CGGTTTCCTA	ATCTATGAGG	AGGGCCTAAG	ATATCACCAC	240
CCATCACTCG	AG					252

- (2) INFORMATION FOR SEQ ID NO:405:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GAATTCGGCC	TTCATGGCCT	AAGAATACGA	AATTTGAGAG	GATGAATTTG	ACCTTTAATA	60
TTGTTGGACT	TTGTATTGGA	TATCTTTCCT	CCATCACTTC	AAAATCGTCT	TGCTTGGCCT	120
${\tt CTTATTGCAA}$	CCACAGCTGC	AGTAGACAGT	${\tt TCCATACAAG}$	CTTCCAAGAA	CTTCATGGGT	180
ACATCTGGAG	AGCACCTCAC	CTGGGGCCAC	ATTCTCTACC	TTTCCTGTCT	TACTCTTCCT	240
CCTCTGGGCT	TCTTTCTGGT	GCATGGGGGT	GGGGGGAGAT	ATTAAGTATT	CCCCAACAGC	300
TCGAG						305

- (2) INFORMATION FOR SEQ ID NO:406:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

GAATTCGGCC	TTCATGGCCT	ACACAGCAAC	AACCAACATA	GCTAATACAG	AAAGCAGTCA	60
GCAGACTCTA	CAGAATTCCC	AGTTTCTTTT	AACAAGGTTG	AATGATCCTA	AAATGTCTGA	120
AACGGAGCGC	CAGTCCATGG	AAAGCGAGCG	TGCAGACCGC	AGCCTGTTTG	TCCAAGAGCT	180
CCTTCTGTCC	ACTTTAGTGC	GTGAAGAGAG	CTCATCCTCA	GATGAGGATG	ATCGGGGGGA	240
GGTTCTCGAG						250

- (2) INFORMATION FOR SEQ ID NO:407:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GAATTCGGCC	TTCATGGCCT	AAAAGAAACT	AGGTGTGATT	GGAAGGAAGA	ATCATGAAAG	60
ATCAGGGTAG	ATACTGGTGG	GGCAGCTATT	AAAGGAGTTT	GAGCAGGGGC	ATGACATCTT	120
CACATTGAAA	GCAATATGGG	AGTCGAATTA	AATTTAGTAC	CCAGTTGAGA	TAAAAGTCCA	180
TTGCCATATT	CACAGTGAGG	TGGGACAAAA	GCAGAGTCAG	AGAGATTAAG	AGGCTGGGAA	240
AGATTGAAGT	GATTTTTAGG	AATCAGAATC	CACATCAGTT	GATGACAAGT	ACAGAAGGGC	300
ACAATAGCAA	GAAGAAGAAG	TAAATGATAA	TTCCTAGATG	CCATTAGTCA	CAATCAAGTA	360
CGGAAGAGAC	ATTATTGACT	GAGGTTGAAT	CAGGGCAGAG	AAGATAATAT	ACCTGATTTT	420
GGAAGTGTTG	CATGTAAGGG	GGCTTCGATT	TCAGCTACTT	ACATACTTGG	GAAGTCTCGA	480
G						481

- (2) INFORMATION FOR SEQ ID NO:408:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs

The second secon

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

GAATTCGGCT	TCATGGCCTA	CCCGGCAATT	GGCTGATCCG	CAGAAACATT	TCTGGGCTTC	60
TTTTCCATAT	CTCTGGAACT	GATAGTCAAA	CGTTAACTCT	GAGCCTGAAG	GAACCAGTTT	120
${\tt GGTGGTAAAA}$	AACCCAACCC	TCAGTTGTCC	GTTCACAGTC	CATTTTTGGG	TTTCACAATT	180
TGGTTCACAG	CTGTGATTCA	TGAAACGAGA	GCAATTTCCT	TTTTGAGTGG	CATCTATTAT	240
CTCATCATTC	TTCAGGGCCA	TGAAATAGTA	ATGGATGTTT	TTGTTTCGTG	CATACTCCTT	300
CACTCGAG						308

- (2) INFORMATION FOR SEQ ID NO:409:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GAATTCGGCC	TTCATGGCCT	ACAATGAGGA	TAATACAAAA	GAGCAATCTG	CCCCACTGTG	60
AGCCTGAGCT	TCCCATACTG	ACTTCTCTCT	CTCCAGAGGG	ATCCACTCCT	ACCAGTCTGG	120
AAAGCACTGG	GCATACAAGC	GCACAAATGC	GTGGCACATA	CTACAAATCC	TTCTAAAGCC	180
ACTGCTGTAC	ACCTGCCTCA	CTTAACCATG	CAGCCTCAAG	GCTGTCTCAT	GTCATTCTTT	240
CCTACAGCTG	CAGAGTTTTC	AACATATGGA	CAGGTGTGCC	AGGATTTATT	TGACTAGTCT	300
CTTACTGATC	TAGCTCACCT	CCTAAATACA	ACTCGAG			337

- (2) INFORMATION FOR SEQ ID NO:410:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

GAATTCGGCC	TTCATGGCCT	AAAATGTGGG	GATTGGGAAC	CACTAGTTCT	TTCAGATGGT	60
ATTCTTCAGA	CTATAGAAGG	AGCTTCCAGT	TGAATTCACC	AGTGGACAAA	ATGAGGAAAA	120
CAGGTGAACA	AGCTTTTTCT	GTATTTACAT	ACAAAGTCAG	ATCAGTTATG	GGACAATAGT	180
ATTGAATAGA	TTTCAGCTTT	ATGCTGGAGT	AACTGGCATG	TGAGCAAACT	GTGTTGGCGT	240
GGGGGTGGAG	GGGTGAGGTG	GGCGCTAAGC	CTTTTTTTAA	GATTTTTCAG	GTACCCCTCA	300
CTAAAGGCAC	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:411:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GAATTCGGCC	TTCATGGCCT	ACCTGAACCC	CTTACTTCGA	AGGATCATAA	GATTCACAGG	60
GGTGTTTGCA	${\tt TTTGGACTTT}$	TTGCTACTGA	CATTTTTGTA	AACGCCGGAC	AAGTGGTCAC	120
TGGGCACTTA	ACGCCATACT	TCCTGACTGT	GTGCAAGCCA	AACTACACCA	GTGCAGACTG	180
CCAAGCGCAC	CACCAGTTTA	TAAACAATGG	GAACATTTGT	ACTGGGGACC	TGGAAGTGAT	240
AGAAAAGGCT	CGGAGATCCT	TTCCCTCCAA	ACTCGAG			277

- (2) INFORMATION FOR SEQ ID NO:412:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B' TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GAATTCGGCC	TCATGGCCTA	GTGGTAGGGC	TGAATTCGCA	CTATAGGGTT	AGATTTTCTA	60
CTGTAGGGTT	$\mathbf{AGATTTTTT}$	AATGGTGTGT	ATATAATAAT	ATAATATTAA	TAATAATCGG	120
AGAGGGTCAA	AGAGGAGGGA	AACTGGGTAA	CCCAAAAACA	TAAGGTCGAG	GTCCCTGTTC	180
TTCACCGGAA	AGAGGGTCAA	GGACCAAAGC	CATAGATTTG	ACTGGTAGTT	TAGTTTAGTC	240
CTGTCTACGA	AGAAGAAGAG	CGGTTGTTTG	TTTTAACAGA	TTCAAGAGCA	GGAAGCACTC	300
ATTTAGATAA	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:413:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GAATTCTAGA	CCTGCCTCGA	GTCAGGCTTT	TAAAAACAAT	CTCATCTGTC	CCTCTAAAAA	60
TTAGCTTCCT	TTAGAACCTC	TTCTCCTTGG	CAATATATTA	GTGATACTAT	TGTTATCTTC	120
ACACTAAAGA	TTCAAAACTT	TAGTTTTTGT	TTTAGGAAAG	TTTTTTTTTT	TTACATTTCT	180
TTCATCCTTC	ATAATTACCC	AGTCATCATG	AACTTTGTAG	TTATCTATTT	CTTCATAGGA	240
ATCCTCGAG						249

- (2) INFORMATION FOR SEQ ID NO:414:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GAATTGATAC	TAGGGACCGA	AGGGAACTAA	GAGACTCCAG	AGACATGCGG	GACTCAAGGG	60
AGATGAGAGA	TTATAGCAGA	GATACCAAAG	AGAGCCGTGA	TCCCAGAGAT	TCTCGGTCCA	120
CTCGTGATGC	CCATGACTAC	AGGGACCGTG	AAGGTCGAGA	TACTCATCGA	AAGGAGGATA	180
CATATCCAGA	AGAATCCCGG	AGTTATGGCC	GAAACCATTT	GAGAGAAGAA	AGTTCTCGTA	240
CGGAAATAAG	GAATGAGTCC	AGAAATGAGT	CTCGAAGTGA	AATTAGAAAT	GACCGAATGG	300
GCCGAAGTAG	GGGGAGGGTT	CCTGAGTTAC	CTGAAAAGGG	TAGGCTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:415:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 529 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GAATTCGGCC	TTCATGGCGT	TAAAACTGTG	CCTAACAGAG	GTGTCCTCTG	ACTTTTCTTC	60
TGCAAGCTCC	ATGTTTTCAC	ATCTTCCCTT	TGACTGTGTC	CTGCTGCTGC	TGCTGCTACT	120
ACTTACAAGG	TCCTCAGAAG	TGGAATACAG	AGCGGAGGTC	GGTCAGAATG	CCTATCTGCC	180
CTGCTTCTAC	ACCCCAGCCG	CCCCAGGGAA	CCTCGTGCCC	GTCTGCTGGG	GCAAAGGAGC	240
CTGTCCTGTG	TTTGAATGTG	GCAACGTGGT	GCTCAGGACT	GATGAAAGGG	ATGTGAATTA	300
TTGGACATCC	AGATACTGGC	TAAATGGGGA	TTTCCGCAAA	GGAGATGTGT	CCCTGACCAT	360
AGAGAATGTG	ACTCTAGCAG	ACAGTGGGAT	CTACTGCTGC	CGGATCCAAA	TCCCAGGCAT	420
AATGAATGAT	GAAAAATTTA	ACCTGAAGTT	GGTCATCAAA	CCAGCCAAGG	TCACCCCTGC	480
ACCGACTCTG	CAGAGAGACT	TCACTGCAGC	CTTTCCAAGG	ATGCTCGAG		529

- (2) INFORMATION FOR SEQ ID NO:416:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GAATTCGGCC	TTCATGGCCT	ACTGAGCCTA	GTAATTCAAG	GCTGCAGTGA	GCTGCGATCA	60
CATCACTGCA	TTCCCGCCTG	GGCAACAGAA	GTAGACTCCA	TCTCTAAAAA	GAAGGAAAGA	120
AAAAAAGGAA	GAAATATACA	GTAATTTTAA	ACTGGGAGAT	GAAATGCTAA	TTTCTAGAAG	180
TCCATTTGGT	TTTGAAGGGT	CTCATGTCAA	AAAAAAAA	AAGTAAGTAA	AATAAGACCC	240
ATCCTACTGT	TTTATATACT	AAAATAGTAA	GTTAATTAAA	TGAAAATGAA	GTACATTTGG	300
GCTTTCATTT	ACCAATCCTG	GAATGTTGAA	AAGTTGCCCA	AAAGACATTT	AGCAAGACTC	360
GAG						363

- (2) INFORMATION FOR SEQ ID NO:417:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

60

120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:
GAATTCGGCC TTCATGGCCT ACCTGAAAGC CCATCTCCTC CAACTTGCAG CGCCGGTAGA GCTCGTAGTG CCGGCTGTGG GTCTGCTCGC GGAGGTCTTC CATGTTCACC CGGATCAACC 1 TGCCTCGAG 1
(2) INFORMATION FOR SEQ ID NO:418:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 284 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:
GAATTCGGCC TTCATGGCCT AGGAGGTGGG TATAGGGAAC ACTTGGGGAG AAATAGTGAA ATCTGAATAT AGACTGTGCA TTGTATCATT TAGTATAAAT GTTGACTTGC CTGATTTTGT TGTTGAAGGC ACTGTGGTTA CACAAGAGAA CGTCTGTCTT CCTAAGTGAT GCATGCCAAG GTTTGCAGGG GCATCCTGTC TGCAATTACT CTCAAATAGA TCAAAATAAT AATAACGTGT GTGTGCATGA TGGAGACAGG GAAGAGAAA GGGAAAGGGCT CCAG
(2) INFORMATION FOR SEQ ID NO:419:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:
GCCAGCACAT TGTGGAACAG AAAAATGGCA AAGAAAGAGT GCCCATCCTC TGGCATTTCC TGCAGAAGGA AGCAGAGCTG AGGCTGGTAA AGTTCCTGCC TGAGATTTTG GCCTTGCAAA GGGATCTAGT GAAGCAGTTC CAGAACGTCC AGCAAGTTGA ATACAGCTCC ATCAGAGGCT TCCTCAGCAA GCACAGCTCA GATGGGTTGA GGCAGCTGCT TCACAACAGG ATCACAGTCT TTCTGTCCAC ATGGAACAAA CTGAGGAGAT CGCTTGAGAC GAACAGCTCG AG
(2) INFORMATION FOR SEQ ID NO:420:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GGAACCAACA GAACAACCTG TGAGGAAGAA CAAAATGGCC TCTAATATCT TTGGGACACC

TGAAGAAAAT CAAGCTTCTT GGGCCAAGTC AGCAGGTGCC AAGTCTAGTG GTGGCAGGGA

WO 98/45437

7	PCT/US98/06956
AGACTTGGAG TCATCTGGAC TGCAGAGAAG GAACTCCTCT GAAGCACTTTAGATCTG AAGGGAGAAG GTGATATTCA TGAAAATGTG GACACACTCGGGGCAG AGTGAAGAGA AGCCCGTGCC TGCTGCGCCT GTGCCCCGAG	AGACT TGCCAGGCAG 240
(2) INFORMATION FOR SEQ ID NO:421:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:	
TAATTTAGAT TATACAGAAC TTGGCCTGCA GAAACTGAAG GAGTCT CTTTGCCTCT TTCTCTGATT ATTATTATAA GTGGTCCTCG GCGGAT TGGATTGATT ACCATCGTGG TACTCCTTGG GATCGCCTTT GTAGTC GAGTGACGGG CAGTATTCTC CTCCACCGTA CTCTGAGTAT CCTCCA CCAGAGACAA CTCGAG	TTCCT GTAACATGAG 120 TATA AGCTGTTCCT 180
(2) INFORMATION FOR SEQ ID NO:422:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 216 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:	
GCGATTGAAA TGGATCCTCC AGCTCTTCCA CCAAAGCCAC CTAAGC GTTCCAAATG GAATGAAGGA CAGTTCTGTT TCTCTTCAGG ATGCAG GATATTTCAA GGGAGGAGGT AAATGACAAA TTGCGGGATA TGCCAG GTCCGAGATG CCTCAACAAA AATGCAGAGA CTCGAG	AATG GTACTGGGGG 120
(2) INFORMATION FOR SEQ ID NO:423:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 389 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:	
GAATTCGGCC TTCATGGCCT AAAATTAATG AGTTGAACCT GTGACC GAGTCACCCA AGAGAGAGGT GGGGAGTCGA ACAGAGCTCC TTTACT	ACTG CATTCAAGAA 60 TTCT CCCACAGAGG 120

AAAAGGTGGA ATTCTGGGCT GGCTTTCCCT CACCAGAGGG TATCCCAAAT CTATGACAAA AGAAAAATGC CAGTCTCTTT TGGAAAGTAG GGAATGCCCT AGTGATGCTG TATGAAGAAG

CAAGCCTCCA TCTTCCCCGG GGAAATTTGA AACCAAGATG GGGTCCTGTC AATGACCCTC

TAGCATTTAT TGAGTGCCTA TTAGACAGGT GGCCTTGGGC TTTGAAATGC AATATCTTAT

231

TTAACTTAAT TCTGAGAACG TATCTCGAG

180

240

300

360

- (2) INFORMATION FOR SEQ ID NO:424:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GCCCGTGCTG	ATGTCTTTGA	AAGAAGGCTA	TAAGAAGTCC	TCAAAAATGG	TATTTAAGGC	60
TCCCATCAAA	GAAAAGAAGA	GTGTTGTGGT	CAACGGAATA	GATTTATTAG	AAAATGTCCC	120
ACCCAGGACA	GAGAATGAGC	TCCTTCGAAT	GTTCTTCCGG	CAGCAGGATG	AGATTCGACG	180
GTTGAAAGAG	GAGCTGGCCC	AGAAGGACAT	CCGCATTCGG	CAGCTCCAGC	TGGAACTGAA	240
AAACTTGCGC	AACAGCCCCA	AGAACTGTTA	GCTCCCCAGC	TGGGCTGTTT	TCTAAGCCGA	300
TCTCTCCGTC	GTTTCTACTC	ATCCCTTAAC	TTCTCCCTTA	CCAGTGACCC	CAGAGACAGA	360
GCCAGGACAG	GAGTGGGGGC	CAGCCTGAGG	ACCCCCCCCCT	ACCACCTCGA	G	411

- (2) INFORMATION FOR SEQ ID NO:425:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 691 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GGTACCAACA	GGACACCCCG	GTGGCCCCCC	GCTTTGACGT	CAATGCCCCG	GACCTCTACA	60
TTCCAGCAAT	GGCTTTCATC	ACCTACGTTT	TGGTGGCTGG	TCTTGCGCTG	GGGACCCAGG	120
ATAGGTTCTC	CCCAGACCTC	CTGGGGCTGC	AAGCGAGCTC	AGCCCTGGCC	TGGCTGACCC	180
TGGAGGTGCT	GGCCATCCTG	CTCAGCCTCT	ATCTGGTCAC	TGTCAACACC	GACCTCACCA	240
CCATCGACCT	GGTGGCCTTC	TTGGGCTACA	AATATGTCGG	GATGATTGGC	GGGGTCCTCA	300
TGGGCCTGCT	CTTCGGGAAG	ATTGGCTACT	ACCTGGTGCT	GGGCTGGTGC	TGCGTGGCCA	360
TCTTTGTGTT	CATGATCCGG	ACGCTGCGGC	TGAAGATCTT	GGCAGACGCA	GCAGCTGAGG	420
GGGTCCCGGT	GCGTGGGGCC	CGGAACCAGC	TGCGCATGTA	CCTGACCATG	GCGGTGGCGG	480
CGGCGCAGCC	TATGCTCATG	TACTGGCTCA	CCTTCCACCT	GGTGCGGTGA	GCGCGCCCGC	540
TGAACCTCCC	GCTGCTGCTG	CTGCTGCTGG	GGGCCACTGT	GGCCGCCGAA	CTNATCTCCT	600
GCCTGCAGGC	CCCAAGGTCC	ACCCTGTCTG	GCCACAGGCA	CCGCCTCCAT	CCCATGTCCC	660
GCCCAGCCCC	GCCCCCAACC	CAAGGCTCGA	G			691

- (2) INFORMATION FOR SEQ ID NO:426:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GCAGACCATA	TATCGAAAGT	TCTTTACTTG	TATCAAGGTG	AGAAAAAATT	AGAAGAGATA	60
TTACCTCTGG	GACCAAACAA	AGCTCTTTTT	TATAAAGGAA	TGGCATCATA	TCTTTTACCA	120

GGACAAAAAT	CTCCATGGTT	TTTCCAAAAA	CCCAAAGGTG	TAATAACTTT	GGACAAACAA	180
GTAATATCCA	CGAGTTCAGA	CGCCGAATCC	AGGGAAGAAG	TTCCCATGTG	TTCAGATGCT	240
GAATCCAGGC	AAGAAGTTCC	CATGTGTACA	GGCCCTGAAT	CCAGGCGAGA	AGTTCCCGTG	300
TATACAGATT	CTGAACTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:427:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GAATTCGGCC	TTCATGGCCT	ATATACTATC	AAATGAAAAT	AGCAAGATGC	TACCATTTAT	60
ATTAAAAAGA	GGACAAAATA	TTAATATATT	CATGGTTGCT	TGTCTATGTG	GAATATTTCT	120
GGATATATAC	ATAAGAAGTT	ACATTGGTTA	CCTATGGGCA	GGTTACTACT	GGGTGGCAGG	180
TGGGCTCGAG						190

- (2) INFORMATION FOR SEQ ID NO:428:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 670 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GAATTCGGCC	TTCATGGCCT	AGGCAAAGCT	GGCCCTGACG	CCTGGGTTTC	TTGGCCCCAG	60
CTGCCCAGCA	GGTGCCTCGA	TTCCCTGCCC	TTGTGACCTC	CCAGGAAACA	GAACTGATCT	120
GGGACACTAT	GTCACCTCTC	CTCTCATCTG	GGGTCAGTCA	GGGTTCGGGG	GCTGCAGCAG	180
CCAAGCGCAT	GAGAGGTGTT	TCCTTGGCCT	TCCAGAAGGC	CCACTGTGGA	GCCAGCCTCC	240
CTATGGGAGG	CAGAGCGGCA	AGGACAGGGC	TTTGGAATCA	$\tt GCCAGGTCGG$	CTCCTGGGCT	300
GTGGCCGTGG	AGAAACACTG	CCCCCAGGAT	GACACAGGCA	AGAGCCCCTG	AGGCATGGGA	360
GGCCCAGGGA	AGACCATGGG	CTGTAGGGGA	GAGTGTGGCA	GGTGACCCAA	AGGCCCAAAG	420
AGGGCCGTGG	GGCCTGAGGA	GGTCATAATC	TCTTCTGAGT	GGGGGCAGGT	CGATTCTTGC	480
ACAAGGTGGG	CTCTTCACTG	AGCCATAAGG	GACAGGGAGG	TATGGGAGAG	CGCTGGGGGC	540
CCATCCCCCT	GTCCACCCAG	TGTCCACTGG	CCTGTCCTTC	AGGGAGCAGA	GCAGAGCAGG	600
TGGTGGACGG	GCCCAGTGCT	GGGTGTTTTC	ACCACCATCC	CCCCATCCCC	CATCTAAGTC	660
${\tt GCTCCTCGAG}$						670

- (2) INFORMATION FOR SEQ ID NO:429:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

entralia Traditional Artifacture (1994) Traditional Artifacture (1994)

GTAAGGATTG	GCGATTCCTA	CAGCGAATGA	TCACCGCTCC	CTGCATCCTC	TTCCTGTTTT	60
ATGGCTGGCC	TGGTTTGTTC	CTGGAGTCCG	CACGGTGGCT	GATAGTGAAG	CGGCAGATTG	120
AGGAGGCTCA	GTCTGTGCTG	AGGATCCTGG	CTGAGCGAAA	CCGGCCCCAT	GGGCAGATGC	180
TGGGGGAGGA	GGCCCAGGAG	GCCCTGCAGG	ACCTGGAGAA	TACCTGCCCT	CTCCCTGCAA	240
CATCCTCCTT	TTCCTTTGCT	TCCCTCCCCA	ACCTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:430:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCTGTTCATC	TTTAAATGCT	60
GTTTTCTCTG	TTCAAAATGC	CCTTTCCTAC	CTTATCTACT	TGTGCCACTG	CATATTCCTA	120
AGGCTCAACT	CAGGGTATCT	TCCCTCGGAA	ACCTTGTCTG	ATCATCCTGG	CCCCTCTGGC	180
GGACAGTAAT	TTCTGCCTCT	GTGCTCCCAT	CACCTGAGCA	CACCTGTATG	GTGCTGCTGA	240
GCCCGCTGAA	TTGGCATTAT	GGGCACGTGC	GTCTCCTCCA	TTCCATGGAG	CTCCTCGAG	299
	GTTTTCTCTG AGGCTCAACT GGACAGTAAT	GTTTTCTCTG TTCAAAATGC AGGCTCAACT CAGGGTATCT GGACAGTAAT TTCTGCCTCT	GTTTTCTCTG TTCAAAATGC CCTTTCCTAC AGGCTCAACT CAGGGTATCT TCCCTCGGAA GGACAGTAAT TTCTGCCTCT GTGCTCCCAT	GTTTTCTCTG TTCAAAATGC CCTTTCCTAC CTTATCTACT AGGCTCAACT CAGGGTATCT TCCCTCGGAA ACCTTGTCTG GGACAGTAAT TTCTGCCTCT GTGCTCCCAT CACCTGAGCA	GTTTTCTCTG TTCAAAATGC CCTTTCCTAC CTTATCTACT TGTGCCACTG AGGCTCAACT CAGGGTATCT TCCCTCGGAA ACCTTGTCTG ATCATCCTGG GGACAGTAAT TTCTGCCTCT GTGCTCCCAT CACCTGAGCA CACCTGTATG	GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCC TCTGTTCATC TTTAAATGCT GTTTTCTCTG TTCAAAATGC CCTTTCCTAC CTTATCTACT TGTGCCACTG CATATTCCTA AGGCTCAACT CAGGGTATCT TCCCTCGGAA ACCTTGTCTG ATCATCCTGG CCCCTCTGGC GGACAGTAAT TTCTGCCTCT GTGCTCCAT CACCTGAGCA CACCTGTATG GTGCTGCTGA GCCCGCTGAA TTGGCATTAT GGGCACGTGC GTCTCCTCCA TTCCATGGAG CTCCTCGAG

- (2) INFORMATION FOR SEQ ID NO:431:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

GTTACATGAC	ACTGTTAATG	ATTGCATTTG	GCTTGCTGTG	GGGGCATCTC	TTGCGGATCA	60
AACCCACGCA	GAGCGTCTTC	ATTTCCACGT	GTCTGTCCTT	GTCAAGCACA	CCCCTCGTGT	120
CCAGGTTCCT	CATGGGCAGT	GCTCGGGGTG	ACAAAGAAGG	CGACATTGAC	TACAGCACCG	180
TGCTCCTCGG	CATGCTGGTG	ACGCAGGACG	TGCAGCTCGG	GCTCTTCATG	GCCGTCATGC	240
CGACTCTCAT	ACAGGCGGGC	GCCAGTGCAT	CTTCTAGCAT	TGTCGTGGAA	GTTCTCCGAA	300
TCCTGGTTTT	GATTGGTCAG	ATTCTTTTTT	CACTAGCGGC	GGCTCTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:432:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GAATTCGGCC	TTCATGGCCT	ACCAGGTTCT	TGCTGCCCTG	CGACTCCAGT	ATCTGCAGGG	60
GGATTATACT	CTGCACGCTG	CCATCCCACC	TCTCGAAGAG	GTTTATTCCC	TGCAGAGACT	120
CAAGGCCCGC	ATCAGCCAGT	CAACCAAAAC	CTTCACCCCT	TGTGAACGGC	TGGAGAAGAG	180
GCGGACGAGC	TTCCTAGAGG	GGACCCTGAG	GCGGAGCTTC	CGGACAGGAT	CCGTGGTCCG	240

GCAGAAGGTC GAGGAGGAGC AGATGCTGGA CATGTGGATT AAGGAAGAAG TCTCCTCTGC TCGAG	300 305
(2) INFORMATION FOR SEQ ID NO:433:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:	
GAATTCGGCC TCATGGCCTA CTCCTCAGCC CCTCATCTTG CCTCCACCCA GCTGCTCCAT TTTTGCCACA TCGTGGCCG CAGCCCCAGA GTCACTGTCC ATGTCACCAT CCTCCTCCTC CTTTGGAATC CTCTCCGCAC ACTGTGGCCC TTGTCTCAGG GCCCACAAGC TGAACTGTGG CATAGCTCTC TCTTCTTCTC CAAGAAGACT CAGCAGCCTA CATTCCCATT CCTGGTATGT GCCATTGGGT TGGATGTCCC CACTTATCTC GAG	60 120 180 240 273
(2) INFORMATION FOR SEQ ID NO:434:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 324 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:	
CGAGTGAGCG GGCGGGACAG TGCTTGTGAA ACTGAACACA ACAAAAGTAT GGATATGGGA AACCAACATC CTTCTATTAG TAGGCTTCAG GAAATCCAAA AGGAAGTAAA AAGTGTAGAA CAGCAAGTTA TCGGCTTCAG TGGTCTGTCA GATGACAAGA ATTACAAGAA ACTGGAGAGG ATTCTAACAA AACAGCTTTT TGAAATAGAC TCTGTAGATA CTGAAGGAAA AGGAGATATT CAGCAAGCTA GGAAGCGGC AGCACAGGAG ACAGAACGTC TTCTCAAAGA GTTGGAGCAG AATGCAAACT ACCCACACCT CGAG	60 120 180 240 300 324
(2) INFORMATION FOR SEQ ID NO:435:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 548 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:	
GAATTCGGCC TTCATGGCCT AAATGATCAA ATTTTGGCTT ACATATTTTG CAACAGTGGT ATAACACAAA GAAGTAAGCA AATATGGCAG AGGTGGTG GCTTTGGCGT CTACTTTTGA CCATAGTGGT GGCCCAAAAAG GTCAGCCAGC TGATGGGTTC TACCACATCCT TCCCGATGGA AGAAGGGGTT GGCCAAAAAG GTCAGCCAGC TGATGGGTTG GACCCAAAA GACAGATGA TAAGAATGAG TGACACCATG TTCTATCATT TTGTATTAGA TGCACCAAAA AACTATTCTG TTATTGTGAT GCTTACTGCT GCTCTCCACG CGTTCAGTTC ATGTGTCATG TGCAAAGGTG CTGCTGAAGA ATTTCAGATC TTGGCAAATT CCTATCAACG CCCTGGTGCA TTCACCACAA	120 180 240 300 360

TAACGTCAGT GTCTCGAG	TCCGAGTTTC TTCCACTTTT CTGCCCAATG GAAATTTACA ACAGATGACA	480 540 548
(2) INFORM	ATION FOR SEQ ID NO:436:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 308 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:436:	
TTATTCTGAG TTGGGGTCCC GTGTGTGTGT	TTCATGGCCT AAAATGAAAT TCAGACAAAA TCACTGGCAC CAAAAATGGT CTGTCTTCAC TTTGACTATT TGGGGGGCTT CTCTCAAGTA CAGATGTGGG CTGGAGCAGG CAGGATTGGC AGTAAGAGAT ATTGGCCACT CAAGTCTACT GCCTCTGGAA GAGTGAAGAA TGGACTTCAA AAGTAACATC AAAAATCTAA CCTGGAGACA TTTTGCAGGG CTTTCCTTTC AAGTCTTCA AGTACAGGAC	60 120 180 240 300 308
(2) INFORMA	ATION FOR SEQ ID NO:437:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 420 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:437:	
CTGCCCACTC GATGTGCCCA TCTACAGACA CTAGAGCAAC GGTGTTCCCG	GATCCCCTCG GCCCCACGC CATATGACCA AAGTCACACC AGGTTCAGAG CCAATGGAAC CACCTTATCA TCTAACCTCA CTGGTGGCAT GCCCTTCATT CTCCCATCTC CTCTGCAAGT TCAGAAGCTG CCTCAGCAGT GGTCAGTCCC GTGGCCTGGA ATTCTCCTCC CAAACCACTT CCAAGGAAGA CCTTACTGAT CTGGCTCTCC AGGGTACAGC ACAGCTACAG AGCCTGGAAG CAGTGAGCTA AGCAGCCTGA CCTCCAGGAA GGGACCCATG TGGAAAAGTC CCAGTCAGCA CCATCCCTGA AGTGTTAGAG GAGTGCACGT CCCCTGCCGA CCAACTCGAG	60 120 180 240 300 360 420
(2) INFORM	ATION FOR SEQ ID NO:438:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 279 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:438:	
AACGTGCTGG CTGCGTGTGG	TTCATGGCCT AATTGAATTC TAGACCTGCT TCTCACTGCA CCTGGATGGC ACCACTTCTC GGAGCTGCGC AGCGTCGAGG GGCTGCAGGA GGGCTCTGTG TGGAAGAGCC GTACACGGTG CGTGAGGCCC GCATCCACGT GCGCCATGTC TCAAGAGCCT GGACCCATCC GATGCCTTCA ACGGGGTTGA CTGCAACTCC	60 120 180 240

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439: GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCA CCCAGCCTC TTCTTTTCAT TATAACCTTT ATACCACAGT AAGCTGTTGC ATCATTCAAA TAGACCTGCA AATTGAATTC TAGACCTGCA GGATTACAGG GTTCTGGGCA TACATGCTTA TATACCACAGT AAGCTGTTGC ATCATTCAAA TAGACCTGCA CATTATCACT TAGACCTGCA TAGACCTCCA TAGACCCA TAGACCACCA TAGACCCA TAGACCCA TAGACCACCA TAGACCACCACCA TAGACCACC	TTGTCCTTCC TGAGTGTCTT CACCGACGGC GACCTCGAG	279
(A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439: GAATTCGGCC TTCATGGCCT AATGAATC TAGACCTGCA CCCAGCCTTC TTCTTTCAT TATACCTTT ATACCACAGT AAGCTGTGC ATCATTCAAA TGACCTGCA TCCTATATTG AATATTCTCC ATTATTCTCT AATATCTTG GGGGTACCCA GGATTACAGG GTTCTGGGCA TACATGTTAAA TCGTTTGCC AGGACTTTC TTTTTATTCA TGTCGTGAC CCATGTCTT TGCTTATATT TAAAGTTTT GCTCTTGATA TCATTGGTTC TTCCTTAAAT CACTTTTCT GGGTAACTGCT TTGGATGAA TCAATCATAT CACTTAGGT TTTCTAAAT CACTTTTCT GGGTAACTGCT TTGGATGAA TCAATCATAT CCACTTACG GAGCTCTCGA G (2) INFORMATION FOR SEQ ID NO:440: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440: GAATTCGGCC TTCATGGCCT ACCAATACTC ATAATTAAAA GTTTTTCGTT GTCAAAACAT TTCACAGTT CAGGAATCAC AGGCTATTT CATCTTTTCA AAATAAAAGTT AAAGTCCATT TTTCTTAAGC CTTATTACAC CATTATCCAA AAACCATACC TAGCATTCAT CTTAGTTTTT CATAACTCCCT TAGCAGATAG TTTAGTATAT TCCATTTTCT AATATTAAAA GTTGTGGAAG CAGTTTCTCA GGAGTCAAGC AAGCCTTTCC ATCATCTTC TATTTTAAAA AGTTCTTCT AGGAGATTAG CATTATCACAA AAACCATACC TAGCATTCAT CTTAGTTTTT CATAACTCCAT TAGCAGATAG TTTAGTATAT TCCATTTGTC TTATTTTAAAA GTTGTGGAAG AAGTTTCCAA GAGGTTCAAG AATCATCTC TATTTTAAAA ATCATCCATT AAGTAAAATGT TTTTGTGTG CAAAAACTGG AG (C) INFORMATION FOR SEQ ID NO:441: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441: GAATTCGGCC TTCATGCCTA GCCAGGAGGA GGAGGACCCT ATGAACATA CTACTGCGGCA (C) STRANDEONESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:	(2) INFORMATION FOR SEQ ID NO:439:	
GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCA CCCAGCCTTC TTCTTTCAT TATACCTTT ATACCACAGT AAGCTGTTGC ATCATTCAAA TGACTCTGCA TCCTATATTC TATATACCTT ATATCTCTC AATATCTTTG GGGGTACCCA GGATTACAGG GTTCTGGGCA TACATATATA TGCTTTTGCC AGGACTTTC TTTTATTCA TTGCTGTAGA GTTCTGGGCA TACATATATA TGCTTTTGCC AGGACTTTC TTTTATTCA TTGCTGTGTCA CACTTTTCT TGCTTATATT TAAAGTTTT GCTCTTGATA TCATTGGTT TTTCCTAAGT CACTTTTCT TGCTTATATT TAAAGTTTT GCTCTTGATA TCATTGGTTC TTTCCTAAGT CACTTTTCT GGTAACTGCT TTGGAATGAA TCATACATAT CTCACTTAGC GAGCCTCGA G (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440: GAATTCGGCC TTCATGGCCT ACCAATACTC ATAATTAAAA GTTTTTCGTT GTCAAAACAT TTTCTTAAGC CTTATTATAC CATTATCCAA AAACACTACC TAGCATTCAT CTTAGTTTTT TTCTTTAGAG AATTATATAC CATTATCCAA AAACACTACC TAGCATTCAT CTTAGTTTTT TTCTTTAGAGAGTAGT GTTAGTATAT TCCATTTTGTC TATTTTTGAG TTTAAAAAA GAATTGGAGC AACTTCCTC AGGAGTACAC AGGCCTTCC ATCTATCTC TATTTTTAAAAAA GAATTGTGATA AACATCCATT AAGTAAAATT TCTTTTTTTTT TATTAAAAAAA GAATTGTGATA TATCTTTTT TAGAATAAAAT TTTTTTTTTT	(A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCA CCCAGCCTTC TTCTTTCAT TATAACCTTT ATACCACAGT AAGCTGTTGC ATCATTCAAA TGACTCTGCA TCCTATATTG ANATATCTCC ATTATTCTT AGAGTCTTTG GAGTATCAGG GTTCTGGGCA TACATGATAA TGCTTTTGCC AGGACTTTC TTTTTATTCA TTGTCGTGAC CCATTGTCTT TGCTTATAAT TAAAGTTTTT GCTCTTGATA TCATTGGTTC TTTCCTAAGT CACTTTTCT TGCTTATAAT TAAAGTTTTT GCTCTTGATA TCATTGGTTC TTTCCTAAGT CACTTTTCT GGTAACTGCT TTGGAAATGAA TCATACATAT CTACCTTACG GAGCTCTCGA G (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440: GAATTCGGCC TCATGGCCT ACCAATACTC ATAATTAAAA GTTTTTCGTT GTCAAAACAT TTTCTTAAGC CTTATTATAC CATTATCAA AAACACTACC TAGCATTCAT CTTAGTTTTT TTTCTTAAGA CTTATTCAAA CATTATCAA AAACACTACC TAGCATTCAT CTTAGATTTTI TTCTTTAAGA GAATGTCAA GAGACTTCAC AAGCCTTCC ATCATACTCA TATTATAAAA 240 GTTGTGGAAG AAGTTCTCA GAGATTCAAC AAGCCTTTCC ATCATACTTC TATTTTAAAA 240 GTTGTGGAAG AAGTTCTCA GAGATTCAAC AAGCCTTTCC ATCATACTTC TATTTTAAAA 240 GTTGTGGAAG AAGTTCTCA GAGATTCAAC AAGCCTTTCC ATCATACTTC TATTTTAAAA 240 GAATGTGATT TATTGTTTTT ATGAATAAAA TATACCTCGT GTGTTTCTCA TATTGATGTTC CATTACATTA ATCATCCATT AAGTAAAAGT TTTTTGTTGTTTCTA TATGATGTTC (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441: GAATTCGGCC TTCATGCCTA GCCAGGAGGA GGAGGACCCT ATGAACAAAC TCAAGGGCA GAAGATGGTG TCCTGCCAGCA TCTGCAAGGG CAGCCAGCACA TCAAGGGCCA GAAGATGGTG TCCTGCCGGA AGCTAGAGGC GGCCCAGCAC TCACCAGGACA CTGAGCGCCA GAAGATCGTG TCCTGCCGGA AGCAGAGCT GGCCCGTTT CTACTGGGGA 240 GAAGGGAAAACCTG CGCCCGGACAG CTGGGCCTTTC TATCTGGGAA 240 GAAGGGAAAACCTG CGCCCGGACAG CTGGGCCTTTC TATCTGGGAA 240	(ii) MOLECULE TYPE: cDNA	
TATAACCTT ATACCACAGT AAGCTGITGC ATCATTCAAA TGACTCTGCA TCCTATATGG AATATTCTCC ATTATTCTCT AATATCTTTG GGGGTACCCA GGATTACAGG GTTCTGGGCA TACATGTTAA TGCTTTTGCC AGGACTTTC TTTTTATTCA TTGTCGTGAC CCATTGTCTT TGCTTATATT TAAAGTTTTT GCTCTTGATA TCATTGGTTC TTTCCTAAGT CACTTTTCT GGTAACTGCT TTGGAATGAA TCATACATAT CTACACTTACG GAGCTCTCGA G (2) INFORMATION FOR SEQ ID NO:440: (i) SEQUENCE CHARACTERISTICS:	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440: GAATTCGGCC TTCATGGCCT ACCAATACTC ATAATTAAAA GTTTTTCGTT GTCAAAACAT TTTCTTAAGC CTTATTATAC CATTATCCAA AAAACATACC TAGCATTCAT CTTAGTTTTT 180 GTTGTGGAAG AAGTTCTCA GGAGTTAGT TCAATTGTC TATTTTGAGG TTTAAATAAAA 240 GTTGTGGAAG AAGTTCTCA GGAGTTCAGC AAGACCTACC TAGCATTCAT CTTAGTTTTT 180 GAATTGGATT TATTGTTTTT ATGAATAAAA TATACCTCGT GTCTATCTTC TATTTTAAAA 300 GAATGGATT TATTGTTTTT ATGAATAAAA TATACCTCGT GTGTTTCTCA TATGATGTTC 360 CATTACATTA ATCATCCAT AAGTAAATGT TTTTGTGCTG CAAAAAACTCG AG 412 (2) INFORMATION FOR SEQ ID NO:441: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441: GAATTCGGCC TTCATGCCTA GCCAGGAGGA GGAGGACCCT ATGAACAAAC TCAAGGGCCA 60 GAAGATCGTG TCCTGCCGCA TCTCCAAGGG CGACCACTGG ACCACCACTA GACCACTGCAA 120 GAAGGAGAGGAGG CTGCCGGGGA AGCTAGAGGCC GGCCGAGGAACA AGACCAGGGGAA 240 GAAGGAGAGAG CTGCCGGGAA AGCTAGAGGCC GGTGCAGGACA AGACAGGGGAA 240	TATAACCTTT ATACCACAGT AAGCTGTTGC ATCATTCAAA TGACTCTGCA TCCTATATTG AATATTCTCC ATTATTCTCT AATATCTTTG GGGGTACCCA GGATTACAGG GTTCTGGGCA TACATGTTAA TGCTTTTGCC AGGACTTTTC TTTTTATTCA TTGTCGTGAC CCATTGTCTT TGCTTATATT TAAAGTTTTT GCTCTTGATA TCATTGGTTC TTTCCTAAGT CACTTTTTCT	120 180 240 300
(A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440: GAATTCGGCC TTCATGGCCT ACCAATACTC ATAATTAAAA GTTTTTCGTT GTCAAAACAT 120 CAGGAATCAC AGTCCTATTT CATCTTTTGA AATAAAAGGTT AAAGTCCATT 120 CATATCTCACAGTT CAGGAATAC CATTATCCAA AAACACTACC TAGCATTCAT CTTAGTTTTT 180 CATATCTCCT TAGCAGATAG TTTAGTATAT TCCATTTGTC TTATTTGAGG TTTAAAAAAA GTTGTGGAAG AAGTTTCTCA GGAGTTCAGC AAGCCTTCC ATCTATCTCT TATTTTAAAAA 300 GAATGTGATT TATTGTTTTT ATGAATAAAA TATTACCTCGT GTGTTTCTCA TATGATGTC 360 CATTACATTA ATCATCCATT AAGTAAAATGT TTTTGTGCTG CAAAAACTCG AG 412 (2) INFORMATION FOR SEQ ID NO:441: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441: GAATTCGGCC TTCATGCCTA GCCAGGAGGA GGAGGACCCT ATGAACAAC TCAAGGGCCA 60 GAAGACTCGTG TCCTGCCGCA TCTCCAAGGG CGACCACTGG ACCACCAGTA GCCCCTTACAAA GGATACGTG GGCCCATGC AGAAGGAGCT GGCCGAGCACA ACCACCCGT GCCCCTTACAAA GAAGGAGAGG CTGCCGGGGA AGCTAGAGGCC GGTGCAGGCCA ACCACCACAA 240 GAAGGAGAAG CTGCCGGGGA AGCTAGAGGCC GGTGCAGGCCA ACCACCACA ACACACCACA ACACACGGGAA 240	(2) INFORMATION FOR SEQ ID NO:440:	
GAATTCGGCC TTCATGGCCT ACCAATACTC ATAATTAAAA GTTTTTCGTT GTCAAAACAT TTTCACAGTT CAGGAATCAC AGTCCTATTT CATCTTTTGA AATAAAAGTT AAAGTCCATT TTCTTAAGC CTTATTATAC CATTATCCAA AAACACTACC TAGCATTCATC CTTAGTTTTT 180 GTTGTGGAAG AAGTTTCTCA GGAGTTCAGC AAGCCTTTCC ATCATCTTCT TATAAAAAAAAAA	(A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
GAATTCGGCC TTCATGGCCT ACCAATACTC ATAATTAAAA GTTTTTCGTT GTCAAAACAT TTTCACAGTT CAGGAATCAC AGTCCTATTT CATCTTTTGA AATAAAAGTT AAAGTCCATT TTCTTAAGC CTTATTATAC CATTATCCAA AAACACTACC TAGCATTCAT CTTAGTTTTT 180 CATATCTCCT TAGCAGATAG TTTAGTATAT TCCATTTGTC TTATTTGAGG TTTAAAAAAA 240 GTTGTGGAAG AAGTTTCTCA GAGGTTCAGC AAGCCTTTCC ATCTATCTTC TATTTTAAAA 300 GAATGTGATT TATTGTTTTT ATGAATAAAA TATACCTCGT GTGTTTCTCA TATGATGTTC 360 CATTACATTA ATCATCCATT AAGTAAATGT TTTTGTGCTG CAAAAACTCG AG 412 (2) INFORMATION FOR SEQ ID NO:441: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441: GAATTCGGCC TTCATGCCTA GCCAGGAGGA GGAGGACCCT ATGAACAAAC TCAAGGGCCA 60 GAAGATCGTG TCCTGCCGCA TCTGCAAGGG CGACCACTGG ACCACCGGT GCCCCTACAA 120 GGATACGCTG GGGCCCATGC AGAAGAGACT GGCCGAGCAG CTGGGCCTGT CTACTGGCGA 180 GAAGGAGAAG CTGCCGGGAG AGCTAGAGCC GGTGCAGGCC ACGCAGAACA AGACAGGGAA 240	(ii) MOLECULE TYPE: cDNA	
TTTCACAGTT CAGGAATCAC AGTCCTATTT CATCTTTGA AATAAAAGTT AAAGTCCATT TTTCTTAAGC CTTATTATAC CATTATCCAA AAACACTACC TAGCATTCAT CTTAGTTTTT 180 CATATCTCCT TAGCAGATAG TTTAGTATAT TCCATTGTC TTATTTGAGG TTTAAAAAAA 240 GTTGTGGAAG AAGTTCTCA GGAGTTCAGC AAGCCTTTCC ATCTATCTTC TATTTTAAAA 300 GAATGTGATT TATTGTTTTT ATGAATAAAA TATACCTCGT GTGTTTCTCA TATGATGTTC 360 CATTACATTA ATCATCCATT AAGTAAATGT TTTTGTGCTG CAAAAACTCG AG 412 (2) INFORMATION FOR SEQ ID NO:441: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441: GAATTCGGCC TTCATGCCTA GCCAGGAGGA GGAGGACCCT ATGAACAAAC TCAAGGGCCA 60 GAAGATCGTG TCCTGCCGCA TCTGCAAGGG CGACCACTGG ACCACCCGCT GCCCCTACAA 120 GGATACGCTG GGGCCCATGC AGAAGGAGCT GGCCGAGCAC CTGGGCCTGT CTACTGGCGA 180 GAAGGAGAAG CTGCCGGGAG AGCTAGAGCC GGTGCAGGCC ACGCAGAACA AGACAGGGAA 240	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441: GAATTCGGCC TTCATGCCTA GCCAGGAGGA GGAGGACCCT ATGAACAAAC TCAAGGGCCA GAAGATCGTG TCCTGCCGCA TCTGCAAGGG CGACCACTGG ACCACCCGCT GCCCCTACAA 120 GGATACGCTG GGGCCCATGC AGAAGGAGCT GGCCGAGCAC CTGGGCCTGT CTACTGGCGA 180 GAAGGAGAAG CTGCCGGGAG AGCTAGAGCC GGTGCAGGCA 240	TTTCACAGTT CAGGAATCAC AGTCCTATTT CATCTTTTGA AATAAAAGTT AAAGTCCATT	
(A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441: GAATTCGGCC TTCATGCCTA GCCAGGAGGA GGAGGACCCT ATGAACAAAC TCAAGGGCCA 60 GAAGATCGTG TCCTGCCGCA TCTGCAAGGG CGACCACTGG ACCACCCGCT GCCCCTACAA 120 GGATACGCTG GGGCCATGC AGAAGGAGCT GGCCGAGCAG CTGGGCCTGT CTACTGGCGA 180 GAAGGAGAAG CTGCCGGGAG AGCTAGAGCC GGTGCAGGCC ACGCAGAACA AGACAGGGAA 240	CATATCTCCT TAGCAGATAG TTTAGTATAT TCCATTTGTC TTATTTGAGG TTTAAAAAAA GTTGTGGAAG AAGTTTCTCA GGAGTTCAGC AAGCCTTTCC ATCTATCTTC TATTTTAAAA GAATGTGATT TATTGTTTTT ATGAATAAAA TATACCTCGT GTGTTTCTCA TATGATGTTC	180 240 300 360
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441: GAATTCGGCC TTCATGCCTA GCCAGGAGGA GGAGGACCCT ATGAACAAAC TCAAGGGCCA 60 GAAGATCGTG TCCTGCCGCA TCTGCAAGGG CGACCACTGG ACCACCCGCT GCCCCTACAA 120 GGATACGCTG GGGCCCATGC AGAAGGAGCT GGCCGAGCAG CTGGGCCTGT CTACTGGCGA 180 GAAGGAGAAG CTGCCGGGAG AGCTAGAGCC GGTGCAGGCC ACGCAGAACA AGACAGGGAA 240	CATATCTCCT TAGCAGATAG TTTAGTATAT TCCATTTGTC TTATTTGAGG TTTAAAAAAA GTTGTGGAAG AAGTTTCTCA GGAGTTCAGC AAGCCTTTCC ATCTATCTTC TATTTTAAAA GAATGTGATT TATTGTTTTT ATGAATAAAA TATACCTCGT GTGTTTCTCA TATGATGTTC CATTACATTA ATCATCCATT AAGTAAATGT TTTTGTGCTG CAAAAACTCG AG	180 240 300 360
GAATTCGGCC TTCATGCCTA GCCAGGAGGA GGAGGACCCT ATGAACAAAC TCAAGGGCCA 60 GAAGATCGTG TCCTGCCGCA TCTGCAAGGG CGACCACTGG ACCACCCGCT GCCCCTACAA 120 GGATACGCTG GGGCCCATGC AGAAGGAGCT GGCCGAGCAG CTGGGCCTGT CTACTGGCGA 180 GAAGGAGAAG CTGCCGGGAG AGCTAGAGCC GGTGCAGGCC ACGCAGAACA AGACAGGGAA 240	CATATCTCCT TAGCAGATAG TTTAGTATAT TCCATTTGTC TTATTTGAGG TTTAAAAAAA GTTGTGGAAG AAGTTTCTCA GGAGTTCAGC AAGCCTTTCC ATCTATCTTC TATTTTAAAA GAATGTGATT TATTGTTTTT ATGAATAAAA TATACCTCGT GTGTTTCTCA TATGATGTTC CATTACATTA ATCATCCATT AAGTAAATGT TTTTGTGCTG CAAAAACTCG AG (2) INFORMATION FOR SEQ ID NO:441: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	180 240 300 360
GAAGATCGTG TCCTGCCGCA TCTGCAAGGG CGACCACTGG ACCACCCGCT GCCCCTACAA 120 GGATACGCTG GGGCCCATGC AGAAGGAGCT GGCCGAGCAG CTGGGCCTGT CTACTGGCGA 180 GAAGGAGAAG CTGCCGGGAG AGCTAGAGCC GGTGCAGGCC ACGCAGAACA AGACAGGGAA 240	CATATCTCCT TAGCAGATAG TTTAGTATAT TCCATTTGTC TTATTTGAGG TTTAAAAAAA GTTGTGGAAG AAGTTTCTCA GGAGTTCAGC AAGCCTTTCC ATCTATCTTC TATTTTAAAA GAATGTGATT TATTGTTTTT ATGAATAAAA TATACCTCGT GTGTTTCTCA TATGATGTTC CATTACATTA ATCATCCATT AAGTAAATGT TTTTGTGCTG CAAAAACTCG AG (2) INFORMATION FOR SEQ ID NO:441: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	180 240 300 360
	CATATCTCCT TAGCAGATAG TTTAGTATAT TCCATTTGTC TTATTTGAGG TTTAAAAAAA GTTGTGGAAG AAGTTCTCA GGAGTTCAGC AAGCCTTTCC ATCTATCTTC TATTTTAAAA GAATGTGATT TATTGTTTTT ATGAATAAAA TATACCTCGT GTGTTTCTCA TATGATGTTC CATTACATTA ATCATCCATT AAGTAAATGT TTTTGTGCTG CAAAAACTCG AG (2) INFORMATION FOR SEQ ID NO:441: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	180 240 300 360

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 222 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:	
GAATTCGGCC TTCATGGCCT ACCGCCTCGC TGCCTGGACA CCTGTCCGTG CCACCCTGGT CACTGAGCAG GACATCCGCG TCTGTGGCCC CTGGGACCCT GCCCCGGACA GCCAGGCCTG GGTTTGTCCT TTTAGGTAGA GTGCCTGGTC CAGGTCATTG GAGGAGAGTC CACATGGCCA CCTCTGGCGT GTTCTAGAGA GGCCCTCCCG TCTAGGCTCG AG	60 120 180 222
(2) INFORMATION FOR SEQ ID NO:443: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:	
CTTTATGACA GCCATGAGCT TTTTCCGGTG CATTGCAATT GTTTTTCCAG TCCAGAACAT TAATTTGGTT ACACAGAAAA AAGCCAGGTT TGTGTGTGTA GGTATTTGGA TTTTTGTGAT TTTGACCAGT TCTCCATTC TAATGGCCAA ACCACAAAAA GATGAGAAAA ATAATACCAA GTGCTTTGAG CCCCCACTAC TCGAG (2) INFORMATION FOR SEQ ID NO:444: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 178 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:	
GAATTCGGCC TTCATGGCCT ACCTGCCTCC CTCCTTGCTT CTTGCTCTGC TAACTCAACT CTGCCTTCCT CTTTTTCATT CTTCTACTCT GCCCTATATG GAGGACAAAT GGACACCAGG GGTGCTAACC TTATTGGTGC CTGCCCCAGC CTACCCCAGG TGCAAGCAGA CTCTCGAG	60 120 178
(2) INFORMATION FOR SEQ ID NO:445:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 251 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:	
GAATTCGGCC TTCATGGCCT AGAAAGCCAC AAACTTTTTA GTTTTTAACT TCAAAGGCTT CTTTCTCTTT AAAAAAAATT ATTTTTAATA TAGAGTCAAA AAATTGGATG TATTATTTTG AGCTTCTAAT TGCTGCCACT TGGAGATGTC CAAGTAAGAA GGCCTTCTTT TTACATGGA TGAATTGTGC ACTTCTACTG ATGATGACTA CAGCAGAAGT GATGTTATAC GTACAGGCAC TTGAACTCGA G	60 120 180 240 251
(2) INFORMATION FOR SEQ ID NO:446:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 301 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:	
GAATTCGGCC TTCATGGCCT AGGGCTTATA TTTTAACTGA ACTATTATTA AATAAAAACA AAATAAAAATC TTATCATATA GGTGTAATCT GTTCTAAGGA AAAAATCCTT CTATCAAGAC TAAACGTCTA ACTGAATACA GAATGACATT TCATGCCTTA AGGTCTCTGT CCATGTTGTT CCCTTCTTTCT ACTGTCCTTT ACTGTATTAG TTCAAAACAT TCTAATTCAC TCTCCAAAAC CCCAATTCAAA CATCACCATC AGAAAGTCTT CCATGATGGG CCAGGTGTGG CGGCCCTCGA G	60 120 180 240 300 301
(2) INFORMATION FOR SEQ ID NO:447:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 150 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:	
GAATTCGGCC TTCATGGCCT AGCTGAAATG CTTTCTATTG GATACTATCT GGGCATATTA CTTCCTGTGG TTCACTGTCT GGGTGACAGG ATTCATAGAA GCCCAAACTT TAGCACCACG CAGCATACCC TTGTAACAAA GCCACTCGAG	60 120 150
(2) INFORMATION FOR SEQ ID NO:448:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 226 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GAATTCGGCC TTCATGGCCT AATTTGATTT TATTAGGTTT AAATTGTATT TCTTCAAATT 120
TCATAAACTA TAGCATTTAT CTCCATATTT TTAATAAATG ATCACAAATA AATCACTGTT 120
AATATCTCCA TTTACACTTT TACAACTCCT GCTATTGCTG GATTTTCAT CCTATGATAT 180

226

GTTAAACCAA TTTAAAATAC ATTTAAAGAA TCACAGCTGT CTCGAG

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 453 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:	
GAATTCGGCC TTCATGGCCT AAGACTGGGG GCATGTACCC CACCTACTTT CTGCACCTGG	60
ACCETGAGGA TGGGAAGAAG GTAAGGTTGG TCTGGGCATG TTATCATCTA GGCTTTACAG	120
CCCTTTGAAA TCCTAGGGGC TGAAATGTGA CTGGAAGTCT CATATCTACC GCTGACCTCT	180
CAGTTCCTCA AAGAAACTGC CTTCGTGTCT GGTCTGTGCA CATCTTTGTG TTTTCCAGTG	240
CATTTGTGTG TGTGCACATA TGTGCGTTTG GGAGCTGACG CAACGGAGAG AGTCTGTGTG	300
AGTGGCTCTC ATGACTGTGT GCAGACCAGA GGCTGAGTCT GGAATATGAC CTCATTCCAC	360
TCCCCAAGGT GTTCCTCCTG GCGGGAAGGA AGAGAAAGAA GAGTAAAACT TCCAATTACC	420
TCATCTCTGT GGACCCCACA GACTTGTCTC GAG	453
(2) INFORMATION FOR SEQ ID NO:450:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 246 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:	
GAATTCGGCC TTCATGGCCT AAAAGCAAAT TAACTTGTTC TGAAAAGAAA GTATAGATTA	60
ATTTTGTTTT CTGTTTAAAT TTTATCTCCT TGGTAAAGAT TTTTTTTCC TGGGCAGAAA	120
ACTTGGCATT TTTAGGCGTA GATACCTTAC CTTACAATGC CAAAATGAAT TTAATTCCAG	180 、
TACTCAGGTT TTTCCCTTTA ACAGACTCTA TGTGTACCAG GCATTGAATT CTAGACCTGC	240
CTCGAG	246
(2) INFORMATION FOR SEQ ID NO:451:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 414 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:	
GAATTCGGCC TTCATGGCCT AGTTTGGTGG GGTTGAAGTT GATGGCAAAC TCATGGGAGA	60 120
CCTTCCAGTC TGGGGGTAAC TGGGCCCCGA ATCCCAGAGC TGGAAACATC TTATCACTGT	120 180
CGTAGTCCTG AATGATCTGC CCAACAGCCC AGATGGCCGA CAGATATTCG TTGGTGCCCA TAGGGTTGAT ATAGTGCAAA GAGGAAGGGT CGAGGGGATT CCCGTTGGAG GCTGTAAAGT	240
CTATTCCAAC GGTGAACATG AGCTGGCAGC CTCCCAGGAT GTAGTCAAGG AAGGAGTAGT	300
CTCGGTTTAT CTTGCAGGAT CGCAGGATGA TGATGCCCGA GTTTTTATAG TTCTTCTTCT	360
240	

TCCTCTGCTT CTTGGGGTTG ATGCACTCGA ACTCCAGCGG GACGCTGTCT CGAG

414

(2) INFORMATION FOR SEQ ID NO:452: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 374 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:452: GAATTCGGCC TTCATGGCCT ACACACTGAC TGACAGACCA CGGTATGCCT TGCACCACCC TGGCTGCTGG GGTCCAAAGA GGGATCTGGT AGACCTGGGC TGGAATCTCA GCTTCACCAT 120 TTACCATCTG GGTGGCCAAT GGAGTGTTAC TTGGCCTCTC TGAGCCTCGG TTTTGCTCGT 180 CTCTGAAACA GTAAGATACC TCCCTTTGGC TGTTGTGATG AGGATGAAGG TTAGCCTATG 240 CCCAGTAGTA TGCCTGTCCC TTCATCGATG CCTGCTCATC TCACTCTTGC TCTGGAAACA 300 360 GAGGTGATCT CGAG 374 (2) INFORMATION FOR SEQ ID NO:453: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 288 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:453: GCGTCCGTCC GCCGCCACCA CCCACTCCGG ACACAGAACA TCCAGTCATG GATAAAAATG AGCTGGTTCA GAAGGCCAAA CTGGCCGAGC AGGCTGAGCG ATATGATGAC ATGGCAGCCT GCATGAAGTC TGTAACTGAG CAAGGAGCTG AATTATCCAA TGAGGAGAGG AATCTTCTCT 180 CAGTTGCTTA TAAAAATGTT GTAGGAGCCC GTAGGTCATC TTGGAGGGTC GTCTCAAGTA 240 TTGAACAAAA GACGGAAGGT GCTGAGAAAA AACAGCAGAT GGCTCGAG 288 (2) INFORMATION FOR SEQ ID NO:454: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 383 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454: GAATTCGGCC TTCATGGCCT AAGAAGTGTC TCCTGTATCC ACCTCTTCCT GGCCTCCCTT 60 CCCCCACTTC CTGGTCCCTG TCCACTCCTC AGGTTGGTGC TCTCACTTCT TGAAAGCTCT 120 AGGCACCCCC GCCTCCCGCC AGGCTCCCCG TTGGCTCCTG GCAGGCCAGC TGAGAATGAA 180 CAGGAGATGG AGGCAGGCAG CCCAGGCTGC AGAGGTGAGG GATGTGGGGC CAGGCCCAGA 240 GGGCTCAGCC TAGAGGCTTC CAATCTCAGA TTCTCCTGCC TGTGGTCATC TGTTTGTCCA 300 TCACCCCAGG ACAGGGCAGA CAGAGGGGCA AAGCACTGGG GGCCCCAGAG CCTAGCTTCC 360 CCTCAGCCTG GGGGAAACTC GAG 383

- (2) INFORMATION FOR SEQ ID NO:455:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

AGAGCACGTC	AATGCCATGA	GGGGCCTGCA	AAGCAGCAAG	GAGCTCAAGG	CTGAGCTGGA	60
CGGGGAGAAG	GGCCGGGACT	CAGGGGAGGA	GGCCCATGAC	TATGAGGTGG	ACATCAATGG	120
	CTTGAATGCA					180
	GCCTTAAAGG					240
GGCCAAGTAT	GAGAGTAAAA	TCCAGATGTA	TGATGAGCAG	GTGACAAGCC	TTGAGAAGAC	300
CACCAAGGAG	AGTGGTGAGA	AGATGGCCCA	CATGGAGAAG	GAGTTGCAAA	AGATGACCAG	360
CATAGCCAAC	GAAAATCACA	GTACCCTTAA	TACGGCCCAG	AATCTCGAG		409

- (2) INFORMATION FOR SEQ ID NO: 456:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GAATTCGGCC	TTCATGGCCT	AAATTTCATG	AAAAACAAAT	GGCTTAAACC	CAGGGAAGCA	60
AGGATTATAA	${\tt TTGATTTTT}$	TGAGCAATGT	CTCTTTTGGT	TACAAAGTAA	AAGGTAAAAT	120
AAAAGTTTAA	AAGCATTTGG	AAAGAATGTT	CTTTGGTTTT	TTCACTCAGT	AACCTAAAGT	180
TTAATGACCC	TTTACAGTGC	TGATAAACAC	TTAAATTTTT	GCAGTAGGCA	TTGCTAGTTC	240
AAATTGAAGG	AAGGTTGCCA	GGCTCATGCC	TATAGTCCCA	ACTACTTAGG	AGGCTAAGGC	300
AGGGGGACGC	CCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:457:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GAATTCGGCT	TCATGGCCTA	CTGCTCTTTG	GCTAAGGTGG	CAGTGTACCT	CTAGATCAAC	60
CTGGGCAACA	GTCACAAGGG	AGTGTGACTT	CTTGGCCATA	ATAAACTCAC	TTGATAGTGT	120
TTATGTTATT	AATCTGAATG	CAACAGAAGA	CAAAAGCACA	GGCATGCACA	CACACAGAAC	180
CCCAAACCAC	TAAAAACTAC	CTAAACACTG	ACTTAGTAAA	TAGTAAAAAG	GTAATGTTGG	240
${\tt GACTTTTAAA}$	CCTTGAATCC	ATTAGCCAGG	CTTGGGATGA	AAGGACCATC	TAAAATCATG	300
CTAGTCTAAA	CCATGCTCTT	CCACACAGCT	GTTTAAAAAC	CACTGGGTAT	GAGGAATATG	360
CTAGAAAGAA	ATGTTAAAAA	TAGATTGTTG	GCTCACACTT	ATTTTTCTAA	TAAATAGGAC	420
CATTATTACT	ACCAGGAAAG	TCTTATTTAT	TTTGCCTGAA	ATTGGCTTAA	AGAAAGTCTC	480

510

ATGACGGGAT GGGATGGGCC GGCACTCGAG

(2) INFORMATION FOR SEQ ID NO:458:

(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 382 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:458:	
AATTAAACCC AGATCATATT GGCATCGCTG AGAGTCTGTA CTGGGAGAAT	TTCATGGCCT AGCGGAAACA ACTGAAACTA ATGGAAGATA TGGATACAGT CGTCCTCAAG TAGTAAAACA AAAAAAACAG CGACCAAAAT CTATTCACAG GAATCCCCCA AAACACCAAT AAAGGGTCCT CCAGTCTCTA GCCTTTCTTT AACACGGGTG ATAACCAGAG TGTACATTCA GGCAAGAGGA CGCCAAGATC GAAGGCTTCT TATCTCCAAG TCGTTGTGGC AGTCGAAATG GAGAAAAAGA GCATCAACAA CTTCTTCAGT GGCTTCTGGA ACAGAATATA CAGGACCAAA GAACACCTCG AG	60 120 180 240 300 360 382
(2) INFORMA	ATION FOR SEQ ID NO:459:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 433 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:459:	
GACTCTGCAG AGGGAGCCTC GGGGTGACGT TTTCACCAAA CCATGTTGTG	TTCATGGCCT ACTGAGTCCC AGGCCGGGGC CCTGCCCCAG CCAGGGCTGG TTGGGAGCTT GTCCAGCTGC CCCCTCTAAT GCTTTTCTCC TCCAGGACAC CGGAAGCACA GTAGTCCCCG TGTGTCACCT TAGGCTGACC TCTGTCCCCA AATGCTGTCA CTGTCTTGAA TTCTTCATCG TTTAACAGGG AGCCCAGTGT AGCAGAATTG GATTTTTTT TTAAGTCGAT AAATTTTTAC TCAAGGAATT ATTTCTTCCA CTGTCCATCA AGGTCACTTT AGATCCTCTA AAGAGCTAGA TTATCTTCAA GTTAGTCCTT TTTAATGAAA CCGATGCTTA TTTTAATCCA GAG	63 120 180 240 300 360 420 433
(2) INFORMA	ATION FOR SEQ ID NO:460:	
(i) :	SEQUENCE CHARACTERISTICS: (A) LENGTH: 305 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:460:	
CAAATTTTAC GCCTTTGTAA	AGTAATCCAG TCACCTGCTG CTGATACTAG AAGGGCTGAG ATGTCACAAA CCCTGACACT CTTGCCCAGA ATGAAGGGAA GGCTATGTCT TATCAGTGTA GTTTCTATCA TCATCCTTTT CCGTGTTAAA AGATCATATT AAGCAACATG TGAAGTGATA CTGATGTGCT CAGAGTGCCA TATTACATCT AGAAGCCAGG	60 120 180 240
	243	

TCGAG

AGGAACTTGA AGCCCACGTG GTGAATGACC ATGACAATGA TGCCAATATC CACACCGAAC

300

(2) INFORMATION FOR SEQ ID NO:461:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 563 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:	
GAATTCGGCC TTCATGGCCT AAGAAATATC AGTCCAAGCA AGAGGAATTA CAGAAAGATA TGCAAGGAAG TGCACAGGCA TTGGCTGAAG TAGTGAAAAA CACAGAGAAC TTCTTAAAAG AGAATGGTGA AAAGCTGTCA CAGGAAGATA AGGCTTTGAT TGAACAGAAA CTTAATGAAG CTAAGATAAA GTGTGAACAG CTTAATTTAA AAGCAGAACA GTCTAAAAAG GAGCTGGATA AAGTTGTGAC AACAGCAATC AAGGAAGAAA CTGAAAAGGT AGCAGCAGTG AAGCACTGG AAGAGAGCAA AACCAAAATA GAAAACCTTT TGGACTGGTT GTCAAATGTT GACAAAAGAC CTGAAAAGGGC AGGGACAAAA CACAAAACAGG TAATCGAACA GAACGGGACC CATTTTCAAG AAGGTGATGG CAAGTCAGCA ATTGGAGAAG AGGATGAAGT TAATGGTAAC CTGTTGGAGA CTGATGTTGA TGGGCAAGTT GGAACCACTC AGGAGAATCT GAATCAGCAA TATCAGAAAG TTAAGGCCCA ACATGGACTC GAG (2) INFORMATION FOR SEQ ID NO:462:	6 12 18 24 30 36 42 48 54 56
(A) LENGTH: 477 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:	
GCGGCTGTGA AGATGGCGGC GGCTGCGTGG CTTCAGGTGT TGCCTGTCAT TCTTCTGCTT CTGGGAGGCTC ACCCGTCACC ACTGTCGTTT TTCAGTGCGG GACCGGCAAC CGTAGCTGCT GCCGACCGGT CCAAATGGCA CATTCCGATA CCGTCGGGGA AAAATTATTT TAGTTTTGGA AAGATCCTCT TCAGAAATAC CACTATCTTC CTGAAGTTTG ATGGAGAACC TTGTGACCTG TCTTTGAATA TAACCTGGTA TCTGAAAAGC GCTGATTGTT ACAATGAAAT CTATAACTTC AAGGCAGAAG AAGTAGAGT GTATTTGGAA AAACTTAAGG AAAAAAGAGG CTTGTCTGGG AAATATCAAA CATCATCAAA ATTGTTCCAG AACTCCAGTG AACTCTTTAA AACACAGACC TTTTCTGGAG ATTTTATGCA TCGACTGCCT CTTTTAGGAG AAAAACAGGA GCTCGAG	64 124 300 360 424
(2) INFORMATION FOR SEQ ID NO:463:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 382 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:	

GTTGCACTCC	TGTTGTACTC	TTTTAGAGGT	GGAAAAGAGG	TGGATACTGA	GATCTAAGAG	60
GAAAGGATAG	TCATTCACGT	TCTGAGATAT	GCGCTCTCTC	TATTGTTCTC	GAACACAAAG	120
GGATAGTCTC	TTTTCTGGAG	CTGATGTCCC	TGCTTGGAGG	TTAGCCCCAA	AACATGGCTC	180
TTGTATTGTT	CTAAGAGAAA	AGGCTTTCAT	TTTGGTTCTT	CTGATTGGTG	TTACCTACTG	240
			GCAGACTATT			300
AGAGCAGTTC	ATTAAGCCCA	TTGCTTTCAG	TAATGTGGCC	TTGACCCCTT	CTGCTTCCCC	360
	GACGAGCTCG				0.001.000	382

- (2) INFORMATION FOR SEQ ID NO:464:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GGACCTGCCT CAAGGACATG GGTGGACATA TGGGCGGACT CTCAGGGACA ACCAAAGTGA	60
TGATCACACT GACCGATGTC AATGACAACC CACCAAAGTT TCCGCAGAGC GTATACCAGA	120
TGTCTGTGTC AGAAGCAGCC GTCCCTGGGG AGGAAGTAGG AAGAGTGAAA GCTAAAGATC	180
CAGACATTGG AGAAAATGGC TTAGTCACAT ACAATATTGT TGATGGAGAT GGTATGGAAT	240
CATTTGAAAT CACAACGGAC TCTAAAACAC TCGAG	275

- (2) INFORMATION FOR SEQ ID NO:465:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GTTCTAGACC	TACCCCGAAC	AGCCCCAAAC	AGTCAGAGTG	GCACAAAATG	ACAGTCTCCA	60
AAAACTGCCC	CGACCAAGAT	CTCAAAATCA	AACTTGCTGT	CCGAATGGAT	AAGCCTCAAA	120
ACATGAAGCA	TTCTGGGTAT	TTATGGGCCA	TCGGTAAGAA	TGTCTGGAAG	AGATGGAAGA	180
AAAGGTTTTT	TGTATTGGTG	CAGGTCAGTC	AGTACACGTT	TGCCATGTGC	AGTTATCGGG	240
AGAAGAAAGC	GGAGCCTCAG	GAACTTCTAC	AATTGGATGG	GTACACTGTG	GATTACACCG	300
ACCCCCAGCC	AGGTTTGGAG	GGTGGCCGAG	CCTTCTTCAA	TGCTGTCAAG	GAGGGAGACA	360
CCGTGATATT	TGCCAGTGAC	GATGAACAAG	ACCGCATCCT	GTGGGTCCAG	GCCATGTATC	420
GGGCCACGGG	GCAGTCACAC	AAGCCTGTGC	CCCCGACCCA	AGTCCAGAAA	CTCAACGCCA	480
TCCTCGAG ·						488

- (2) INFORMATION FOR SEQ ID NO:466:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GAATTCGGCC TTCATGGCCT AGCCGCTGCG GTGAGCCTTG AAGCCTAGGG CGCGGGCCCG	60
GGTGGAGCCG CCGCAGGTGC AGATCTTGGT GGTAGTAGCA AATATTCAAA CGAGAACTTT	120
GAAGGCCGTC TGAGCTAAAA AATAATGCTG ATTTGGCCTC ATCATATTTA TGAAGGAGGG	180
AGAAATAGAA GCATGTATAA TGTAGAAAAA CATATCTTAT CCTTATGTTT GCATATATTG	240
TTGAATAAAT ATAGTTTAAT GAATATGTTT TCTCACCTTT CTTTGCTTGC ACTTCTCGAG	300
(2) INFORMATION FOR SEQ ID NO:467:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 381 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:	
- · · · · · · · · · · · · · · · · · · ·	
GTTCTAGACC TGCCTCGAGA TATGCCGGAA GGTTGCATGG CTGGTCCCAG GGCCAGCACA	
GGCCCGAGGC CGGGCTGCCT GGTTTTATTT TTATTTAACT TTATTTTCTG TTTTATGAGT	60
GTGTGTCCGC CCACCCCCAC CCCCTTCAGT GTTAAGTGGG GAGCCCTGGG GGAGTCTCTC	120
CTGCCTCCCA GCCTCTCCCA AGACCTCCCC CCTCGTCACC AGCCATCCCT CTGGACCAGG	180 240
CAGAGGGCGG ACCGGGTGGG CAGGGGCCTG AGGGTGGCTC GGGCCAGCCC ACCAGCCAAT	300
GGACCCCTCC TCAGGCCGCC AGTGTCGCCC TGCCCCTTTT TAAAACAAAA TGCCCTCGTT	360
TGTAAACCCT TAACGCTCGA G	381
(2) INFORMATION FOR SEQ ID NO:468:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 304 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:	
(AL) SEQUENCE SECRETION. SEQ ID NO:400:	
COMMUNICATION OF THE PROPERTY	
GCTGTCCAAT TATACTGACC TGGCCATGAG CACGGTGAAG CAGACCCAAG CCATTCCATA	60
TACTGGTCCC TTTAATTTGC TCTGTTACCA GCTGCAGAAA TTGACAGGTG ATGTGGAAGA ATTAGAAAATT CAAGAAAAAC CTGCTCTGAA AGTGTTCAAA AATATTACTG TAATACAAGA	120
ACCAGGCATG GTGGTATTAG AATGGCTGGC AAACCCTTCT AATGATATGT ATGCAGATAC	180
AGTAACAACT GTGATATTGG AAGTTCAGTC AAATCCCAAA ATAAGAAAAG GCGCAGAACT	240
CGAG	300 304
	502
(2) INFORMATION FOR SEQ ID NO:469:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 346 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:	
GCGATTGAAT TCTAGACCAC CCCGCACTCC AGCCTGGGCA ACAGAGCAAG ACTCTTTCTT	60
	~ ~

120

AAAAAAATTA AAAAAAAAAG GAGTACCCAT TGGGATAAAC CTCTTTGGAG GAGAGGACAT

PACCECTAGE TRANSPORCE ACCAMPAGE ALGARIAGE ALGARIAGE TAGITGGGAT PACCECTAGE TAGETTAGAT TAGITGGGAT CACCATCACT CACCATCACT CACCATCACT TAGETTAGAT CACCATCACT CACCATCACT TAGETTAGAT CACCATCACT TAGETTAGAT CACCATCACT CACCATCACT TAGETTAGAT CACCATCACT CACCATCACTACT CACCATCACT CACCATCACT CACCATCACT CACCATCACTACT CACCATCACT CACCATCACT CACCATCACT CACCATCACT CACCATCACT CACCATCACT CACCATCACTACT CACCATCACTACT CACCATCACTACT CACCATCACTACT CACCATCACTACT CACCATCACTACTACTACTACTACTACTACTACTACTACT	240 300
FTTTTTATTT GCCATCTTGG CAGGTTTAGG GCAGAGCATG CTCGAG	346
(2) INFORMATION FOR SEQ ID NO:470:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 321 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:	
SAATTCGGCC TTCATGGCCT AGGATTTCA GCAAGAATTA AATTATTCTG CATATTGGAC AGGCCTATT TAGAGGCCTG CACATCTGTT TTTATCCATT TGTGTAACGA TACCGTGTGT AGAAGTAGGT TCATGGATCA GATGAGAAAA GTCAATTCTC TAAGATACCT TCCCTTGTGG CTGTGGATTC TCACCTTGAT GATTCAGCTT TGTGTGATGG AGGTGTCTGC CAGAGAATTC CTGGCCACCC AGCTCCTCAG CCCTCTGCCC CCACCCCCAA TACACACACC TTTCTCCATT GTGACCAGATG CTGGTCTCGA G	60 120 180 240 300 321
(2) INFORMATION FOR SEQ ID NO:471:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 417 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:	
GAATTCGGCT TCATGGCCTA CTTCATTCAC TGTAAAACCA ATAGCAAACA ACGGAAGAGA ACGGAAGCCCT TGAAGCAACA AAGAGAGGA GAAGCAACAT GGCAAGAGCA GGAAGCCCCT GGGAAGAGACA CTCCCACCGA AAGTTCTTGC GCAGTGGCCG CCATTGGCAC CCTCAGAGGC GGCACCCCCAC GTATCTCCAC CTCCTCTTT AGGAAGGTGC TGGCTGGCCC CCTCAGGCTG CCGAGGGACC TGTGTAACTG GATGCAGGA CTCCTGCAAG CTGCTGGCCT CCATATCAGG ACAATGCTT ACAACTACTG CTACATGTAC GAGCTCCTGA GCCTGGGGCT GCCACTCCTC CTGGGCGTTCT CTGAGGTCCT CTGAGGCCAT TACAGGGAAT CTGAGGGCTC CCTCGAG	60 120 180 240 300 360 417
(2) INFORMATION FOR SEQ ID NO:472:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 331 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:	
SAATTCGGCC TTCATGGCCT ACAAGAGGCA GCTTATAGAC AACCGCAAGC TCATTGAGAC	60 120

GGGCCTGGGC CTGGCCCAGA AGGTAGATCC TGCCCAGAAG GAGAAGGAAG AGGTTGGCCA

GTGGCTCACG AATACCATCG ACACGCTCAA CATGCAGGTG GACCAGTTTG AGAGTGAAGT GGAGTCACTG TCAGTGCAGA CACGCAAGAA GAAGGGCGAC AAGGATCAGA AGCAGGACCG GATTGAGGGC TTGAAGCAGC AGCATCTCGA G	240 300 331
(2) INFORMATION FOR SEQ ID NO:473:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:	
GAATTCGGCC TTCATGGCCT AGAGGTGCTT CAGTGGTACA ATCAGTTAGC ACACAGTACG TATACAGCAG TATGTGTGTG AGAAATTATT TTAAATATAA GAATTATCAA AAATTATAAG AAGACCATCC CTTTAACTGA ATAGTTTCAC CAAAAATCAG AAAAATATGT AAGTGATACA TTTTGTTTCT TGGATATAGC AATGTACCAC CTTGCATAAA TGAGACTATT AAAATGATCA CCTGAGGTCA GAAGTTCGAG	60 120 180 240 260
(2) INFORMATION FOR SEQ ID NO:474:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 511 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:	
GAATTCGGCC TTCATGGCCT ACAAAGATTT GAGGAAAAGA GGTTCAAATT GGACCACTCA GTGAGTAGCA CCAATGGCCA CAGGTGGCAG ATATTTCAAG ATTGGTTGGG AACTGACCAA GATAACCTTG ATTTGGCCAA TGCAATCCTT ATGTTGGAGT TACTAGTGCA GAAGAAGAA CAACTGGAAG CAGAATCACA TGCAGCCCAA CTACAGATTC TTATGGAATT CCTCAAGGTT GCAAGAAGAA ATAAGAGAGA GCAACTGGAA CAGATCCAGA AGGAGCTAAG TGTTTTTGGAA GAGGATATTA AGAGAGTGGA AGAAATGAGT GGCTTATACT CTCCTGTCAG TGAGGATAGC ACAGTGCCTC AATTTGAAGC TCCTTCTCCA TCACACAGTA GTATTATTGA TTCCACAGAA TACAGCCAAC CTCCAGGTTT CAGTGGCAGT TCTCAGACAA AGAAACAGCC TTGGTATAAT AGCACGTTAG CATCAAGACT GAAAACTCGA G	60 120 180 240 300 360 420 480 511
(2) INFORMATION FOR SEQ ID NO:475:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 610 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:	
GAATTCGGCC TTCATGGCCT AGTCACAGCT GTCTATTTTT GTCACTGTCG GAACATTGTT CATCGTGATT TAAAAGCTGA AAATTTACTT CTGGATGCCA ATCTGAATAT CAAAATAGCA GATTTTGGTT TCAGTAACCT CTTCACTCCT GGGCAGCTGC TGAAGACCTG GTGTGGCAGC	60 120 180

CTGCACCTGA	ACTCTTTGAA	GGAAAAGAAT	ATGATGGGCC	CAAAGTGGAC	240
TTGGAGTTGT	CCTCTACGTG	CTTGTGTGCG	GTGCCCTGCC	ATTTGATGGA	300
AGAATCTGCG	GGCCCGCGTG	CTGAGTGGAA	AGTTCCGCAT	CCCATTTTTT	360
AATGTGAGCA	TTTGATCCGC	CATATGTTGG	TGTTAGATCC	CAATAAGCGC	420
AGCAGATCTG	CAAGCACAAG	TGGATGAAGC	TAGGGGACGC	CGATCCCAAC	480
TAATAGCTGA	ATGCCAACAA	CTAAAGGAAG	AAAGACAGGT	GGACCCCCTG	540
TCCTCTTGGC	CATGGAGGAC	ATGGGACTGG	ACAAAGAACA	GACACAGAAG	600
					610
	TTGGAGTTGT AGAATCTGCG AATGTGAGCA AGCAGATCTG TAATAGCTGA	TTGGAGTTGT CCTCTACGTG AGAATCTGCG GGCCCGCGTG AATGTGAGCA TTTGATCCGC AGCAGATCTG CAAGCACAAG TAATAGCTGA ATGCCAACAA	TTGGAGTTGT CCTCTACGTG CTTGTGTGCG AGAATCTGCG GGCCCGCGTG CTGAGTGGAA AATGTGAGCA TTTGATCCGC CATATGTTGG AGCAGATCTG CAAGCACAAG TGGATGAAGC TAATAGCTGA ATGCCAACAA CTAAAGGAAG	TTGGAGTTGT CCTCTACGTG CTTGTGTGCG GTGCCCTGCC AGAATCTGCG GGCCCGCTG CTGAGTGGAA AGTTCCGCAT AATGTGAGCA TTTGATCCGC CATATGTTGG TGTTAGATCC AGCAGATCTG CAAGCACAAG TGGATGAAGC TAGGGGACGC TAATAGCTGA ATGCCAACAA CTAAAGGAAG AAAGACAGGT	CTGCACCTGA ACTCTTTGAA GGAAAAGAAT ATGATGGGCC CAAAGTGGAC TTGGAGTTGT CCTCTACGTG CTTGTGTGCG GTGCCCTGCC ATTTGATGGA AGAATCTGCG GGCCCGCGTC CTGAGTGGAA AGTTCCGCAT CCCATTTTTT AATGTGAGCA TTTGATCCGC CATATGTTGG TGTTAGATCC CAATAAGCGC AGCAGATCTG CAAGCACAAG TGGATGAAGC TAGGGGACGC CGATCCCAAC TAATAGCTGA ATGCCAACAA CTAAAGGAAG AAAGAACAGGT GGACCCCCTG TCCTCTTTGCC CATGGAGGAC ATGGGACTGG ACAAAGAACA GACACAGAAG

- (2) INFORMATION FOR SEQ ID NO:476:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GGAGATTGGC	CACCTCCAAG	ATATGGTAAG	GAAAAGTGAA	CAAGGTCTTG	GCTCTGCAGA	60
AGGACTTATT	GCTAGTCTTC	AGGACTCCCA	GGAAAGGCTT	CAGAATGAGC	TTGACTTGAC	120
TAAAGACAGC	CTAAAGGAGA	CCAAGGATGC	TCTATTAAAT	GTGGAGGGTG	AGCTAGAACA	180
AGAAAGGCAA	CAGCATGAAG	AAACAATTGC	TGCCATGAAA	GAAGAAGAGA	AGCTCAAAGT	240
GGACAAAATG	GCCCATGACT	TAGAAATTAA	GTGGACTGAA	AATCTTAGAC	AAGAGTGTTC	300
TAAACTTCGT	GAAGAGTTAA	GGCTTCAACA	TGAAGAGGAT	AAGAAGTCAG	CAATGTCTCA	360
ACTTTTGCAG	TTGAAAGATC	GAGAGAAAA	TGCAGCAGAG	AAACTCGAG		409

- (2) INFORMATION FOR SEQ ID NO:477:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GTATGCCTGT TCCAGACCAG	CCTTCATCAG	CCTCAGAGAA	GACGAGTTCC	CTGAGCCCCG	60
GCTTAAACAC CTCCAACGGG	GATGGCTCTG	AAACAGAAAC	CACCTCTGCC	ATCCTCGCCT	120
CAGTCAAAGA ACAGGAATTA	CAGTTTGAAA	GGCTGACCCG	AGAGCTGGAG	GCTGAACGGC	180
AGATCGTAGC CAGCCAGCTG	GAGCGATGCA	AGCTCGGATC	CGAGACTGGC	AGCATGAGCA	240
GCATGAGTTC AGCAGAAGAG	CGGATACTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:478:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GAATTCGGCC TTCATGGCCT ATGCGTGGGG GTGGGGGGGC AGGCTAGAAA GGAGCCCTCC CTCCTCGGGG TGTCTAGGGT GTGCTGGCCA CTGGAAGATT GGAGTCGCTG ACCCAGTGCT GACCCTGACC CTTGGCTGGG TCCACTCTGC AGACTCCACC TGAGGAGACC CACCCAGGGT GAAGCTCGGT GCCCAGGCCT GAACTGAGCC CGGCCGGGTG CAAGGGCTGA GGTGTGAGGT CGGCCCAGGC CTCTTCCCAG GCCTGAGGGT GGCTACAGCT CGAG	60 120 180 240 284
(2) INFORMATION FOR SEQ ID NO:479:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 352 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:	
GAATTCGGCC TTCATGGCCT ACTAAATTTT CCAAAACGTT GATTTGCATA ATACAGTGGT ATGTGCAATG GATAAATTGC CGTTATTTCA AAAATTAAAA TTCTCATTTT CTTTCTTTTT TTTCCCCCCT GCTCCACACT TCAAAACTCC CGTTAGATCA GCATTCTACT ACAAGAGTGA AAGGAAAACC CTAACAGATC TGTCCTAGTG ATTTTACCTT TGTTCTAGAA GGCGCTCCTT TCAGGGTTGT GGTATTCTTA GGTTAGCGGA GCTTTTTCCT CTTTTCCCCA CCCATCTCCC CAATATTGCC CATTATTAAT TAACCTCTTT CTTTGGTTGG AACGACCTCG AG	60 120 180 240 300 352
(2) INFORMATION FOR SEQ ID NO:480:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 263 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:	
GAATTCGGCC TTCATGGCCT ATTAAAAGAA TGTTCTTTCA TTAAAAGACC AAAAAGAAGT TAAAACTTAA ATTGGGTGAT TTGTGGGCAG CTAAATGCAG CTTTGTTAAT AGCTGAGTGA ACTTTCAATT ATGAAATCTG TGGAGCTTGA CAAAATCACA AAAGGAAAAT TACTGGGGCA AAATTAGACC TCAAGTCTGC CTCTACTGTG TCTCACATCA CCATGTAGAA GAATGGGCGT ACAGTATATA CCGTGTTCTC GAG	60 120 180 240 263
(2) INFORMATION FOR SEQ ID NO:481:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:	
GGAGCAGGAA GAAATGCAAG AGGAGATGGA GAAGCTGCGA GAGGAAAACG AGACTCTCAA GAACGAGATC GATGAGCTGA GAACCGAGAT GGACGAGATC AGGGACACTT TCTTCGAGGA GGATGCCTGT CAACTGCAGG AAATGCGCCA CGAGTTGGAG AGAGCCAACA AAAACTGCCG GATCCTGCAG TACCGCCTCC GCAAAGCCGA GCGCAAAAGG CTCCGCTACG CCCAGACCGG	60 120 180 240

GGAAATCGAC GGGGAGCTGT TGCGCAGCCT GGAGCAGGAC CTCAAGGTTG CAAAGGATGT

ATCTGTGAGA CTTCACCATG AATTAGAAAA TGTGGAAGAA AAGAGAACAA CAACAGAAGA

300

360

TGAAAACGAG AATCTCGAG	379
(2) INFORMATION FOR SEQ ID NO:482:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 301 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:	
GAATTCGGCC TTCATGCTTT CTAGGCAAGA GGTCATCAGA AGA.TGAGAG AAAGAGGAGA ACCAATCAGA CTATTTGGAG AGACTGATTA TGATGCTTTT CAACGTTTAA GGAAAATAGA GATCCTCACA CCAGAAGTTA ACAAGGGATT GAGGAATGAT TTGAAAGCAG CCTTGGATAA GATTGATCAG CAGTACCTCA ATGAAATCGT CGGCGGTCAG GAGCCTGGAG AGGAAGACAC ACAGAATGAT CTGAAAGTTC ATGAGGAAAA CACCACAATT GAAGAGTCAG AGGCCCTCGA G	60 120 180 240 300 301
(2) INFORMATION FOR SEQ ID NO:483:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 168 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:	
TGGTCTCCAG AAATGCTTTG GGTTCATCTT TCATTGCTGC AAGGAACTTC CATGCCTCTA ACACTCATCT TCAAAAGACT GGGACTGCTG AGATGTCCTC TATTCTTGAA GAGCGTATTC TTGGAGCTGA TACCTCTGTT GATCTTGAAG AAACTGGGCT ATCTCGAG	60 120 168
(2) INFORMATION FOR SEQ ID NO:484:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 452 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:	
GCAAGCTCTC CATGGAAACC CCTGCCAAAA CAGAAGAGAT AAAACTGGAA AAGGCTGAGA CAGAGTCCTG CCCAGGCCAA GAGGAGCCTA AATTGGAGGA ACAGAATGGT AGTAAGGTAG AAGGAAACGC TGTAGCCTGT CCTGTCTCCT CAGCACAGAG TCCTCCCCCAT TCTGCTGGGG CCCCTGCTGC CAAAGGAGAC TCAGGGAATG AACTTCTGAA ACACTTGTTG AAAAATAAAA AGTCATCTTC TCTTTTGAAT CAAAAACCTG AGGGCAGTAT TTGTTCAGAA GATGACTGTA CAAAGGATAA TAAACTAGTT GAGAAGCAGA ACCCAGCTGA AGGACTGCAA ACTTTGGGGG CTCAAATGCA AGGTGGTTTT GGATGTGGCA ACCAGTTGCC AAAAACAGAT GGAGGAAGTG	60 120 180 240 300 360 420
AAACCAAGAA ACAGCGAAGC AAAGGACTCG AG	452

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GTTTGTAAAT	CACCTGATGA	TGGTGATATA	GCTGTGGCCA	ACGAAATGTC	AAGGGAAGTC	60
TGCTGGGGAA	GGTAGACGTA	GGATAGGAGT	ATGGGAAAAA	ATTATTCACT	CAAAAGCATG	120
ATGCACAGAG	GAGCTATGAT	CTTTTCTTGT	TTTCCTCACT	${\tt GGATGTTGTC}$	ATGTCTGTAT	180
GTACTTCCTG	GAACTGTGGC	ACCATCTTAC	AACCATGAAA	GGAGCTCACA	TGAAATCATG	240
TTGAACATAG	CAGAGCGGGA	AGATGGAAGG	AATCCGAGAT	CTATGTTTGA	TGTTAAGCGA	300
TGATGTTAAA	AACTTAAAAA	ACTCCAGAAC	TCTCTTACCC	CTGGTGCTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:486:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

GAATTCGGCC	TTCATGGCCT	ACTCAGCTGG	AAGCTTTACT	CCCTCCTCGA	CAGAAAGTGA	60
GGATTACAGA	TGACATGGAT	CAGGTGGAGC	TGAAGGAGTT	TTGTCCCAAT	GAGCAGAACT	120
GGCGTCAGCA	CAGGGAGGCC	TACGAGGAGG	ACGAAGACGG	GCCCCAGGCT	GGAGTGCAGT	180
GCCAGACGGC	ATGACGTGGT	GCGGGGCAGC	GTGGCCCCAC	CGGACTAGCA	CATGATGAAT	240
GTAAAGTTGG	CACAATGAAA	ATGACATCGC	TTTAATGGCC	TTGTGTTTGG	GATGTCCTGT	300
GTATGTGTTC	AGCATTCTTA	ATTGCTGAGT	GTCTTTTTGG	CTTTTCTTTT	GGTTGTAACT	360
TAAGTTATAG	CTTAATTTAT	ATTTAAATGT	TTTAAGTATA	AATCACCTCT	AGGCCTCGAG	420

- (2) INFORMATION FOR SEQ ID NO:487:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GGAGTGTCAA	GAATAACCGC	TCAGGTTGAG	TGTAAAAATA	TTTTATGGTC	CCATCAGCAT	60
CAACCTGCCT	TAATGCTTCT	TTGGTTGTCT	CTTCAGCTAG	TTCTTATTTT	ACAGCACATG	120
ATATATGAAG	TGATTTCACA	CCATGCCCAA	GATACGGGCC	ACCCACCAGC	TACATGGCAT	180
GATGACTCTG	CAGGCCGAAC	GGCAGCCTTG	ATAATTATAA	GGCCATGGGT	AATAGCCCCC	240
CAGGGGTTCA	CAGATCTTCT	GGCAGTGGGT	GTAGCTCCGC	CTACATTCTA	TACAACAGAT	300
TCCTTCGCCT	GCCTCGAG					318

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 487 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:	
ACTACTACAA GGGAAAGGGG AATGTGGTTT CAAAAAGGGT TTTGCCTTAT TTATTTTAT 1 AGTAGATACT TATTAATCAA ACATTTAAGA GCAACTCAGT AAGTATTTGT CCAGAATGAA 1 CTGTTCTCAA GACTAGGTTT ACTGCTTGAC ATTAGAGGTT AAGGTGTTGC AATTCTGAGT 2 CTTGTTTTTT ATTACTACCA ACCCCCACCC CCGCCGATAT TACTTCATCT CCCTCCAAGG 3 TCACTGAAGT TTTTCATAAC TATTTTAACA GATATTGCAA TAAATGTACA GTAATTTAAC 3 TATCCTTCTT GCTGGGCATG TCAAAGTGTT TTCTATTATT ACAGATAATG CTGCAATGAA 4 TCTTTATTTA TATAATACAC TTTTATCCAG TTGTCATTTT TTCTTTGTCT TATATTCTCA 4	60 20 80 40 00 60 80
(2) INFORMATION FOR SEQ ID NO:489:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 149 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:	
AAAAAATAAA CTGAAAGGAA AATTGTTGAA TGTTTGAATC TTGCCTAGTC CCCTCACCCC 1. CAAGGCTGGC TTCTAGAGTT AAGCTCGAG 1.	60 20 49
(2) INFORMATION FOR SEQ ID NO:490:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 259 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:	
TTTCTCCCAC TCCTCCCAT CACCTTCTGG CACTTCCATT GTTCATATAT TGATATGCTT AATGATGTTT CTGAAGATTT ATTCATTTTT CCTTTATTCC TTTTTATTCT GTTCCTCAGC 1 CCAGATCATT TCAATGCACA TATCCTCAAG TTTGCTGATT CTTTCATTTC CTGCTCAGAT 2	60 20 80 40 59
(2) INFORMATION FOR SEQ ID NO:491:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 320 base pairs (B) TYPE: nucleic acid	
253	

- (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GAATTCGGCC TTC	CATGGCCT ACAAATGTTT	AATCAGAGAC	TCATATTCAC	CTTTAAGTAA	60
AAAACATACT TCT	TTTCCCCC TAATAGTCAC	AGCATTCTGC	AGAGCTAAAG	AAGGAGACCA	120
GGAGTCTGTG GGA	AGCAAAGA TCATTTTGTG	AAGCTAGAGG	ТССАДТТТАД	AAGCAGTTCC	
TGCTACAAAT TAA	AAACATAT TTGCATTCTG	ССТАВАВТАС	TOG: WILLY III	CAACCUTTCCC	180
TGCCTTTTTT AGG	GTTGCTTT GTGAATAATA	TOCACAAAAT	CANANTORMA	DAACGI IGGG	240
GTAGCCTGCT AAC		IGCACAAAAI	GAAAAIGITA	AAAAAAACAT	300
OTAGECTOCT AAC	CCICGAG				320

- (2) INFORMATION FOR SEQ ID NO:492:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

GAATTCTAGA	CCTGCCTCCA	GCCACTTCAA	ACCTTTGGTG	ACCAAAGTGG	GGTAAAAACA	60
					TTAAGAAGTT	120
					TAATTAGTGT	180
		CGTGTTGGTT				224

- (2) INFORMATION FOR SEQ ID NO:493:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GAATTGCCTT CAT	GGCCTAC CGAATCAGAC	AGAAGAAAGC	CCAGGGCTCC	ACTTCTTCTA	60
CAAGGTTGCA TGA	GCCCGAG AAGAATGCCA	GAGAAATAAC	ACAGGACACA	AATGATATCA	120
	GAACCTG CCCAAGGGGA				180
ACAACCACAC GGA	GTATGCC AGCATTCAGA	CCAGCCCGCA	GCCCGCGTCG	GAGGACACCC	240
TCACCTATGC TGA	CCTGGAC ATGGTCCACC	TCAACCGGAC	CCCCAAGCAG	CCGGCCCCCA	300
AGCCTGAGCC GTC	CCTCGAG				320

- (2) INFORMATION FOR SEQ ID NO:494:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GAATTCGGCC	TTCATGGCCT	AGGTAGCTCT	ATGGTTTTCC	TCGCGTTCTT	GAGTCGGGAA	60
ATGGCCGCTG	TGTGGTTGCA	ACGGAGATAA	ATTCCCGGAA	CCGCGATTCG	GCGTGTCAGG	120
AATTCGAATT	TAGAGTTTAA	TTTCTCAGAG	CATTCTCTCC	AGGAAGAATT	TTTACAGTAT	180
CTCAAAGACT	TCACTTGACT	TCTTGATCCT	GCATAAAACC	AAGGAGAAAA	GAAATGGGTC	240
GCTCCAATTC	TAGATCACAT	TCTTCAAGGT	CAAAGTCTAG	ATCACAGTCT	AGTTCTCGAT	300
CAAGATCAAG	ATCTCATTCT	AGAAAGAAGC	${\tt GATACAGTTC}$	${\tt TAGGTCTCGT}$	TCCAGAACAT	360
ATTCAAGGTC	TCGTAGTAGA	GATCGTATGT	ATTCTAGAGA	${\tt TTATCGTCGC}$	GATTACAGAA	420
ATAATAGAGG	AATGAGACGA	CCTTATGGGT	ACAGAGGAAG	GGGTAGAGGG	TATTATCAAG	480
GAGGAGGAGG	TAGAAACCCT	CGAG				504

- (2) INFORMATION FOR SEQ ID NO:495:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

GAATTCGGCC	TTCATGGCCT	ACCAACTTAG	TCATTTGAAG	CCCAAGAGTC	TAATTTTATA	60
TGCCCTGCCA	ATGTCCTCAT	CTATTGCAGA	ATGNATAATT	ATCTATTTGT	TTTGGACTAT	120
ATGTTACAAA	AATTTAAAAC	ATAAGATCCT	CTCTCTATAT	TTCATTATTG	GTGAACCCAC	180
ATTGCTCGAG						190

- (2) INFORMATION FOR SEQ ID NO:496:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

GAATTCGGCC	TTCATGGCCT	AGGTAAGAAA	ATCGTCAATG	AATTGTGGCA	TGACCAGGTG	60
GAGAGTAAGT	GTCATAAAGA	GGGATAGTGG	ATAGTATAAT	GTCAGGCACC	TCAAAGGAAC	120
TGGGCAGGGA	GTTAGGGAGT	AAAAAGGGCG	GTGGTCTGGA	AGCAGAAAGG	AGGAGCAGTG	180
GTCCAGTAGG	GGCTGCAGAG	CTGCAAGGCT	TTGCCTCAAT	CCTGTCAAAG	GCAACTTCAA	240
GCTTTCCAGG	AGCCATACTC	CTTCATTTGT	TCATTACTTT	CTAGATTAGG	AAATCACCAC	300
TCGAG						305

- (2) INFORMATION FOR SEQ ID NO:497:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GGTGGACTAT CTTCCTGGGA CAATGAGCCA AAGCTGTGAG	TTCATGGCCT AGGTGGACCA ATGTACAGCA CTCAGGTTCA TGGCCAACTG TTCAGTACTC TACAGGTGCC TCAGTGGAGG GAGAGCCCAT TGTCCAGGTG CAATACCAGA GCGCTCTGGG AAAAGGGCTG CTTGCAGGCA CGAGGGCTCA TGGTGGGCCA CCGCCACGGC CCATGCAGCC TAATAGCAAG CCÁAGGCAGG AGCTGCTCAAAG GCAGATTTCT CGAG TTCATGGTCA TGGCCCACTGC TAATAGCAAG CCÁAGGCAGG AGCTGCTCAAAG GCAGATTTCT CGAG	60 120 180 240 300 334
(2) INFORMA	ATION FOR SEQ ID NO:498:	
(i) :	SEQUENCE CHARACTERISTICS: (A) LENGTH: 160 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:498:	
GTATCTGCTC	CTTTTCATC CTTAGGAGAC CTGAGTCCTC AAGAAAACCC TTTTCTGGAA CTTCAGAACA TTTTATAGAA AAGAATAATA CAAAACACAC AACTGCAAGA AAGAAAATGA TTTTATGGAA AACACTCGAG	60 120 160
(2) INFORMA	TION FOR SEQ ID NO:499:	
(i) !	SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:499:	
CCAAGCACTA CCAAGCACTA CTTGGTGCTT	TTCATGGCCT ACTCGATCTC CTGACCTCGT GGTCCACCCG CCTCGGCCTC GGGATTACAG ACGTGAGCCA CCGCGCCCGG CCTTGTCCTG GATTTTTTAA TTATTTATAG TTGCGTTAAA ATAAATAGGG ATGGGTTTGA TAAGTCACCA TAAATTCTGC CATCATCTTT TCTAGGAGTG TAAGATATAG AGATACACAT TTTTTTTTTAA CATGAGGATA CTCGAG	60 120 180 240 276
(2) INFORMA	TION FOR SEQ ID NO:500:	
(i) s	SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:500:	
TTGTTCTCTC ACACTGCTCA	TTCTGGCCTA GACCTGCCTC TGATATGTAC TTGGTTTTTA AAAACCCATT TTGTTTCCTC TCTATTTCAG CCTAGTATCA GAAGGCCAGG CGAGACTGCA TCACCCCGCG GCGTGATCCC TGCTCTTAGG TGCTGGGCAG AGGGGAAGGG GAGGATGGTG AGGGAGGGCT GGTGAGGGGC TCAGAGGAAT ACTTGGAACA CTCGAG	

- (2) INFORMATION FOR SEQ ID NO:501:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 635 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

GAATTCGGCC TTCATGGCCT	AGTGGTTTTG	TTGTTGTTGT	CGGAGACAGG	GCCTCGCTTG	60
GTCTCCCAGG CTAGAGTGCA	GTGGCATGAT	CACGACTCAC	TGCAGTCTCG	ACCTTCTGGG	120
CTCAAGTGAT CCTCCTGTGT					180
CATCCAGCTA ATTTAAAAAA	CATTTTTTT	GTAGAAATAG	GGTCTTACCA	TGTTGCCCAG	240
GCTAGTCTCA AATTCCGGGG					300
ATTACAGGCA TGAGTCACCA					360
AGCCTGGGCT ACAGAGCAAG					420
AGAAAGAACC AGAGAAACAT					480
AGAAATGAAA AAGAAATGAA					540
TGAATGGAGG CCTTTAGGCC	AAAGGCTATG	ATTAATTTCA	AGCTATGTTA	CTGAAGTCCA	600
TAAACAAAGG ACTCAGATCT	AAATGGGTAC	TCGAG			635

- (2) INFORMATION FOR SEQ ID NO:502:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

GAATTCGGCC	TTCATGGCCT	ACCCGTAGAA	ATCCCCCTTT	CTCTAATAGC	GAGGCTCTAA	60
CCACACAGCC	TACAATGCTG	CGTCTCCCAT	CTTAACTCTT	TGCCTTTGCC	ACCAACTGGC	120
CCTCTTCTTA	CTTGATGAGT	GTAACAAGAA	AGGAGAGTCT	TGCAGTGATT	AAGGTCTCTC	180
TTTGGACTCT	CCCCTCTTAT	GTACCTCTTT	TAGTCATTTT	GCTTCATAGC	TGGTTCCTGC	240
TAGAAATGGG	AAATGCCTAA	GAAGATGACT	TCCCAACTGC	AAGTCACAAA	GGAATGGAGG	300
CTCTAATTGA	ATTTTCAAGC	ATCTCCTGAG	GATCAGAAAG	TAATTTCTTC	TCAAAGGGTA	360
CTTCCACTGA	TGGAAACAAA	GTGGAAGGAA	AGATGCTCAG	GTACAGAGAA	GGAATGTCTT	420
TGGTCCTCTT	GCCATCTATA	GGGGCGCTCG	AG			452

- (2) INFORMATION FOR SEQ ID NO:503:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GAATTCGGCC TTCATGGCCT ACAAAATTGT CTTGACATAA GTAATTTGGG TATGCTGTAT 60
AAAGGCTTCT AAGAATTAAG AAACATGGCC CGGGTTGCAA ATTTTAATGC ATGACTACCT 120

TTTTTTCTAT AGAATATAGC TTTTGTCAGA TTCTCAGCAG TGGCTCTGAT CCAGAAAACA TTAAGAACCA CTGGTCATGA GTGGTGATTT TCAGCTTTTT TGGTCTTAAC CCACTTAGGT GGGACAGAAG CTCCTTATCT CACCTATACC ATCCAGCATC CTCGAG	180 240 286
(2) INFORMATION FOR SEQ ID NO:504:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 424 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:	
GAATTCAGCC TTCATGGCCT AGAGGGGTTT AGGATTCAAA GCAAAGGGGA GACAGCTACT AAGTAAACTA CAAAATAATT GCTAAACTGA AAATTGTATA AAGTGTACTG GACAGATGAT GTTCCTAATT CTTATCCATG AAATATTTC TGCCTTCTTA GAGGAAATAG CACCTGACAC AACACTAGCC ACATTGTAGG TGATCAATCA GCACATGTCT AAATAAATAA ATTAAAAAAAG AATCAATTAG AAATTCCACT GAAAATTCTT CTTAAATATA ACCAACTTCA TTATGACAAG CTATGAATAT AGAGCTTACA TACATGTTAT ATATCAATAT GTGAGATG GGGTCTCACT CGAG	60 120 180 240 300 360 420 424
(2) INFORMATION FOR SEQ ID NO:505:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 204 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:	
GAATTACTCA GTTTTCAGGT TCTTCCTAGC TCGGGGCTTT TAAATTTTGA AATCTAAACA TTCTTTCCCA CCATCCTTTT TGACTGTTGA CCTTGGTTTT CTCTCTAAG TTCTGTCCC TCTGCTTCCT TACTTTTTTT CCTTTTTGAA TTCTATCTTT ATCTGTCTTT TGTTCACTTT TTAATGCTAT ATATGGATCT CGAG	60 120 180 204
(2) INFORMATION FOR SEQ ID NO:506:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 218 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:	
GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGAGA TGTACAGTAA TAAGTATGCA CAGAAATGTT AGATTATTT TGAAGATGTG GAGAAACTAC TGTTATTTTT GCTTATATTC TTCTCTAAAA ATTCACTAAA TGAATAACAG TTATTGGTTT TGCTATTCAA GATAATTATA AAAATATCTA TTATAGCTAA TCTTCACATG AACTCGAG	60 120 180 218
258	

(2) 7	INFORMATIO	M EOD	SEO	TD	MO . Sc	7.

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GAAGTTTAAC	ATTTCAACTG	TTGGTAAAAT	CTCCCTGGTG	CCACCTTGTC	GCACCCCCT	60
GTTATGAGGC	ACAGTTAGTG	GGTTTATGAG	AGGTTTGTTC	AGTGAAGCTC	CTGCCACTGT	120
AGACCTAAAT	GTTTCTCTCC	CTGTTGAAGT	GACCTGCCTT	CCTCTTTAGT	ACCTAACACA	180
					CCCTTTCTCT	240
CTGGCAGGTA	TATTAAAAAA	TTACAAAATA	GTAAATTTGC	CAAATTTTTC	TTGGTGTGTA	300
		AATATCTTAT				352
						222

- (2) INFORMATION FOR SEQ ID NO:508:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GAATTCGGCC TT						60 120
GAGATGAAAA TO	BATATGGTG	TGCAGAACTG	GACTCAGTAA	GGTGCGGAAA	GGGGAAGGAT	180
CGTGTGGAGT TO					OICACIIAOA	283

- (2) INFORMATION FOR SEQ ID NO:509:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

GAATTCGGCC	TCATGGCCTA	CTCTCCTTTC	TTAACTTGTG	TACTTGGGGG	CACTTTTGAT	60
TTTGGTCCCA	CATCATTGAG	GAAGCTGGCC	CAGAGTTCGT	CCTCCTTCTT	TTTCCTGGCA	120
TCCTCTGATC	CAATGCCTTT	TTCCTGCTCT	GCAGCGTCAT	CTTCCTCCTC	ACTACTGCTT	180
CCCTCAGATT	CTGAATTGGC	ATCCTCCTCT	TCCTCTTCTT	CTAATGAGAG	GCCACCTTGT	240
CTTCTCTTCC	TGGCTGGAAT	GCTCTGGGCC	TTTCTTTTTT	TCCCTTGGGT	TTTCTGTGTC	300
TGCTCTTCAC	CATTAGGCCA	TGAAG				325

- (2) INFORMATION FOR SEQ ID NO:510:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:	
GAATTCGGCC TTCATGGCCT AGACAGGAGG TCATTGGGGA TTTTAGAAGG TTACACTGGA TACATTTCCA TTAAGCTTCA CGATATCCCA CAGGTCCATT CTGTGTGAAA TGGTCTAAAA ATTTCCTGTT CTCATGCTTC ATTTTTTCT TTTAGTAATA TTCCTAATTG TGTAAAATAG TATTTCTTTT CATTTATCTT AATTATGTTA TATTAAGATA TCATGTGTAT GCTTAAATTA TACTTTTGGG CTTCAAATGA GTGACCCCAC TCAGACTCGA G	69 129 180 240 283
(2) INFORMATION FOR SEQ ID NO:511:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 250 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:	
GAATTCGGCC TTCATGGCCT AATTCCCTTG ACTCAAGACA GCTAACTTCA TTTTCAGAAC TGTTTTAAAC CTTTGTGTGC TGGTTTATAA AATAATGTGT GTAATCCTTG TTGCTTTCCT GATACCAGAC TGTTTCCCGT GGTTGGTTAG AATAATATTTT GTTTTGATGT TTATATTGGC ATGTTTAGAT GTCAGGTTTA GTCTTCTGAA GATGAAGTTC AGCCATTTTG TATCAAACAG CACGCTCGAG	60 120 180 240 250
(2) INFORMATION FOR SEQ ID NO:512:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:	
GAATTCGGCC TTCATGGCCT AATTGATTCT AATCTTTCCC AAACAGTGCT GTGGCAATGT ATGAAAGTAA TAAAAATAAT CCTTTTTCTG TTAAAAAAAA AATTGCTGTT ACTTGCTGTT TTGTTATGCT TTTGCTGGAG ATTTTCCCAC CCATCTTAAA GCAGCAACTT CAGGATGGGG GAATCAAGCA AAACCATGGT GAAGAGATTC ATTTAAAGAG GACAAGTCTC GAG	60 120 180 233
(2) INFORMATION FOR SEQ ID NO:513:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 358 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GAATTCGGCC	TTCATGGCCT	AGTCACCTTT	TGTGGGAACT	TCTCTCAGCG	AAGCGGAGCA	60
					AAAGAGCTCC	120
CTATGCCCAG	GGCTTGCAAT	GCTAAGAGAA	GGAGGCAGGA	GAGAGACAGG	GAGCGACACT	180
ACATTTGGTG						240
GGTGATGGCT						300
CCCATCTGTG	GACCACAGCA	GTGCCTCTCA	ACAAACATGT	GCCCCAAGGA	GTCTCGAG	358

- (2) INFORMATION FOR SEQ ID NO:514:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GAATTCGGCC	TTCATGGCCT	AGAATAGAGG	AAAATAGCCG	CCTGGTGGCT	AGACAATTTA	60
GGTGTAGAAA	ACACATTTAT	ATGGTTCTTT	GAATGTAACA	GTGGTAAAGA	ATATAGGTTT	120
AGTTGTTGCT	GCTAAGTAGG	GGGAAATGAC	ATTTTTATCT	GGTATGTTTG	AGAATAAAGT	180
AAATTTCAAA	ATTTGAGATG	ATCGAAGTTT	TTATTTATAA	ACTTAAGTAT	TATTATAATA	240
TGTTACATAT	TTTATTCTTT	AAAAATTGTA	ATTCAGAGAG	TGTAACAAAA	TGTACTTCCT	300
CACTTTCTTG	CTTTTTGTTT	CCCAGAAGTA	ACTCGAG			337

- (2) INFORMATION FOR SEQ ID NO:515:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GAAAAGATGG	AAGAAAACCA	CCATAGCACT	GCAGAAGAAC	TACAGGCTAC	TCTACAAGAA	60
TTATCAGACC	AGCAACAAAT	GGTACAGGAA	TTGACAGCTG	AAAATGAGAA	GCTGGTGGAT	120
GAAAAGACGA	TTTTAGAGAC	ATCCTTTCAT	CAGCATCGAG	AGAGGGCAGA	GCAGCTAAGT	180
CAAGAAAATG	AGAAGCTGAT	GAATCTTTTA	CAAGAGCGAG	TAAAGAATGA	AGAGCCCACC	240
ACTCAGGAAG	GAAAAATTAT	TGAACTGGAG	CAGAAGTGCA	CAGGTATTCT	TGAACAGGGC	300
CGCTTTGAAA	GAGAGAAGCT	ACTCAACATT	CAGCAGCAGT	TGACCTGTAG	CTTGCGGAGA	360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:516:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GCGAGTGAGC	CGGGGTAGCA	TCACCTCACT	CCAGCCTAGG	TGATGACAGA	GTTAGATTTT	60
GTCTCAAAAA	AGAAAAAGAA	AACAATTCCA	GGATTATTAT	TTCTACGTAA	ATGTGACATA	120
TTATTTCTAT	GATATTATTT	CTTTGATCTC	GTAGCCACAC	TGTTCCCAAT	AATGATTATG	180
AGAAAAAGTA	CCCTCTGTTT	GAAGGCAATC	ATGGGGAAAA	TATAATTCAC	AAAGTATTTT	240
AAAATTAAAA	TCCTGTGTAT	TTCAAAAGAC	GATGGTCCTA	TTTTAAGAAA	AATAACCTTG	300
CAATTCATTT	GCTTTTTCAT	TGGCTCGAG				329

- (2) INFORMATION FOR SEQ ID NO:517:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GAATTCGGCC	TTCATGGCCT	AGTCCTTTCA	AGTACACAGA	GAAATTTTGC	TTGAATTTCT	60
GGAGGAAGAG	TCCAGGGTTC	GGGAAAAGGG	ACTGGGTGGT	ATCTATCTGG	GGCCCCAGAC	120
AGCGGCACTI	CTTTCTTCTG	TGCTGGAATT	CGGCGAACAA	TCATATCATC	TTTTTCCAAA	180
TCCGGAAGTA	CAAGTTCACC	TTCTCTACAC	TGTAAAATTA	TATCTCGCTC	TACAGAATCA	240
TCTTGCTCAG	AGAACTTTCT	AAAGTCTTCA	AAAGCTCGGA	GAACATATGG	ATTTGCATGG	300
AAAGCCCCAG	TCTTTCTGAC	AAAGAAATCA	TCATTCTCTA	AGTCAGGATC	CAGGGCTGCC	360
ATCTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:518:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GAATTCGGCC	TTCATGGCCT	ACGCTGAGAT	CAAGATTCGG	AGTTTGGGCT	GCCTAATAGC	60
TGCAATGATA	CTGTTGTCCT	CACTCACCGT	GCACCCCATC	TTGAGGCTTA	TCATCACCAT	120
		TCTTCATCTT				180
ACCCTTCATC	CTGTGGCCCA	TTTCTGACCT	CTTCAACGAC	CTGATTGCTT	GTGCGTTCCT	240
TGTGGGAGCC	GTGGTCTTTG	CTGTGAGAAG	TCGGCGATCC	ATGAATCTCC	ACTACTTACT	300
TGCTGTGATC	CTTATTGGTG	CGGCTGGAGT	TTTTGCTTTT	ATCGATGTGT	GTCTTCAAAG	360
AAACCACTTC.	AGAGGCAAGA	AGGCCAAAAA	GCTCGAG			397

- (2) INFORMATION FOR SEQ ID NO:519:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 640 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GAATTCGGCC	TTCATGCCTA	CTTTGGTAAC	AGAAGAGAAG	ACTGTGGAGC	CAGCTACCGT	60
CTCAGAAGAA	GCAAAGCCTG	CATCTGAACC	TGCTCCTGCC	CCTGTGGAAC	AGCTGGAACA	120
AGTAGACCTG	CCCCCAGGAG	CAGACCCCGA	TAAAGAAGCT	GCCATGATGC	CTGCGGGTGT	180
TGAGGAAGGT	TCATCAGGTG	ACCAGCCGCC	TTATCTGGAT	GCCAAGCCTC	CAACTCCCGG	240
GGCCTCGTTT	TCCCAGGCAG	AGAGCAACGT	AGATCCAGAG	CCTGACAGTA	CCCAGCCACT	300
TTCAAAACCA	GCTCAGAAGT	CTGAGGAAGC	CAATGAGCCA	AAGGCCGAAA	AGCCAGACGC	360
CACTGCAGAT	GCTGAGCCTG	ATGCAAACCA	GAAAGCCGAA	GCTGCTCCTG	AGTCTCAGCC	420
CCCAGCTTCT	GAAGATTTAG	AGGTTGATCC	TCCAGTTGCT	GCAAAGGATA	AAAAGCCAAA	480
CAAAAGCAAG	CGTTCAAAGA	CCCCTGTTCA	GGCAGCTGCA	GTGAGTATCG	TGGAGAAGCC	540
CGTCACAAGG	AAGAGTGAGA	GGATAGACCG	GGAAAAACTC	AAGCGGTCCA	ATTCTCCTCG	600
GGGAGAAGCA	CAGAAGCCTT	TGGAATTAAA	GACACTCGAG			640

- (2) INFORMATION FOR SEQ ID NO:520:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 469 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GAATTCGGCC	TTCATGGCCT	AGCAAGAGAA	AGAGAAGTGC	AAACACTCCC	ACGGCGAAGC	60
GCCCTCCGTG	GACGCGGATC	CCAAGTTACC	CAGTAGCAAG	GAGAAGCCCA	CTCACTGCTC	120
CGAGTGCGGC	AAAGCTTTCA	GAACCTACCA	CCAGCTGGTC	TTGCACTCCA	GGGTCCACAA	180
GAAGGACCGG	AGGGCCGGCG	CGGAGTCGCC	CACCATGTCT	GTGGACGGGA	GGCAGCCGGG	240
GACGTGTTCT	CCTGACCTCG	CCGCCCCTCT	GGATGAAAAT	GGAGCCGTGG	ATCGAGGGGA	300
AGGTGGTTCT	GAAGACGGAT	CTGAGGATGG	GCTTCCCGAA	GGAATCCATC	TGGATAAAAA	360
TGATGATGGA	GGAAAAATAA	AACATCTTAC	ATCTTCAAGA	GAGTGTAGTT	ATTGTGGAAA	420
GTTTTTCCGT	TCAAATTATT	ACCTCAATAT	TCATCTCAGA	ACGCTCGAG		469

- (2) INFORMATION FOR SEQ ID NO:521:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GAATTCGGCC TTCATGGCCT	ACCCGTTTCC	TCTAGTTTCT	TCCTGTAGTA	CTCCTCTTTT	60
AGATCCTAAG TCTCTTACAA	AAGCTTTGAA	TACTGTGAAA	ATGTTTTACA	TTCCATTTCA	120
TTTGTGTTGT TTTTTTAACT	GCATTTTACC	AGATGTTTTG	ATGTTATCGC	TTATGTTAAT	180
AGTAATTCCC GCGGCCTTCA	TG				202

- (2) INFORMATION FOR SEQ ID NO:522:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GAATTCGGCC	TTCATGGCCT	AAATTTAATG	AAGCAAAATT	CCATACATCA	TTTTGAAAAT	60
AGTGTTTCTT	TCCCTGATAG	GCCTGTTCTG	CATCATTCTT	TTAGCTTCCT	TCTGCCCTGT	120
TTATCACTTG	GTCCCACTTT	TATATTTTTC	CTCTTCGGTC	CAGAATTTCT	TATTTAGTTT	180
CTTGTATTTT	GCCTACTCCC	TCCCTTCTCC	ATGATTCAGC	CTAGTCTTTC	CGTCCTCTGT	240
GGACTTGGGT	GTGCCTTCCT	CTGGGCCACC	TCGTCTTTTG	CTGCTGTTAG	CCCTCCCGCC	300
TGCGCACCTG	CCACTTCACC	CTCGCCTGTG	GTCCACTTAC	GTTCCACTCA	GCCCGGTCAG	360
TCCTGCTTTG	TTCTTCTCCA	CCGCCTTGGT	CTCCCGTGTG	TCTTATCTAG	CTCTGGTTCC	420
TTCTCGTCTC	CACATTTATT	TTGTTTTCTT	CCTGTGCTTG	TTAGTCCTTG	TGCACTTGGC	480
CCTTTTCTCG	AG					492

(2) INFORMATION FOR SEQ ID NO:523:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

GAATTCGGCC	TTCATGCCTA	GGAAATTTCA	CCATTTGGTC	TCCCCCTTTG	TGGGTCAGCA	60
GGTGGTCAAG	ACAGGGGGCA	GCAGTAAGAA	GCTACAGCCC	GCCAGCCTGC	AGTCTCTGTG	120
GCTCCAGGAC	ACCCAGGTCC	ATGGAAAGAA	ATTATTCCTT	AGATTTGATC	TAGATGAAGA	180
AATGGGGCCC	CCTGGCAGCA	GCCCAACACC	AGAGCCTCCA	CAAAAAGAAG	TGCAGAAGGA	240
AGGGGCTGCG	GACCCAAAGC	AGGTCGGGGA	GCCCAGCGGG	CAGAAGACCC	TTGATGGATC	300
CTCACGGTCT	GCAGAGCTCG	TCCCCCAGGG	CGAGGATGAT	TCTGAGTATT	TGGAGAGAGA	360
CGCCCCTGCA	GGAGATGCTG	GGAGGTGGCT	CGAG			394

(2) INFORMATION FOR SEQ ID NO:524:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

	CGATTGAATT	CTAGACCTGA	CCAAAGACCT	TCCGTACAGA	TTGACCGCAG	AATGTCAGGG	60
	AAAGTTAGGA.	GAAGAAGTTC	TGAGAAGACT	GACTACAGAT	TGGCTGGCCT	GGCTGACCCA	120
	GGAACTTCTG	AGCAGACTGA	CCTCAGATTG	TATGGCCTCG	TTGACCACAA	AACATCTGTA	180
,	AAGACTCACC	ACCAAGTGTA	CGGCCAAGCC	ACTGAACTAG	CTGAACACCA	GGCTATTGAC	240
	CAAGCTCATA	GTAATGCTGA	TCAACCTCCA	GTTGACAATG	CTCACTACAC	TGAATCTGAC	300
	CAGACTGACC	ACTTAGCAGA	CAGACAAGCT	AATCATAAAG	ACCAGCTGTC	TTACTATGAA	360
	ACACGTGGCC	AGTCTGAAGA	CAGAATATTT	CCCCAGTTAG	GCAACAGCAA	AGAGGACAAA	420
	GAGGCTGACT	ACAGAGTACA	ACCCTGCAAA	TTTGAGGATA	GCCAAGTAGA	CCTCAATTCC	480
,	AAGCCTTCAG	TTGAAATGGA	AACTCAGAAT	GCAACCACTA	TCCCACCCTA	CAACCCAGTT	540
	GATGCCAGAT	TCACCAGTAA	ATTCCAAGCA	AAAGACCAAG	CTCTTTTCCC	AAGACTCGAG	600

- (2) INFORMATION FOR SEQ ID NO:525:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 466 base pairs

the second of the

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GAATTCGGCC	TTCATGGCCT	ACTTTCTTCT	GCTGGCTTCC	ATCTTGCCAC	ACTTTCTTGC	60
TCTTCCTTCT	AACTGAAAGA	${\tt CTACTTCTCC}$	ATCCCCTCTG	CAGGCTCTTT	TGCTCCACCT	120
GATATTTAAA	TGTTGGAATG	CCTAGAGTTG	TTCTGACCCT	TCTTTATCTA	CCCCGATTTC	180
CTCAGTGATC	TTATGCAGAG	GTCTCCCAAA	${\tt GTTTACATGG}$	CTATCCTTGA	CCTCCTTCCT	240
GAACTGCAGC	TGGTGTCAGC	TGCCGTCACT	TGGATGTTTA	ATCAGCAACT	CAAGGTTTAC	300
GTGATGATTA	GACCGCAGTT	ACCCCCAGAC	TTCCTTATCC	CTTAGTTTTC	CCCATCTCAT	360
TAAGTTCACT	TCCATTCACC	TTCTTGATGA	AGCCAAGTAT	TTCAGAACTA	GCCTTGTTTC	420
TTCTTTTTCA	CTTTCCCCCA	TATCAATTCC	AGACTACCCA	CTCGAG		466

- (2) INFORMATION FOR SEQ ID NO:526:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 559 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GAATTCGGCC	TTCATGGCCT	ACATTGTAGA	AGAGATCACA	GAAACCACAA	AAGGTTTTCT	60
GAAGTATATG	GATAATCAAT	CATTTGCAAC	TGAAAGTCAG	GAAGGAGTTG	GTTTGGGACA	120
TTCACCTTCA	TCCTATGTGA	ATACTAAGGA	AATGCTAACC	ACCAATCCAA	AGACTGAGAA	180
ATTTGAAGCA	GACACAGACC	ACAGGACAAC	TTCTTTTCCT	GGTGCTGAGT	CCACAGCAGG	240
CAGTGAGCCT	${\tt GGAAGCCTCA}$	CCCCTGATAA	GGAGAAGCCT	TCGCAGATGA	CAGCTGATAA	300
CACCCAGGCT	GCTGCCACCA	AGCAACCACT	CGAAACTTCC	GAGTACACCC	TGAGTGTTGA	360
GCCAGAAACT	GATAGTCTGC	TGGGAGCCCC	AGAAGTCACA	GTGAGTGTCA	GCACAGCTGT	420
TCCAGCTGCC	TCTGCCTTAA	GTGATGAGTG	GGATGACACC	AAATTAGAGA	GTGTAAGCCG	480
GATAAGGACC	CCCAAGCTTG	GAGACAATGA	AGAGACTCAG	GTGAGAACGG	AGATGTCTCA	540
GACAGCACAA	GGCCTCGAG					559

- (2) INFORMATION FOR SEQ ID NO:527:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

GAATTCGGCC	TTCATGGCCT	ACGCAGTGGT	TCAATTTTCT	TCGAAACGGT	GTGGTCCCTG	60
CAAAAGGATG	TTTCCTGTTT	TCCATGAGCT	GGCTGAAACT	TGTCACATCA	AAACAATACC	120
CACATTTCAG	ATGTTCAAGA	AAAGCCAGAA	GGTAACCCTA	TTCTCAAGAA	TCAAAAGAAT	180
AATTTGCTGT	TATAGAAGTG	GATTCATGAG	CAACCTGATT	TTTGAGTTTT	GTGGAGCCGA	240
TGCTAAAAAA	TTGGAAGCCA	AGACTCAAGA	ATTAATGTAA	GCTGATCTCC	AAGGCAAAAT	300
ACACTTGTGC	CGCTCGAG					318

- (2) INFORMATION FOR SEQ ID NO:528:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GGCACAGACT	TACCGGACAC	ACAGGTCATG	GGACACAGAG	TCATGGGGCA	CACAGGTTCA	60
CAGGGCACAC	AGGCTCACGG	GACACAGAGT	CATGGGACAC	ACAGGCTCAC	AGGGCACACA	120
GGCTCACAGG	ACACACAGGT	TCATGGGGCA	CAGAGTCATG	GGGCACAGAC	TCACAGACTC	180
ACAGGTCATA	GACGCTCATG	GGGCGCAGGC	TCACAGGGCA	CACAGACTCA	GGGCACACAG	240
GCTCATGGGG	CACAGAGTCA	TGGGGCAGGG	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:529:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GAATTCGGCC	TTCATGGCCT	ATTCTGTTCT	TTAAATTTGA	ATGAAAGTTT	GGCATTTTAA	60
AAAACTTTAG	GTGATTTAGG	AGTATAATTT	TAAGCAGATT	TTTAGAGTAC	GAGTGTCCAC	120
ATATTTAACT	AAACATTCAA	AAATTAGTTA	AAATCAATGA	ACTTGGGAAG	GATCCTCGAG	180

- (2) INFORMATION FOR SEQ ID NO:530:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

GGGGACAGAA	GATGTGCTCC	AGGGTCCCTC	TGCTGCTGCC	GCTGCTCCTG	CTACTGGCCC	60
TGGGGCCTGG	GGTGCAGGGC	TGCCCATCCG	GCTGCCAGTG	CAGCCAGCCA	CAGACAGTCT	120
TCTGCACTGC	CCGCCAGGGG	ACCACGGTGC	CCCGAGACGT	GCCACCCGAC	ACGGTGGGGC	180
TGTACGTCTT	TGAGAACGGC	ATCACCATGC	TCGACGCAGG	CAGCTTTGCC	GGCCTGCCGG	240
GCCTGCAGCT	CCTGGACCTG	TCACAGAACC	AGATCGCCAG	CCTGCCCAGC	GGGGTCTTCC	300
AGCCACTCGC	CAACCTCAGC	AACCTGGACC	TGACGGCCAA	CAGGCTGCAT	GAAATCACCA	360
ACGAGACCCA	GGCCCTTCAG	CACCGTTCAC	AGTATTTTGA	AGGTGTTGTG	AAGTGCAATA	420
AGCTGGAAAT	ACTGGAGACC	ATCGTGGACA	GAATAGTAAG	AGCCCTCGAG		470

- (2) INFORMATION FOR SEQ ID NO:531:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

GAATTCGGCC	TTCATGGCCT	AGAAAATTCC	AGAAAGGATA	TTTAAGAAAA	TACAATAAAC	60
TATTGGAAAG	TACTCCCCTA	ACCTCTTTTC	TGCATCATCT	GTAGATACTA	GCTATCTAGG	120
TGGAGTTGAA	AGAGTTAAGA	ATGTCGATTA	AAATCACTCT	CAGTGCTTCN	TACTATTAAG	180
CAGTAAAAAC	TGTTCTCTAT	TAGACTTTAG	AAATAAATGT	ACCTGATGTA	CCTGATGCTA	240
TGGTCAGGTT	ATACTCCTCC	TCCCCCAGCT	ATCTATATGG	AATTGCTTAC	CAAAGGATAG	300
TGCGATGTTT	CAGGAGGCTG	GAGGAAGGGG	GGTTGCAGTG	GAGAGGGACA	GCCCACTGAG	360
AAGTCAAACA	TTTCAAAGTT	TGGATTGTAT	CAAGTGGCAT	GTGCTGTGAC	CATTTATAAT	420
GTTAGTAGAA	ATTTTACAAT	AGGTGCTTAT	TCTCAAAGCA	GGAATTGGTG	GCAGATTTTA	480
CAAAAGATGT	ATCCTTCCAA	TTTGGAATCT	TCTCTTTGAC	AATTCCTAGA	TAAAAAGATG	540
GCCTTTGCTC	GAG					553

- (2) INFORMATION FOR SEQ ID NO:532:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 843 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GAATTCGGCC	AGAGAGGCCT	ACTTCTCTTA	GTGATTTCAT	GTTTCAACCA	GTACATTGTG	60
GTGAATACTG	AAATATCTTG	TTTAATTCAG	ATAATTAAAA	TGGTGGCAAA	GGAAGCTGTT	120
TAGCCAGAGC	CCTTCTTGAC	TTTGAGGAAC	AGTGGTAGTA	TAAGACTTGA	AGACAGACGT	180
GTAAAAAGTA	CTACTCACTG	GTAGGCTCAG	GTCTGGTTGA	TTGACTGATT	CTTGAGACGG	240
AATGTCGCTC	TGTCGCCTAG	GCAGGAGTGC	AGTGGCCCAG	TCTCGGCTCA	CTGCAGCCTC	300
CGTCTCCGGG	TCCAAGCGAT	TCTCCTGCCT	CAGCCTCCCG	AGTAGCTGGG	ACTACAGGCG	360
CCCGCCACCA	CACCGGGCTA	ATTTTTGTAT	TTTTAGTAGA	GACGGAGTTT	CACAATATTG	420
GTCTCGAACT	CCTGACCTCA	GGTGATCCAC	TCGCCTGGCC	CACCCAAAGT	GCTGGGATTA	480
CAGGGATGAG	CCCCTGCGCC	TGGCCTCGGT	TGAATTTATT	AAACAACTTT	TGTGGGCAGC	540
AAGCTGTACG	AGGTTAACTA	TGTGATGAGA	AGACTTAGAA	ATGGAGAAAA	GTTTTATCAG	600
TTCTACATAG	GACTTAGTTT	GGGAGTTTCT	GGAAACTACG	TTGGAAATCA	GTAGTTGCAC	660
ACTAGCTGAA	TTCAGCTGTG	TAATTTACAG	TGATTTGTTA	TTTACCAAAT	AAGTAGAAGA	720
GGGAATTAAG	AAGCTAAAAT	CTCTGGGTAC	TTGTTTGATA	TGAATTTGTT	AATTGTTTAT	780
ACTCAGGTAA	TAAGTGTTAC	CTCAGTCATA	GCATTTAATA	TTTTATCTGA	CTGTCCTCTC	840
GAG .				•		843

- (2) INFORMATION FOR SEQ ID NO:533:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

SAATTCGGCC AAAGAGGCCT ACATCCAGAA ATTTAGGGAC TCAGCCCTGG TCAGGGTGGC	60
AAGGGTCTG TTTGTCTTTC CCCATTAGAC AGAGGTCTTG TCCTGCTACC CTAATTGTAA	120
AGGGGTGCCT GGGAAGGGGT GGTAGGGACA TGGTGGCGGT GGAGACTCCG GCCCCACTTC	180
CCAGGCTTT GCTGACAGGG GCCTGCTTTT AATTTTTATT TTTATTCCAT GACTTTTTAA	240
AAAGAATCC CGTAACTTCT TTTTCATAAC TTTTTTTGTA ACTTTTCATA ATACTGTTTT	300
TACTTTGTT CCCACAAGTT TTTTTGCCAC AACGTTTTTA CATTTTTTAT CCCATAACTT	360
TTCACCCCA TAACTTTTT AAATAAAGTT ATTTAATAAA ATAACTTTTT ATAAAACTTT	420
ATAAAAGTT TTTTAATTAA CCCATAACTT TTTTATTTTG GTTTTTAATA AACACTTGCA	
	480
AGTTATATT ACAACTTTGT AAAAATGAAA CACATTATCT CAGGC	525
2) INFORMATION FOR SEQ ID NO:534:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 268 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
· · · · · · · · · · · · · · · · · · ·	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:	
HAATTCGGCC AAAGAGGCCT AGAAAACCCT TGAAGACATG TTGAAAAATAC ATACTCCTGT	60
AGCCAAGAA GAAAGATTGA TTTTCTTAGA CTCCATTAAG TCCAAATCCA AAGACTCTGT	120
TGGGAAAAA GAAATAGAAA TACTTATAGA GGAAAATGAG GACCTCAAAC AACAATGTAT	180
CAGCTAAAT GAAGAGATTG AAAAGCAAAG GAACACTTTT TCATTTGCTG AAAAAAACTT	240
GAAGTTAAC TATCAAGAGT TACAAGAG	268
2) INFORMATION FOR SEQ ID NO:535:	
() ADAMMACA CULTURATED CONTROL	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 224 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(12) NOT BOWN D. MINDS DIVI	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:	
GCTTGCACC TCGGCGATCC CCGACTCCCT TCTTTATGGC GTCGCTCCTG TGCTGTGGGC	60
CGAAGCTGGC CGCCTGCGGC ATCGTCCTCA GCGCCTGGGG AGTGATCATG TTGATAATGC	120
CCGGAATATT TTTCAATGTC CATTCCGCTG TGTTGATTGA GGACGTTCCC TTCACGGAGA	180
AGATTTTGA GAATGGCCCC CAGAACATAG ACATTCCTCT CGAG	224
(2) INFORMATION FOR SEO ID NO:536:	
,	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 303 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
15/ 15/ 2000	
(ii) MOLECULE TYPE: cDNA	
/ I) CHONENCE PROGRESSION CHO TO VO TO C	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:	

60

120

GAATTCGGCC TTCATGGCCT ACCACTCTGG CCCCAGCGTC ACTGGCCTAG GGACACATGG

GGGTGGGGAT TGTTTGGCCT TCCTGGCTTA GGTCTCTGGA AGAGAAGA ACCCCATGGG

PCT/US98/06956 WO 98/45437

GCAGACCCAG GCCACGGGCA GTACATGCCT CCCACACTAC TGACACCGCC AGTGTCTTCT	180
GTGAAGCCAC CTTTGAGCAA CGGAAAGGAA GGGGGATGGG CAAGATCAGT GCAAGGTTGG	240
CCAAAAGCCT GGGGCTGGCC TTCTGCTGGC ATGAGAGGGC CAGGCCGCCC CCAGCTCCTC	300
GAG	303
(2) INFORMATION FOR SEQ ID NO:537:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 350 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:	
GAATTCGGCC TTCATGGCCT AGAACAAAAT CTGAAATTCA GAAATAAACA ACAGTTGGAA	60
AATATTTTCC ATTTTTTCC CTATTAAATA TGATAATTTC AGGTGCAAAG AGTGTTTTTT	120
TTTTTTTTT TTTCTCCACA GTGCTTTTCA CGGTGGGGAC TAATGGATAT AGAGGGTGGG	180
AGGCCAGAAT AACCAAGTAC CTGGAAGTGA ATCTTTGTGG AGATAATGAA ATAATTTTAT	240
TCGAAAGGTG CAAAAGGAAG TCTTCCATCA CTAGCTCAGC TGTTATGGTC CTTGAACTGC	300
CCTTGCCCGT CTGTCTTTTT ATTAATCCTT TTTACCTGTC GAGTCTCGAG	350
	330
(2) INFORMATION FOR SEQ ID NO:538:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 344 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) TOPOLOGI: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:	
GAATTCGGCC TTCATGGCCT AGAGTTGCAC AGATGTCTTT TGTTAGCTTT GGTGGCGGAG	60
TCATCCTCAC AGACCGTTAC TCAGATAATT AAGTGCCTTG CAAATTTAGT ATCAAATGCA	120
CCTTATGATC GTCTAAAACT CAGCCTGCTG ACCAAAGTCT GGAACCAGAT AAAGCCTTAT	180
ATTCGCCACA AAGATGTTAA TGTTCGTGTG TCAAGTCTCA CACTCTTGGG AGCTATAGTG	240
TCCACCCACG CACCTTTACC TGAAGTCCAA CTACTTCTGC AACAGCCATG TTCTTCTGGA	300
CTCGGTAATA GCAATTCAGC AACCCCTCAC CTCAGCCCCT CGAG	344
(2) INFORMATION FOR SEQ ID NO:539:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 343 base pairs	
(E) DEPOTAL SES NODO POTED	

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

ra.	TCGGCC	TTCATGGCCT	ACAACTCCAT	TAAACCACCA	CCAGCTCCCC	AAGCCACCCC	60
rc <i>i</i>	AGCCATG	AAGTTCCTGC	TCCTGGTCTT	GGCAGCCCTC	GGATTCCTGA	CCCAGGTGAT	120
CF	AGCCAGT	GCAGGTGGGT	CAAAATGTGT	GAGTAACACC	CCAGGATACT	GCAGGACATG	180
rge	CACTGG	GGGGAGACAG	CATTGTTCAT	GTGCAACGCT	TCCAGAAAAT	GCTGCATCAG	240

CTACTCCTTC CTGCCGAAGC CTGACCTACC ACAGCTCATC GGTAACCACT GGCAATCAAG

300

GAGAAGAAAC ACACAAAGGA AAGACAAGAA GCAACCCCTC GAG	343
(2) INFORMATION FOR SEQ ID NO:540:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 248 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:	
GCGATTGAAT TCTGAAGACC TCTCAGCCTC TTATGACCAC TCCTGGCACC CTGTCAAGCA CAGCATCTCT GGTCACTGGC CCTATAGCCG TACAGACTAC ACCTGGAAAA CAGCTCTCGC TGACCCATCC TGAAATACTA GTTCCTCAAA TCTCAACAGA AGGTGGCATC AGCACAGAAA GGAACCGAGT GATTGTGGAT GCTACCACTG GATTGATCCC TTTGACCAGT GTACCCACAA ATCTCGAG	60 120 180 240 248
(2) INFORMATION FOR SEQ ID NO:541:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 433 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:	
GAATTGGCCT TCATGGCCTA GATTGTCTTT ATAGGAAATG TCTTTAGCAA AATACTACGG GTTCTATAAA ACCCATTAAC GGGTTATCAG TGTCTAGGAC ATAAATGGCT TCTGGTAAGA AAATTAAGGT CTACTCTCC TAAAAATCAA CATAAATACA AAGGTTAAGA AAAAAGAAGT AGAGTAAAAC ATGTGTCCCT TAAAAAATCAA ACATGAGTGG TCACAAGGTC CTAAGAAGCA GAGAATGAGA ACTCCAGTTG CTTGTTTATC TCTCAGGCTG AGCATGGTTG GTTACAATGA GGGGTAGCAG GAAGAGCACA GCCTTGGACT CCAGTCCAAG GAACTCCAGT CTCTCCTGCA ATTTCCCAGT GTTTGACCTT GGGCCACTTA CTGTTCCTTT CTCAGGCTCC ATTTTCATAT CTAAAACCTC GAG	. 60 120 180 240 300 360 420 433
(2) INFORMATION FOR SEQ ID NO:542:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 493 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:	
GAATTCGGCC TTCATGGCCT AGACACGGGA CATAAAAACT TTTAATGAAG GAGGACACAG CTCAGAGCCC TTCCACATGC GGCCCAACCC TGCCCCACGG AGACCGGCCA TGGCAACCGC TCAATCAGAA GGTGTTCTTG ATGCGGCCGG CCACCAGCCT AAGGATGTCC CCGATCTTCT TCTGCCAGTT GGCGATGTCC TTGGACACGG CGCACCACAG CTCCCCATGC CGAGGCTCTG	60 120 180 240
CACTCTCACA GCGCTTCCTC ACCTCCTCCT GCTGCTCCTC AGTGCCATGC TGCAGCTCAA	300

ACTTGTAGAA GAAGGCCCAG GCATCCCCCA GGTCCGAGTC AATCTTCACA GTGCGGTGGA ACCACTCCCT GGCCTTGGTG ATCTTCCGCT GACTCCAAAA CAGCTTGGCC ACGGCCAGGA GCACATGGGG GTCATGCTCA CACTTCTTCA GGGCATCCAC GCTCTTGGTC CTCCTCTGGG GCCTTGCCTC GAG	360 420 480 493
(2) INFORMATION FOR SEQ ID NO:543:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:	
GAATTCGGCC TTCATGGCCT AGTCAGGGAG AAGGGAAGGT GAGAAGGGGG GGAAAAAAGA AGCAAAAAGC CCAAAGAAAA AAACATTTA TATTCATCTG TATAAACATA TCCGCTAAGG CAAACGCAAT CCGGGTCCGA GGCTGCGC CTGGGCTCGG TGCCTCCTAA TTTCTGCAGA TTCTAAGGCC AAAAAATAAA ACCTCTGCAA GTCCGCGTAG CTTCCAGGAC TCCTGGGCAT TTTACTAAAA TAAAGAGTTA TCGAGTTTAA AAAGCAGTGA CGTCGTTATG ACACACACTG AAAGTTGCAT AACTGTGGCC TCGAG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:544:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 473 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:	
GAATTCGGCC AAAGAGGCCT AAGAATTCCT TATGAAAGTG ATGCTTGAGT CAAAATATGA TGGATGAAGA GAGTTTAAAT AGATTACATA GAATTTTTAA TAATGTCGAT TGGTTATATA CTGGGCACTG ATAGCTGATT TTCTTTGGG GAAAGGTATG TCAGCCTAGT CATTCAGATT CCTTTATTTT TTTAAATGTT TTTCATTTT TTGCTTTGCA TTGCATTCAT TTGCTGAAGA GCTGGCTTGT ACTTGGCAG GTGTCATACT TGGTTATTCT CCTTAGGATA TTGGCCCAAC AATCTGGGAT TTGTGAAAGG CGCTTCGCTT TTCAGACCTG GGCGTCTGTA TCATGACTAT CATAAATTTA GGATTAAGAC ACCTAGCCTC CTACCAGGAT GAATGAGGTG TCCATGTGAC CTGCTGTGCC CTGGAATTTT ATACATCTTT CTCTCATAGC ACACGGACTC GAG	60 120 180 240 300 360 420 473
(2) INFORMATION FOR SEQ ID NO:545:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:	
GAATTCGGCC AAAGAGGCCT AGTCGAGAAG GAAGAGGGAA GAAGAAAAAC TATAAAAGTG TGCTAAATGT TTTATTTTCT CTGGAAGAAT AGTTATATTC TACTCTTTGT GGCTCTCGAG	60 120

- (2) INFORMATION FOR SEQ ID NO:546:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GCTAGACCTG C	CCCCTTAGA	AATGGAAAAA	GCATGCAAGA	GAGATGTTAA	AGGAGACTAT	60
TGGAGCAACT G	TGTCCACAC	CCTCTGTGAT	AGAAATGGAA	AAAATATCCC	CAGAAGATCG	120
TGGTGAGAAT A	TTGGGAAAC	ACAAAGTGTT	ACCCGCAGTG	GTAGACATTG	AGAAAATACA	180
TGGAACAGGA C'	TAGAATTGA	CCACTAAACA	AGGGGAGGCC	ATGCTTCCTG	CATTTGAAAG	240
TAAAACACCA C	AAGAGTATG	CTGAAGGGAG	TGTTGAAGAA	ACAATGGAAA	ATACTTACCA	300
AAAGGATGCT G	AAGGGGATA	TTGGAAAGGC	TGAAGTGATG	CCTGTGAGGT	TAGAAATGGA	360
AAATACTTAC C	CAAAGGATA	CTGAAAGAGA	CGGTGGCAAA	ACTGAGGTGA	TGCCCCTTGC	420
ATTAGAGGTA G	TAAATACTT	ACCAAAAAAA	TGCCAAAGGT	TTTACCGGGA	ACAATCTCGA	480
G						481

- (2) INFORMATION FOR SEQ ID NO:547:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

GAATTCGGCC	AAAGAGGCCT	AGAAACCTGA	GGCTGCTGCC	CTTTATCTGC	CTTCACGGTA	60
CTGTCCCCTT	CCCCCAGCTC	CTCCCTGACC	CCATGGGCCA	GGCCTCAGAC	CTTCCAGCTA	120
ACCGCTTCCC	ATGAGCCACT	ACTCTGATGT	CAGCCTATAA	CCAAAGGAGC	TGGGGGGTCC	180
AGGCCTGGTG	ACCAACCTTT	CTCAGCCCAC	TCAATCAGGG	TGCTCCCCAC	CTGCAGGCAG	240
GAGGCAACAC	CCTATCTGCT	ACCATCAGCC	CCTTCCAGAG	CCCATCTGCC	CCGCCCAGCC	300
CTGCCCTGCC	CAGCCATACC	CTGCTCTGCC	CCATCTGGGG	GTGCCCTGCT	CAGGGATGGG	360
CTGGCAGGGC	TGTACCCAGC	CTCCCTGGTA	AGCAAAGAGC	TCGAG		405

- (2) INFORMATION FOR SEQ ID NO:548:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GCGATTGAAT	TCTAGACCTG	CCTCCCTGCT	TTCTAATAAA	TCTGACTAAC	CTTAGACATT	60
TTGTATCTTA	CTAAGAACAT	CCCTTCAATA	TCTACTTCAT	TATCCCATGC	CATTTCCCCA	120
CTGTCTCAAC	ACGAATCTCG	AG				142

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:	
GAATTCGGCC TTCATGGCCT ACTATGGTAT TGCTAAACAA GGGTGGGAGG AGAGAGAGGT AATCAGGGAG GACTTCCCAC AGGAGGTGGC ATCTGCAGAT GTCTCAAAAA AGAAAAGAAT TAGCCTGGCA AGAGGTGAGG ATTGTGTAGA GGTCACTCAC TTTCCTTGTG GGTGGAGGAA ACCATTCCAG GAGCTGTAGG AAGCTTGGTG CTGGTGAAGG AGGCAGGAGA GGAGAGAAGA GGAGATGACC TTAGAAATCA CATCCAAGAG CCTCTGATCC CAGGAGGCAG CTCGAG	60 120 180 240 296
(2) INFORMATION FOR SEQ ID NO:550:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:	
GCAGGAGAGA AAATTGAGGC TTAGGTTAAG AAACTTACCC AAAGTCAAAC AATTTAATTG GTTTGGGAAG ACCAGGAAGA CTTTAAGTTC CTAAGATCGT TTGAGATTCT GCATCAGGGA ACACTTGACA GCAGGTTTAT ACAAAGACAG ATTTGGTATC TTTGGAGGGA ATGAGTTTCC AGTCATTGCA GGTGGTCCAG CAGAGAGGGC CACTCTCCTT TTTTTCTTTC TTTACTCCCT TTTTGATTCT CGAG	60 120 180 240 254
(2) INFORMATION FOR SEQ ID NO:551:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 278 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:	
AGGCCATGAA GGCCCTTTCC ATTTCTTTT GTTCCATCAC TCTTCTCTCA ACCTGTGTTT CTTTTTTTAC TGAGGAGTTA GTCCCCATTA GTTCTTGTAT CACATTTCA TTTGCACGAC ATTACTCGCA GGTGGTGGG AGCCTGGGCT TTTGGGGAAC CAGGCTGCTC TGGTCCCAG CATTGCCTCC TCCTAGCCCC TCTAGTCCAG TTTGCCTCCC TTACCCTCAT TTTCCAAACC TCTTGTACCC TCCTCTCCCT CCCCCAGCTG GCCTCGAG	60 120 180 240 278
(2) INFORMATION FOR SEQ ID NO:552:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 322 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
273	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

GAATTCGGCC	TTCATGGCCT	ATGCACTTCT	TCTTTCTCTC	CTCCTTTTGC	TGGGTGCTTA	60
CCGAGGCCTG	GCAGTCCTAC	CTGGCTGTCA	TTGGGCGGAT	GCGCACCCGC	CTCGTTCGCA	120
AGCGCTTCCT	CTGCCTGGGC	TGGGGTCTGC	CTGCCCTGGT	GGTGGCCGTG	TCTGTTGGCT	180
TTACCCGAAC	GAAAGGATAC	GGTACATCCA	GCTACTGCTG	GCTCTCCCTG	GAGGGCGGCC	240
TGCTCTACGC	CTTTGTGGGC	CCTGCAGCCG	TCATTGTCCT	GGTGAACATG	CTCATCGGAA	300
TCATCGTCTT	CAGCAGCTCG	AG				322

- (2) INFORMATION FOR SEQ ID NO:553:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: GDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

GCCAAAATCA	AGCAAAGTAT	GAAGAAAGAT	AAAGAAGGGG	AAGAAAAAGG	GAAGCGAAGA	60
GGATTCCCCA	GCATCCTGGG	ACCCCCACGG	AGACCAANCC	GTCATGACAA	CAGTGCAATT	120
GGCAGAGCCA	TGGAACTACA	GAAGGCGCGC	CACCCTAAGC	ACTTATCCAC	ACCCTCATCT	180
GTGAGTCCTG	AACCTCAGGA	CTCTGCCAAG	TTGCGCCAGA	GTGGGTTAGC	AAATGAAGGA	240
ACAGACGCTG	GATACCTGCC	TGCCAATTCC	ATGTCTTCTG	TAGCTTCAGG	GGCCTCTTTT	300
TCCCAGGAAG	GAGGGAAAGA	GAATGATACA	GGATCAAANC	AAGTTGGAGA	AACATCAGCA	360
CCTGGAGACA	CCTTAGATGT	CACCCTCGAG				390

- (2) INFORMATION FOR SEQ ID NO:554:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

GACGGCTACA	CCATGGGCCG	GCTGCTGCGG	GCCGCCCGGC	TGCCGCCGCT	GCTTTCGCCG	60
CTGCTGCTTC	TGCTGGTTGG	GGGAGCGTTC	CTGGGTGCCT	GTGTGGCTGG	GTCTGATGAG	120
CCTGGCCCAG	AGGGCCTCAC	CTCCACCTCC	CTGCTAGACC	TCCTGCTGCC	CACTGGCTTG	180
GAGCCACTGG	ACTCAGAGGA	GCCTAGTGAG	ACCATGGGCC	TGGGAGCTGG	GCTGGGAGCC	240
CCTGGCTCAG	GCTTCCCCAG	CGAAGAGAAT	GAAGAGTCTC	GGATTCTGCA	GCCACCACCA	300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:555:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

the second second second

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

GAATTCGGCC	TTCATGGCCT	ACCCTCTCAC	GCCACCCCCG	CCCCCACCGG	GCTGCAGGTG	60
CTGCTGATGC	GCTGGGATCT	GATTGAGGAT	AAAAAGGAAG	GAGAGATGAC	CCCTACCCCC	120
TCATCCCCCA	${\tt GTTTTGAAAA}$	GGTCTAAGCA	AGTGAGTCTG	GTGGAGGAGC	TGAGGGAGGG	180
AGCCATGGAA	GGTGCCAGAA	GGAAGGTTGG	CGGGGGCACG	TGTGGGCCGT	GGCTTGGGCT	240
GGTCAGAGTG	GCGTGAGCTG	CCCGGCGCCT	GCCCTGCCCA	AGTGACCAGG	GAAGTGTGTG	300
TGTGTCCATG	TGTATGCGTG	GCTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:556:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GAATTCGGCC	TTCATGGCCT	AGAGAAGGAG	CCAGCTGGGG	CCGAATCCAT	CCGCTTGAAC	60
ACCAAAGAAG	ACAAAAATGG	TGTCCCCGAC	TTAGTGGCCC	TGCTGGCTGT	GAGAGACACC	120
CCGGACGAGG	AGCCGGTGGA	CAGCGACACT	TCGGAGAGCG	ACTCGCAGGA	AAGTGGGGAC	180
CAAGAAACAG	AGGAGTTGGA	TAATCCTGAG	TTCGTGGCCA	TTGTGGCCTA	TACCGACCCG	240
TCGGACCCCT	GGGCCCGGAA	GGAGAACTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:557:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GAATTCGGCC	TTCATGGCCT	ATTTCCGATC	TATGTATCTG	TACTCATACA	GCCTCATCGG	60
GCTAAACAGC	CTTCTTTTCA	GAACAGTAGA	TCACTCAACT	GGGTTTTCAA	GTGACTGTTT	120
ACCTTTCAAG	GCTGGCTTTA	TAGGTCTTGC	CTCACTGTAT	CCAGCAATCC	AAACTTTACC	180
CTATCCCAGT	CAGGACTGCA	CACCTCATAT	TGAAAGACAT	ACCTTAGAAC	CAGACTCCCC	240
AAACCTTACA	AATATCCCAC	CCTTGACTCC	CGTTCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:558:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GCAATGGTCT CCAGGATGGT CTCTACCATG CTATCTGGCC TACTGTTTTG GCTGGCATCT

GGATGGACTC	CAGCATTTGC	TTACAGCCCC	CGGACCCCTG	ACCGGGTCTC	AGAAGCAGAT	120
ATCCAGAGGC	TGCTTCATGG	TGTTATGGAG	CAATTGGGCA	TTGCCAGGCC	CCGAGTGGAA	180
TATCCAGCTC	ACCAGGCCAT	GAATCTTGTG	GGCCCCCAGA	GCATTGAAGG	TGGAGCTCAT	240
GAAGGACTTC	AGCATTTGGG	TCCTTTTGGC	AACATCCCCA	ACATCGTGGC	AGAGTTGACT	300
GGAGACAACA	TTCCTAAGGA	CTTTAGTGAG	GATCAGGGGT	ACCCAGACCC	TCCAAATCCC	360
TGTCCTGTTG	GAAAAACAGC	AGATGATGGA	TGTCTAGAAA	ACACCCCTGA	CACTGCAGAG	420
TTCAGTCGAG	AGTTCCAGTT	GCACCAGCAT	CTCTTTGATC	CGGAAACACT	CGAG	474

- (2) INFORMATION FOR SEQ ID NO:559:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GAATTCGGCC	TTCATGGCCT	AATTTTTTTG	TTGTTGTTTC	CTTTTTGTAT	TTTACTGATA	60
TCACCAGGAT	AGTTTACTCT	CCTTCTAGCT	TTCTGCTTAC	CGCACACTGG	ATAACACACA	120
CATACACACC	CACAAAAATG	CTCATGAACC	CAATCCGGAG	AAGGTTCCAG	CAGGTCCCCC	180
ACCCTCCCCT	CCTCCTCCTA	CTTCTCCTCT	TGACAGCGAG	GACAGGAGGG	GGACAAGGGG	240
ACACCTGGGC	AGACCCGCCG	GCTCTCCCCC	CACCCCACCC	CGTCCTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:560:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GTGTATGTGG	GGGGTAAGTG	TGTGTGTGTG	CGTGTGCGTG	TATGTGCACG	TGTTGTGTGT	60
GTGCGCCTGC	ACACGGAGAG	CCCACTCATA	CGTAGCAGAA	AATCAAATGG	CCCCAAATCA	120
GAAACATGGC	GCATGTGAGC	ATGCCACTTC	TTGTGTGCCT	GTGACTGTTC	AGAATGTACA	180
CGGCCCTGCA	GCTCCCGAAG	GCCAGCTCTG	CTGCAACCCC	TCCTCTGTCC	AACACAGTCC	240
TCACTGGTGT	CTTTTCCTCT	TCAAATCTAC	AGCATTTCTG	ATCTCTGCAA	ACAATTTAAC	300
CCAAAACCAA	GTTCTGGCTG	ACAAGGCTAC	ATCTTGTTTC	TTGTGCGTGA	TTAGCCTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:561:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

the survey of the state of the

GGCCCGAGGC	CGGGCTGCCT	GGTTTTATTT	TTATTTAACT	TTATTTTCTG	TTTTATGAGT	120
GTGTGTCCGC	CCACCCCCAC	CCCCTTCAGT	GTTAAGTGGG	GAGCCCTGGG	GGAGTCTCTC	180
CTGCCTCCCA	GCCTCTCCCA	AGACCTCCCC	CCTCGTCACC	AGCCATCCCT	CTGGACCAGG	240
CAGAGGGCGG	ACCGGGTGGG	CAGGGGCCTG	AGGGTGGCTC	GGGCCAGCCC	ACCAGCCAAT	300
GGACCCCTCC	TCAGGCCGCC	AGTGTCGCCC	TGCCCCTTTT	TAAAACAAAA	TGCCCTCGTT	360
TGTAAACCCT	TAACGCTCGA	G				381

- (2) INFORMATION FOR SEQ ID NO:562:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GCACTCATAA	AAATCTTACT	CAGAAATCTT	CAGAGGTTTG	CTAAGGATAC	AATTTGATTC	60
TTACACATTT	AATGCTCACC	AGCTGCTTAG	GCCCACACCA	TTTATCCACC	CTGATTTGCT	120
ACTGCTCTTT	GAAATACAAC	CAGTGTTTCA	GCCAGACTGT	TTTCCTGCTT	CTGCTCCCCT	180
TCTCCTCCTC	CCAGCACATC	TGTGAATTCT	TTGACTGGTT	TACCACTCCC	ACACTCCTCC	240
CCAGCAATGC	AGATCTTCTA	CACCCTTTAG	GATCTAAGCT	AAGTCTGCTT	CCCAGATATC	300
CTCCCGAACA	GCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:563:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GAATTCGGGC	TTCATGGCCT	ACTTTAATGA	GATAGGAACT	AGTATATTCA	CCGTCTATGA	60
GGCCGCCTCA	CAGGAAGGCT	GGGTGTTCCT	CATGTACAGA	GCAATTGACA	GCTTTCCCCG	120
TTGGCGTTCC	TACTTCTATT	TCATCACTCT	CATTTTCTTC	CTCGCCTGGC	TTGTGAAGAA	180
CGTGTTTATT	GCTGTTATCA	TTGAAACATT	TGCAGAAATC	AGAGTACAGT	TTCAACAAAT	240
GTGGGGATCG	AGAAGCAGCA	CTACCTCAAC	AGCCACCACC	CAGATGTTTC	ATGAAGATGC	300
TGCTGGAGGT	TGGCAGCTGG	TAGCTGTGGA	TGTCAACAAG	CCCCAGGGAC	GCGCCCCAGC	360
CTGCCTCCAG	AAAATGATGC	GGTCATCCGT	TTTCCACATG	TTCATCCTGA	GCATGGTGAC	420
CGTGGACGTG	ATCGTGGCGG	CTAGCAACTA	CTACAAAGAA	GAAAACCTCG	AG	472

- (2) INFORMATION FOR SEQ ID NO:564:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

en de la companya de la co

TCATGCCGG TACAAAGAGT TCCGCGAACA TCGCTGTGGC AGTCAGCTCA	TCCCCCTTCG GGCCCTGTGG TTGGTCTGGG CGCTTCTAGG AGTGGCCGGA AGCCGTGCGC CTGCGTGGAC AAGTACGCTC ACCAGTTCGC GGACTGCGCT TGCGTGAGGT GCCGGAAGGA CTGCCTGCCA ACGTGACGAC GCTTAGTCTG AGATCACTGT GCTGCGCGC GGGGCCTTCG CCGACGTCAC ACAGGTCACG TGGCGCACAA TGAGGTGCGC ACCGTGGAGC CAGGCGCACT GGCCGTGCTG AGAACCTCGA TCTGAGCCAC AACTTCATAT CCAGCTTCC GTGGAGCGAC TGAGCGCGCT GCAGCTGCTC AAAATGAACC ACCACCTCGA G	60 120 180 240 300 360 411
(2) INFORMA	TION FOR SEQ ID NO:565:	
(i) :	SEQUENCE CHARACTERISTICS: (A) LENGTH: 270 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:565:	
ATTAATTAAG GTATTCATTA GCAACATTTA	CCTCAGACTT TCAAAGAGCC AGGAAATCGG TATAAAATTT TTGAGATAAC CTTTTTGCAG TTTTTCCTAG GACCAGATTA AACAGAAGTT TTCCTTTACA TGGTTGGTAT CTCCAGAGTT CATCCTTTTT TTGTGGTACT GGGAAAAGTT CCTTTGCAGG GACATGGATG GAGCTGGAGG CCATTATCTT TAGCAAACTA AAAGACAAAA ACCACTCGAG	60 120 180 240 270
(2) INFORMA	ATION FOR SEQ ID NO:566:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 272 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:566:	
CCATGTCACT TGGAAATTAC TTATACTGGG	ACTAACGGCT CATCTTTCC TTGTTTTGT TTTTTTTTT TTCTTTTTTT AAAGGCCAAA ACTGGAACCA AGGATTTAAT AACTATTATG ATCAAGGATA AATAGTGCCT ATGGTGGTGA TCAAAACTAT AGTGGCTATG GCGGATATGA TATAACTATG GGAACTATGG ATATGGACAG GGATATGCAG ACTACAGTGG ACTTATGGCA AGGCATCTCG AG	60 120 180 240 272
(2) INFORMA	ATION FOR SEQ ID NO:567:	
(i).	SEQUENCE CHARACTERISTICS: (A) LENGTH: 306 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:567:	
AGAAGAGGTA	GAATTCGAAA TATTGGCATA TGGTTCTTTT GGATTAGATT ATATAAAATC GAACCAGGCC CCAAGCACTC CTTTTTCTCT GCATGATACT TCTGCTTATT CTAGCTACAT GATTTATAGT CTTGCTCCCC AATATGTTAT GTATGGAAGC	60 120 180

CAAAATTACT TAATAGAGAC TAATATAACT TCTGATAATC ATAAAGGCAA TTCAACCCTT

TCTGTGCCAA AGAGATGTGA TGCAGAAGCT CCTGAAGATC AGTGTACTGT TACCCGGACG

240

300

CTCGAG		306
(2) INFORMA	TION FOR SEQ ID NO:568:	
(i) 5	SEQUENCE CHARACTERISTICS: (A) LENGTH: 253 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:568:	
AATGGGTGGC AGCAACTGCA	CACAGTTCGG GACCTATGGT AGAAAAATAC TCAGTAGCTA CCCAGATTGT GTTACTGGCT GGTGTGCAGG ATTTCTGTTC CAGAAAGTTG GAAAACTTGC GTAGGTGGTG GCTTTCTTCT TCTTCAGATT GCTAGTCATA GTGGCTATGT TGGAAGAGAG TTGAAAAAAGA TGTAAATAAA GCAAAAAGAC AGATTAAGAA GAG	60 120 180 240 253
(2) INFORMA	TION FOR SEQ ID NO:569:	
(i) :	SEQUENCE CHARACTERISTICS: (A) LENGTH: 544 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: eDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:569:	
CGCTTGGTGC GGACGGCGGT GGAAGTCGGA AAAACCCTTC TCGCCATAAA GCTTACACAC ATCCACCTGC	GCTCACAACA AGATGCTCAA GGTGTCAGCC GTACTGTGT TGTGTGCAGC AGTCAGTCTC TCGCAGCTGC CGCGGCGGTG GCTGCAGCCG GGGGGCGGTC NATTTTCTGG ATGATAAACA ATGCCTCACC ACAATCTCTC AGTATGACAA CAGTGGAACA AATTCCGAGA CGATGATTAT TTCCGCACTT GGAGTCCAGG GATCAGGCT TAGAATCAGC TAAGGATCCA TGCTTAAAGA TGAAATGTAG GTATGCATTG CTCAAGATTC TCAGACTGCA GTCTGCATTA GTCACCGGAG AGGATGAAAG AAGCAGGAGT AGACCATAGG CAGTGGAGGG GTCCCATATT AAGCAGTGCC CAGTGGTCTA TCCCAGCCCT GTTTGTGGTT CAGATGGTCA TTCCAGTGCA AACTAGAATA TCAGGCATGT GTCTTAAGGA AACAGAATCT	60 120 180 240 300 360 420 480 540
(2) INFORMA	TION FOR SEQ ID NO:570:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 330 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:570:	
	TCATGGCCTA CATTAAAGAA AAGCTTCCCA CACATCCATT TGAAGCTGAT TGGCAGAAAT GATTGCAGAA GATGAAGAGA AGAAGACTCT ATCTCAGGGA	60 120

GGAAGTACAT GAAGAGCTGA	CTTCTGAACA CGAACTCTTT CTAGACACCA AGATATTTGA AAAAGACCAA ACAGTGGTGA TCTTGAATCA GAGGCAGTAT CTACTCCACA TAGCTGGGAG ATCACTATGC CTTAAAGTCA AATGCTGTGC AAGAGGCTGA TTCAGAATTG CAAAAGGGGA AACCCTCGAG	180 240 300 330
(2) INFORM	ATION FOR SEQ ID NO:571:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 312 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:571:	
TCTTTAAAAA AAACAAAATG TGCGTTAAAA	TTCATGGCCT AAGGGAAAAC ATTTTGCATG TGTAAAGCTT CATGAAGTTC ATACCAAAGC TTGTTTATTT CTGATAATTA ACCTAAGCCC TTATGAAAAT AAGGGATTAT GACAGGTATT ACCAAAAACA CCAAAAGGAA CAAAGGGGCC CCTAATTGCT AATGCTTCAC AACTAGGAGA GCATGCCGTC TTGATGTTTA GGTCTCCACC CTTCCTTTGA TTTGTGCAAT TCTGTCTTCC ACAGTTCCGG AG	60 120 180 240 300 312
(2) INFORM	ATION FOR SEQ ID NO:572:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 391 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:572:	
CTGGGGTCAA GCTCTTCTCC CACGGTGACA CCTGTACACG CCAGGTACTG	ATGGCCGCAG CAGGAGTAGA GGTCCTGAGC CTCCTATTTT TCTGCATCTA TATGCCACCG ATGGCATTGG CAACGAGAGT GTGAAGATCT TGGCCAAGCT TCCAGCTTCC TCATCTTCCT GCTGATGCTT ATCCTCCTGG GGAAGGGATT CGGGGCCGCA TCAGCCACGC GGGCTCCGTG AAGTTGTCT TCTACATCAC CTCACCCATG TGGTGCTGCT CATCTACGAG GCGGAATTCT TTGACCCAGG TACACGTATG AGTCGCCGGC CGGCTACGGG CTCATTGGAC TGCAGGTGGC TGGTTCTGCT ATGCTCTCGA G	60 120 180 240 300 360 391
(2) INFORMA	ATION FOR SEQ ID NO:573:	
(i) _.	SEQUENCE CHARACTERISTICS: (A) LENGTH: 377 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:573:	
TTTGTTAATT	TCATGGCCTA AAAAAAACTC CAGAAAAAAA CAACAGCGCG GTGGTGGGGT TCGCCTTTTT TTTTTTTTGC ACGCGCCACG AAATTCAGGC TGCGTTTAGC TATCCAAAGT AATTGCAGAT TGCGGAGACG CACAGCATTA GTTCAAAAAA	60 120 180

GACCCGAGGC ATTGGGGCAG GGTTAGGTGG AGGGCACCGG AGGCTCTACA CAAGAAAAGC AGGAACCTGC AAACCCACGT AGATTTCCAC TACAACCTTC CCTTTTCTTC TGGCTAGCCA TCCAGGCGCTC TCCATGGCAC TGCATGGCAC AAGTTGCTTC TGATAGTCTT TTAAGTTTGC TAAGGGAACT CCTCGAG	240 300 360 377						
(2) INFORMATION FOR SEQ ID NO:574:							
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear							
(ii) MOLECULE TYPE: cDNA							
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:							
AACCGCAGAA GCCTCCCCAG CTCACCCCTG GAGGACGGCC GGCTCTCTAT AGCACCAGGG CTCACGTGGG AACCCCCCTC CCACCCTCGC GAGTCTGTTT CCAAGGAGGA GAAGGAGCAG AACTATGACT TAACTGAAGT CTCAGAGAGC ATGAAAGCTT TCATATCCAA AGTCTCAACC	60 120 180 240 300 325						
(2) INFORMATION FOR SEQ ID NO:575:							
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 438 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear							
(ii) MOLECULE TYPE: cDNA							
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:							
GAATTCGGCC TTCATGGCCT ACTCAGCCTC CCTAATAGCT GGGATTACAA GCGTGAGCCA CCACACCCCG CTGGGAAATA TCTTAAAAGA ATCAAAATAA GAAAGTTACT CTACTTAAAT CGTGTGCTTT TTCTGTGTGT GATTTATGGT AATCTTACCA TGGGGTATCT GATTACTTTA GAAAGATCCA TTTAGCTTAT TTTTTCTTC TTTGGGTTAT TTTTTTCTTC CTTCCATTTG CACAGCCTCC CCCCAAATAA AAAATAAAGA TATAAAGTCT ATCTTCTCC TCTTGTCAGT TTAAGTAAAA AGAACTTTTG CTTCCATTTT AATAATAGAA TTTGTGTGTA TATAATATAG GCAGTGATTT GGCCTCAAGC TGAGTTTAGA TTTGAAAAGA TGAGAATATT AAAGCTTGTC AGCCAGCCCCA CTCTCGAG	60 120 180 240 300 360 420 438						
(2) INFORMATION FOR SEQ ID NO:576:							
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 510 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear							
(ii) MOLECULE TYPE: cDNA							
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:							

6**0**

120

GAATTCGGCC TTCATGGCCT ACTGTNTTCC ATAAAGGCTG TACTAATTTC CATTCTCACC

AACAGTTCAC TAGGGTTCCC TTTTCTCCAC ATTGTTGCCA ACATTCTTTA TCTTGTGTTT

NTTAATAACA	GCTATCCTAA	CAGGTATGAG	GTGATCTCTC	TCATTGCGGT	TTTGATTTGC	180
ATTTCCCTAA	CGGTTGGTGA	TACTGAGCAT	TTTTGCATAC	ACCGGGTCAT	TTGTTCTTTG	240
TTGTTGACTT	GAGTCCCTTA	TATAGTTTGG	ATACTGCTGT	GGCCTGAATG	TTTGTGTCCC	300
CCAAAAATTC	GTATATTGAA	CTCTCATCCC	TAAGGTCAAC	AGTTTAGGGA	AGCGATTAGG	360
TCCTGAGGAC	TCTGCCCTCT	TGCATAGAAT	TAGTGCTCTT	ATAAAAGATG	CCĆGAGGGAG	420
CTCTTTTGCC	CCTCCTGCCA	TGTGAGGACA	CAGCTAGAAG	CTACCATCTG	TGAACCAGGA	480
AGCCCCCCTC	ACCAGACACT	GTATCTCGAG				510

- (2) INFORMATION FOR SEQ ID NO:577:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GAATTCGGCC	TTCATGGCCT	AAAAAATAAA	AATAAAATAT	ACAACCAAAG	GCAGTATTCA	60
CAGAGGTATT	TCTTGGGAAT	AAAAGAAGGA	ATATAGTCAT	TCCTTGGTAT	TCTCTTTGGT	120
GTCCAGAGTT	ACTTAAAAAT	TCTTGGTGTT	TATTGCCTTT	TAGTCACAGG	GATACACCTT	180
TTATTCATTT	ATTTATTTAT	TTACCAGTCT	CATTTAGCAG	TAGGAATGCA	TCTTAGCATT	240
TTTATACTGC	TGCTCAACAC	AGTGCTTTCA	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:578:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

GAATTCGGCC	TTCATGGCCT	AAATCCTTCC	AGATGTCCTG	TGAAAATGTT	TGAATGCTAC	60
TTGTCTAAAA	GTCCACAGAA	TCTTAATCAG	AGGATGGATG	TTTTTTTTTT	GCAACCAGAA	120
TGCTCTAGTT	CTACAGATAG	CCCTGTCTGG	TATACGTCTA	CTTCACTGGA	CCGAAACACC	180
TTGGAAAATA	TGCTTGTACG	GGTTCTTCTA	GTAAAAGATA	TTTATGATAA	AGACAATTAT	240
GAACTGGAGG	AAGACACTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:579:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 439 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GAATTCGGCC	TTCATGGCCT	AATTTAGGAC	CATTTAAGAG	AGTTTGACTA	AGAAAGAGCT	60
GTTTGAAACC	TCCTGGCTTA	TGTATTTTTA	GGGGTGTGGT	GATCGAGGCT	TTCTCCTCTG	120
AGTAGAGTTT	GTGCATTTGC	AGTATAAGAT	TATCATTATC	AAACATTCCT	ACTAGGCCTT	180

TCTCCTCAGC	CCCTAAAAAA	ATATGTATAG	TAATGAAGTA	GGAAGATCAT	GTTTATATTT	240
GACTTCACAA	ATTCCTCAGG	CTAAGTTGCT	TTCTACTGGG	GTGTGGCTGG	AGACAAAAAT	300
TACAGGTAAG	ACTTGACTTA	ATTTTTGATA	GGGAGGTTCT	TAAGAGGCTT	TTTCGGAATC	360
ACTCACCTCG	CCCACTTCCA	TGCAGGGATG	TGGTGAGAGC	CCTTCAGTCT	ACTTAGGAAA	420
ACCTGGCACA	TGACTCGAG					439

- (2) INFORMATION FOR SEQ ID NO:580:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GAATTCGGCC	TTCATGGCCT	AGATATTCTC	AGGGTCATCA	AGACTCCTGA	GATAGCAAAC	60
TTGGCCTTGC	TTGGCTTTGG	AGATATCTTT	GCCCTGCTGT	TTGACAACCG	CTACCTGTAC	120
ATCATGGACT	TGCGGACAGA	GAGCCTGATT	AGTCGCTGGC	CTCTGCCAGA	GTACAGGAAA	180
TCAAAGAGAG	GCTCAAGCTT	CCTGGCAGGC	GAAGCATCCT	GGCTGAATGG	ACTGGATGGG	240
CACAATGACA	CGGGCTTGGT	CTTTGCCACC	AGCATGCCTG	ACCACAGTAT	TCACCTGGTG	300
TTGTGGAAGG	AGCACGGCTG	ACACCATGAG	CCACCAGCCG	CTCGAG		346

- (2) INFORMATION FOR SEQ ID NO:581:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 740 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GAATTCGGCC TTCATGGCCT	AGACCTGCCT	CGAGATTGCC	ATCTTGGTTT	TGGTGGGTTT	60
CGGCCGACTT CTTTGCCACT	TGCTATTTTA	TTTTCTAGGT	CTTTGTGCCC	CGTATTGTGT	120
GCTGAACTCC NGTCTCATCC	TGTGACTAAG	ATTGCCTAAC	CTCCTGGGAA	TGCAGCCCAG	180
TAGATCTCAG CCTTACTTTA	CCTAACCCCT	TTTCAAGATG	GAGTCACTCT	GGTTCAAACA	240
CCTCTGACAT TCGCAGTGGA	ATCCATTAAA	AGATGTTAAG	GAGATATGAT	TATATTTCTA	300
AATTGTCACT CCAGCATCCC	CTACGCCAGA	CATTATGCCA	GTCTCTATCC	ATACAGTATC	360
TCATTTAATC CTCCCGTCAT	TAATCTCATT	TTACCAATGA	GTAAACTTGA	AGCAAATGAG	420
TGACTTTCTC AAGGCTACCT	ACTTACGCCT	TACCAGGGCC	AGGATTCAAA	CCTAGACTTG	480
TTCAGCGACA GAACACACAC	TTAACCATCA	CCCACTTAGG	CCATGAAGGC	CGGCCTTCAT	540
GGCCTAAACT. GCTGTTATTT	TGGATTATAT	GGAGTTATGA	AAATCTAAAT	GTTTTACAAA	600
GTTAAAAAGT ATTCTTTTTT	TGCTCACTTA	TAACTCAAAA	ATCACTAAAG	TCATTCTGCT	660
AAACATGCCA CGAAGCCAAG	CTTCTTGCCA	TATGTCTGCA	TAATTTTATT	AAATCACTGC	720
TATTGACGTG CAACCTCGAG					740

- (2) INFORMATION FOR SEQ ID NO:582:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GAATTCGGCT	TTCATGGCCT	ACAAAGGGGT	AGCAAGGCAT	GTCTTACATG	GTGGCAGCAG	60
AGAGAGAGAG	CAGGGAAAAC	TGTCATTTAT	AAAACCATCA	GATCAGTTGG	GTTGTGCAAA	120
TGGTGGAGAA	GAAAACTTCA	GGAAGAGTGC	ATAGACTGAG	CAGAGAAGAG	GACCAGCTAC	180
CTCCGTAGAG	GCAGGGAGAG	CAGCCAAGCT	${\tt GGAGCCTGAG}$	CAGCATTGCT	GGACATGGAG	240
AAGGTCTGGA	ATCTTGTCAA	GGAAGCAAGC	AAAGGGTTTC	TTTCTATTCA	ATGAAGTCCA	300
CTCCCAGGAC	CCTGGGCAGC	AACGGGTGCT	GGACTGGGCC	ACCTGGCAGC	GTCACATCAA	360
CTGGCAGCTA	GAAGTCCTGG	AGAATGACAA	CTTCCAGGAC	GACCCCCATG	TGGGACTCCC	420
TCAGCTCAGC	AAGAGACTGC	CACAGTTCGA	TGATGATGCA	GACACCAGAC	AGTAAAAGAA	480
GAAAACTCGA	G					491

(2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 566 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GAATTCGGCC	AAAGAGGCCT	AAACAGTCCA	GAGAGGCATA	AATCAGACCC	AGTTCCTAGC	60
TGGCTTGTCC	TTATCAAGTA	AATGGAAAAG	GGGCCAGGCC	AAAGCAGGGC	AAGATGACCT	120
TGGACTTGGG	AGAGACTTGG	ACTCATGCCA	CAATCCTAGG	GTGCCCACTG	GACCATTGCT	180
TTTCTGAGTT	TTGTAGTCAT	TCGGTGTCTG	AAGTAAGGTA	GATTGAAGTG	AGGCCTTCGG	240
TTTCCATCTG	GACCCTTTCT	CTCCTGTTTT	CTTTTTTTCC	GCCTTGTCCT	AGGGATGTTC	300
AATAGCCCAG	AAATGCAAGC	CCTCCTCCAG	CAGATCTCTG	AGAACCCCCA	GCTGATGCAG	360
AATGTGATCT	CAGCACCCTA	CATGCGCAGC	ATGATGCAGA	CGCTTGCCCA	GAACCCCGAC	420
TTTGCTGCTC	AGATGATGGT	GAATGTGCCG	CTCTTCGCGG	GGAACCCCCA	ACTGCAGGAG	480
CAGATCCGCC	TGCAGCTCCC	AGTCTTCCTG	CAGCAGATGC	AGAACCCAGA	GTCACTCTCC	540
ATCCTTACCA	ATCCCCATAC	CTCGAG				566

(2) INFORMATION FOR SEQ ID NO:584:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GAATTCGGCC	TTCATGGCCT	AGTTGAAAAT	GATCATTACA	CAATATATTC	CTAAACATAA	60
ACTGAGTAAA	CTTGAAACAG	CTCACTGTGT	GGAGAGGACC	ATTCCCGTTT	TGCTCACCAG	120
AACTGGAGAT	TCTTCTGCCC	GCCTCCGCGT	CACAGCTGCA	AATTTTATTC	AGGAAATGGC	180
CTTGTTTAAA	GAAGTTAAGT	CTCTCCAAAT	TATTCCATCC	TACCTGGTGC	AGCCATTGAA	240
AGCAAACTCT	TCAGTTCACC	TGGCAATGAG	TCAGATGGGC	CTCCTGGCCC	GGCTGCTGAA	300
AGACCTGGGC	ACTGGCAGCT	CGGGCTTCAC	CATTGACAAC	GTGATGAAGT	TTTCAGTGAG	360
TGCCCTGGAG	CATAGAGTGT	ATGAGGTCCG	CGAGACGGCG	GTTCGAATTA	TTTTGGACAT	420
GTACAGACAG	CACCAGGCTT	CCATCCTGGA	GTACCTTCCT	CCAGACGACA	GCTAATCTCG	480
AG						482

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:	
CAAATTGTAG GTAGCCTGTT TTTTAAAACA TTTATTCAAC AAATATTTAG TCCAAGCCAC TATTACTTAC TACCTTCTCT ACTATTGTAT GGACTTTTAA CTATCTCTGA CACTATTCAC TATTCTTCCA CATTCTCTAT TATTTATACC TATGGTAAAA TTTGCCAGTT TGACCATACA	60 120 180 240 265
(2) INFORMATION FOR SEQ ID NO:586:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:	
	60 120
(2) Information for phy in no.307.	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 503 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:	
AAGACAATTT AAGAGAAGAA CTAAAGAAAA GAACAGAAAC TGAGAAGCAG CATATGAACA CAATTAAACA GTTAGAATCA AGAATAGAAG AACTTAATAA AGAAGTTAAA GCTTCCAGAG ATCAACTAAT AGCTCAAGAC GTTACAGCTA AAAATGCAGT TCAGCAGTTA CACAAAGAGA TGGCCCAACG GATGGAACAG GCCAACAAGA AATGTGAAGA GGCACGCCAA GAAAAAGAAG CAATGGTAAT GAAATATGTA AGAGGTGAGA AGGAATCTTT AGATCTTCGA AAGGAAAAAG	60 120 180 240 300 360 420 480 503

- (2) INFORMATION FOR SEQ ID NO:588:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 567 base pairs
 (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GCCACTATGG	TACCAAAACC	TCAGTCTTCA	CATAGTCAAA	CTTGGACACA	AACAGCACCT	60
CCCACAAACA	TTCTTATCCT	CATCCCAGCA	TTGGTTACTG	ACCACACACT	CTAGCAGGTC	120
ACTCAAGCGC	TAATGCTGGG	AAGGACCTCT	GAATACTTCT	CTTTGTCTTG	TGCCACACAG	180
CCAGGGTCAC	CAAAGCCTGT	TAATGCTACC	TCCAAAAAAG	GCAAATCTGA	CCCCTCTTCC	240
TCAAAACCCA	GCCACATAGT	AAGTTCAAGG	ATTCAGTCAC	AGGTCTGCCT	TAGTGCACTA	300
		TCACTTCCCC				360
		ACTTTTCTAA				420
		TAATTCCTTC				480
GTTTGGTCTA	GTGTCCTTTT	AAAGACACTA	GATTTCTCAT	CACCATACCG	CATGTACCCT	540
ATACGACTTA	TCAATTCCCT	ACTCGAG				567

- (2) INFORMATION FOR SEQ ID NO:589:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAATTCGGCC	AAAGAGGCCT	AGGCATGGTG	AGTTTTGATC	TTCTTCCCCT	TCTTTTCTTC	60
CCCTTCTTCT	TTCCTTCTTT	GATCTTCTTC	CCCTTCTTTT	CTTCCCCTTC	CCCTTCTTTT	120
CAATTTCTCC	CACGTCAA					138

- (2) INFORMATION FOR SEQ ID NO:590:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAATTCGGCC	AAAGAGGCCT	AGAGAGAATG	GAAAAGATAA	GGAACAGAAA	CAAACAAATA	60
CCGATAAAGA	AAAAAATAAA	AGAGAAAGGG	AGCTTCTCTG	ACACAGGCTT	GGGTGATGGA	120
AAAATGAAAT	CTGATTCTTT	TGCTCCCAAA	ACTGATTCTG	AGAAGCCTTT	TCGGGGCAGT	180
CAGTCTCCCA	AAAGGTATAA	GCTCCGAGAT	GACTTTGAGA	AGAAGATGGC	TGACTTCCAC	240
AAGGAGGAGA	TGGATGATCA	AGATAAGGAC	AAAGCTAAGG	GAAGAAAGGA	ATCTGAGTTT	300
GATGATGAAC	CCAAATTTAT	GTCTAAAGTC	ATAGGTGCAA	ACAAAAACCA	GGAGGAGGAG	360
AAGTCAGGCA	AATGGGAGGG	CCTGGTATAT	GCACCTCCAG	GAAAGGAAAA	ACCGAGGCAG	420

- (2) INFORMATION FOR SEQ ID NO:591:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 611 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

			TCAAATAACT			60
CATGTGGCTA	CTTTAGTAAT	ATTGCCAAGA	AGAGCACAGT	TTTTACACTA	GTGGCATCTC	120
AGTGAAATTA	ACCAAAGATG	AAGCTTTGGC	TTTGCTGGTG	AGATCAGAGC	CCTCCTGAGC	180
			CTGCACAGGC			240
GGGCTGAGAC	GCCATGGGGC	CGCTGCTGCT	TATGTGGTTG	GATTGTTTAC	AAGCCTCATT	300
			CTGCCTTTCC			360
			CTTTTTAAGC			
						420
			CCTCATGATG			480
GATGTGAGGT	GGGGACTTCA	TTCATTGTCC	TATTTCTATC	TNCACTTTGT	GCCTGGAGAG	540
CTTTCAGGGG	AGGTGGAGGA	GGAGGGTCTG	CCAAGCTACT	GCAACATCTG	TCACCCACTA	600
NACCCAGACC						611
						011

- (2) INFORMATION FOR SEQ ID NO:592:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

GAATTCGGCC	AAAGAGGCCT	AATTGAATTC	TAGACCTGCC	TGAAACCTGT	CCCTCCTAGG	60
AAATTGAATA	GCTTGAGTTA	CGAAGGAACT	GCATGGGACA	GACTGAGTTT	TGTTCCTCTC	120
TTCCCTGGAA	GCTGGATGTC	CTTTACAGCT	TTGCCCAGTA	TGTCATGTGG	CCCCTGAAGT	180
ACATAATCCA	GAGTGGACTG	CCTTTCAGGG	TCCCTCAGCT	GTGAAAGTGG	AGCATTCATA	240
TCAAGACTAC	ATCTTTCCTG	TTCAGCTTTC	TTCAGCCTTG	GAGGAACCAC	ACACAATGGA	300
TCCAAGACTT	CTGTCCCTTG	CTAATTATCT	ATAAGAAGTA	AACCCATTTC	ACATAACTTG	360
TGAATATGTT	TTCTTTCACT	GGATTTTGGC	AAATAGGTAC	CCAGTGCATG	GTGGACCTAC	420
ACAGTTAGGC	CTCTTTGGCC	GAA				443

- (2) INFORMATION FOR SEQ ID NO:593:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

GAATTCGGCC	AAAGAGGCCT	AAAAGCATTC	AGTATTGGTA	AAATGAGTAC	AGCTAANCGA	60
ACTTTAAGTN	AAAAGGAGCA	GGAAGAATTA	AAGAAAAAGG	AGGATGAAAA	GGCAGCTGCT	120
GAGATTTATG	${\bf AGGAGTTTCT}$	TGCTGCTTTT	GAAGGAAGTG	ATGGTAATAA	AGTGAAAACA	180
TTTGTGCGAG	GGGGTGTTGT	TAATGCAGCT	AAAGAAGAAC	ATGAAACAGA	TGAAAAAAGA	240
GGTAAAATCT	ATAAGCCATC	TTCAAGATTT	GCAGATCAAA	AAAATCCTCC	AAATCAGTCT	300
TCCAATGAAA	GACCACCATC	TCTTCTTGTG	ATAGAAACCA	AAAAACCTCC	ACTTAAAAAA	360
GGAGAGAAAG	AAAAGAAAAA	AAGCAATTTG	GAACTCTTCA	AAGAAGAATT	AAAGCAAATT	420
CAAGAGGAAC	GTCGACTCGA	G				441

- (2) INFORMATION FOR SEQ ID NO:594:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 562 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

		AAGAAAACCT				60
		GTGAATCATC				120
TCGAGATCGT	GAGATAAACA	GCCTCCGGCG	CCAGCTTGAT	GCAGCTCACA	AAGAACTCGA	180
		AAATCGCTTT				240
GGCTACAATG	GCAAGAGAAA	ATCAAGAAAT	CTCATTGGAA	TTGGAAGCAG	CAGTGCAAGA	300
AAAAGAAGAA	ATGAAGAGCA	GAGTTCATAA	ATACATAACA	GAGGTGTCAC	GATGGGAGAG	360
		AAGAAAATCA				420
TAACCGTGCT	GAAGACTGGG	AGGTCAAAGC	CCATCAAGCT	GAGGGAGAAA	GCAGCTCAGT	480
TCGACTGGAA	CTTCTTTCTA	TTGACACTGA	GAGGAGACAT	CTTCGGGAAA	GAGTGGAGCT	540
	GAAAATCTCG				0.101001001	562
		-				202

- (2) INFORMATION FOR SEQ ID NO:595:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

GGAAGAGCAG	AATTTGGTGG	CTTATCCTCA	TGATGGAAAA	ATCTTTTTCT	GCACCTCACA	60
AGATATCCCT	CCTGAAAATG	AACTGCTTTT	TTATTATAGC	CGAGATTATG	CTCAACAGAT	120
TGGTGTTCCT	GAACACCCAG	ATGTGCATCT	CTGTAACTGT	GGCAAGGAGT	GCAATTCTTA	180
CACAGAGTTC	AAAGCCCATC	TGACCAGCCA	CATCCATAAC	CATCTTCCTA	CCCAGGGACA	240
		GTCACAGCAA				300
		CCAAACTTCA				360
GCCCCACAAG	TGTGATTTCT	GTAGCAAGGC	TTTTAGTGAT	CCCAGCAACC	TGCGAACCCA	420
CTCGAG						426

- (2) INFORMATION FOR SEQ ID NO:596:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

GAAAAATCAG TCGACTGAA	T GACACCATCA	AATCTTTGAA	ACAACAGAAG	AAACAAGTGG	60
AACATCAGCT GGAAGAAGA	A AAGAAAGCAA	ACAATGAGAA	ACAGAAAGCT	GAAAGGGAGC	120
TAGAGGGTCA AATCCAGAG	A TTGAACACAG	AGAAAAAGAA	ACTAAATACG	GACCTGTATC	180

ACATGAAACA	TTCTCTCAGA	TACTTTGAAG	AAGAGTCCAA	GGATCTGGCC	GGCCGCCTGC	240
AACGTTCATC	${\tt GCAGCGTATA}$	GGAGAGTTAG	AGTGGTCTCT	CTGTGCTGTC	GCCGCCACAC	300
AGAAGAAGAA	GCCGGATGGG	TTCTCGAG				328

- (2) INFORMATION FOR SEQ ID NO:597:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 529 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

GAGAAGTGCG	AGAGGGGCCA	GTGTTGTTGT	TACCTGAAAG	GTAAGTGCAG	CCCACAAAAA	60
TGCAGTGAAG	AAGAAGATAT	ATGCATATGT	TTAAGTTAAT	ACAATTGAGA	TACATTTAGC	120
AGACAGAATC	AATAGAGTTG	ATGAGTGACT	GACTGGATGT	GTGGGGAGTT	TATATCACTC	180
CCAGGTTTTT	GACTTGGGCC	ACCGGGCACT	CAAGAAGGAA	AAAGAGGATC	CAGGGAGAGG	240
AACTTTTCTG	AGGACTGGGG	TAGGGCTGAA	CAGCTGCATT	CGAGACTGGT	GGAGGGTGGG	300
			ACTGGGTCTG			360
CCAGCATAGA	GATAGAGAGG	CCCCAGTGCT	GCTGAGTAAC	TGTGATTCCC	CAGGTGATGG	420
CATCAGCTGA	GAAGGGAAGG	AAGCCCATGT	GAGGACACTG	AAGAAGGAGT	GAGCAGACAA	480
TAAGAAGCCC	ACAGAAGACA	GAGAAGGAAC	AACTAGAAGG	AGGCTCGAG		529

- (2) INFORMATION FOR SEQ ID NO:598:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

GAAAAAGATG	AAATCTGATG	GATTAGGAGC	ATCTGGACAT	TCGTCAAGTA	CCAATAGAAA	60
TAGTATAAAT	AAAACTCTGA	AGCAAGATGA	TGTAAAGGAA	AAAGATGGTA	CAAAAATAGC	120
ATCTAAGATT	ACAAAAGAAC	TTAAAACTGG	GGGAAAAAAT	GTTTCTGGAA	AGCCCAAAAC	180
TGTAACAAAA	TCCAAAACAG	AAAATGGTGA	TAAGGCACGG	TTGGAAAACA	TGTCACCTAG	240
ACAAGTTGTA	GAAAGATCAG	CAACAGCAGC	AGCAGCAGCA	ACTGGACAGA	AGAATTTACT	300
AAATGGAAAA	GGAGTGAGAA	ATCAGGAAGG	GCAAATTTCA	GGTGCCAGAC	CCAAGGTACT	360
CACAGGAAAC	TTAAATGTGC	AAGCCAAAGC	AAAGCCTTTG	AAGAAAGCTA	CAGGGAAGGA	420
TTCACCATGC	${\tt CTCAGCATCG}$	CAGAACCCCT	CGAG	•		454

- (2) INFORMATION FOR SEQ ID NO:599:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

GAATTCGGCC	TTCATGGCCT	AGGTCCTCAA	GCATTGCTTC	AATATCAATA	TCGTCTGCCA	60
${\tt TTTTCTCTAA}$	ACGCCTGTTC	CGGCCTTCGG	GCGCCTGTGG	TGCTCGTGTT	CGGGAAGAGA	120
TTGCTGCTGC	TGCTGCTGCT	GCTGCCGCCG	CCGCCGCTTC	TGTTGCTACT	GTTAAGCCCC	180
TAGGCCCAGG	CCGCGGAACC	GCCCAGCCCG	AATATCGGGT	TCCAAGGACG	GCTAGGCCCG	240
AGAGAATCTA	АААААААСАА	TGGAATTAGA	GAAGCCCACG	CGGGAGAGCA	GGACGCCGC	300
TTCGGCAGCT	CAGGATCCAC	CCCNGCGACA	GCGTCGACAA	GTTCCCTGAA	ATGGCGGCCG	360
CTGCTTCCCT	GTACTCANAN	TCCACCCCCC	GAATTCTAGA	CCTGCCTCGA	G	411

- (2) INFORMATION FOR SEQ ID NO:600:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

GAATTCGGCC	TTCATGGCCT	AATTAAGCCT	GCCTACTTCT	ACAATGCATT	CTGTTACCTA	60
TTTGAACAGT	ATGTTTGTAA	CTATGGCAAT	GAAGTCAGTA	GATAGGAAAC	CAGTTATTCC	120
TTCTACCTTT	AAAAATTTTG	AGAACTTGCC	AACCAGGGAC	TAAAGCTATT	ATCTTGAACA	180
GAGTCCCTAA	AGCTAGTCTA	GTTTTTGCCA	CATCTGCAAT	GATTATTGTT	TAATTTCAAA	240
AGAATCCTCA	GGCTCTACAA	TCTAGGGGTG	GTAAATGTGT	TTCCACTATA	CTTGGGACCG	300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:601:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

GAATTCGGCC TTCATGGCCT	AGGAATCTCC	TCTTAAACCA	GGTGAAGTGG	GAAAGCAGGG	60
ACCATACCAC CCTGAGTGAC	ATCTACCTGA	ATAATATCAT	TCCTCGATTT	GTACAAGTCA	120
GCGAGGACTC AGGAAGACTC	TTTAAAAAGA	GTAAAGAAGT	CGGCCAGCAG	CTCCAAGATG	180
ATTTGATGAA GGTCCTGAAC	GAGCTCTACT	CGGTCATGAA	GACATATCAC	ATGTACAATG	240
CCGACAGCAT CAGTGCTCAG	AGCAAACTAA	AGGAGGCGGA	GAAGCAGGAG	GAGAAGCAAA	300
TTGGTAAATC GGTAAAGCAG	GAGGACCGGC	AGACCCCATG	CTCCCCTGAC	TCCACGCCA	360
ACGTTCGCAT TGAGGAGAAA	CATGTCCGGA	GGAGCTCAGT	GAAGAAGATT	GAGAAGATGA	420
AGGAGAAGCA CCAAGCCCTC	GAG				443

- (2) INFORMATION FOR SEQ ID NO:602:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

```
GAATTCGGCT TCATGGCCTA CAACATGTCA GTTTTTTTT TCATTTTCCT CAATATTTTT
                                                                       60
CTTCTNGCTT TCTCTTCTCC TGGTTCCCAG CCTCTACTCA ATAGTCCCCC CAGCTTTGTG
                                                                      120
TGCTGGTCTC GGGGCTTCAT GGAGATGAAT GGGCGGGGG AGTTGGTGGA GTCACTCAAG
AGATTCTGTG CTTCCACGAG GCTTCCCCCC ACTCCTCTGC TGCTATTCCC TGAGGAAGAG
                                                                      240
GCCACCAATG GCCGGGAGGG GCTCCTGCGC TTCAGTTCCT GGCCATTTTC TATCCAAGAT
                                                                      300
GTGGTACAAC CTCTTACCCT GCAAGTTCAG AGACCCCTGG TCTCTGTGAC GGTGTCAGAT
                                                                      360
GCCTCCTGGG TCTCAGAACT GCTGTGGTCA CTTTTCGTCC CTTTCACGGT GTATCAAGTA
                                                                      420
AGGTGGCTTC GTCCTGTTCA TCGCCAACTA GGGGAAGCGA ATGAGGAGTT TGCACTCCGT
                                                                      480
GTACAACAGC TGGTGGCCAA GGAATTGGGC CAGACAGGGA CACGGCTCAC TCCAGCTGAC
                                                                      540
AAAGCAGAGC ACATGAAGCG ACAAAGACAC CCCACACATC TCGAG
                                                                      585
```

- (2) INFORMATION FOR SEQ ID NO:603:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GAATTCGGCC	TTCATGGCCT	AGTCTGGTAG	TAAGGTGGAG	TGGGTTTGGG	GCTAGGTTTA	60
GCTCGGGGGA	GGTGGTGTTG	GGGGCCGCAG	GCTGCGCGGT	GCCTGGGTAC	ATCTCCAGGC	120
CCACGCCCCG	GGCTTGGGAA	GTCACATCCA	TGTCTCTGCG	CCGTGCAGCT	TTCAAGATTT	180
GCCGAAAGGC	TCCCAGAGCT	CTGTTTTAAA	TGGTGAATCC	ATCTTTAGAA	AGAAGCGTGA	240
TTCTCCTTGA	AGTGAGCCTG	GCATTTGTCA	GACAGGAAAC	TCCCCAGGAG	GAGCACCTGT	300
GGTGGTTTGG	GTTGGGTTTG	TTAACTGCAG	AGAGTGGGAA	GAACAGATGC	TCCTCACACC	360
GTCTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:604:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 604 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GAATTCGGCC	TTCATGGCCT	AGGAAAGACC	ATCAGCCTGG	GAGTCAGTGA	ACCTGACTCT	60
		TCAGCTGTGT				120
GCCACAGTTT	ATCTGTCTGT	AAACAGGGGT	ATTGGACTGG	ATTCTCTGTT	ATCTCTCATG	180
TCTCTGTGAA	AGGTCTGTGT	TTTCAAATAC	TCCTTAGGGA	CATGACCTCA	CATAGAAAGA	240
GGGGGTGCCA	CGAACTGGAT	TCCCAGCACT	CCCCCTTCCC	AGCTCTGCTC	AAGCTGAGGG	300
ACCTTGGAAC	ATGGTACTTG	GACCTAAGTA	CTCTCTCTGG	GCTTCAGTGT	CCCCAGCTAT	360
AAAATGGGGG	AAATGCCTAA	CTCAGGAGGT	TGAGGTAAGG	ACAAAAGGAA	TTAATACATG	420
GAAAGTGCCT	GGAACAGTGC	CTGGCACAGT	CTGCTTTCAG	AAAAAGCTGC	AAGGTGGCTA	480
CTCTCAGCAG	ATATAAGTTA	ATGCAGGAAC	AGCAACTAGC	AGCTCTTGGA	CATGCAATAT	540
ATTATATATT	TTTTGCATCT	TTTACCCTTC	ACGGCACTGA	GCCTCACAAT	CCGTTGACCT	600
CGAG				•		604

- (2) INFORMATION FOR SEQ ID NO:605:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GCGCAGCCAG	CGCCTGCCTC	CGACTCGACT	CCACACCTGC	TTGCTACAGC	GGGTGAGGAA	60
GCAGGAAAGG	GGGAGGGAGG	GATGTCGTCT	GGATTCCTGT	AATAATTTGT	TTCATTGTTT	120
CCAATCGACT	TAGTCACCAG	GTTAAATAGT	AGCATAGACC	TTTCAAAAAA	GTAGCTAGCT	180
TATAAGTAGA	TGTATTGAAA	ACACCTGCTT	GTTGAGTCGT	AGACAATTCC	TCATTTACTG	240
TGTGAACTCT	AGGGGGTGAA	ACACGGGCGG	AGAGCGGCTG	TGAGCTCACG	CGGCTCCATC	300
CCCACAGCGG	CCCAGGGTCA	CTCGGGGCCA	TTAATCAGGC	CGCAGAGCTG	CCCTCTGAGC	360
CGGGCCGCCA	GCGCCCACAG	GGCCCAGACC	AGGGCTCCCT	GGGCGGGATG	TTTTAAATCG	420
CACAGGGACA	AAGGAAAGGA	AAGACGCTGG	GGCCCAAGCC	CGAGCTTATG	AAACGTTATC	480
AAGGAGCGAC	TCGAG					495

- (2) INFORMATION FOR SEQ ID NO:606:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GAATTCGCT TCATGCCT	GACTTCCAAG	GACATGCTTC	GAACTCTGGC	CCAAGCCAAG	60
AAGGAATGCT GGGATCGGT	CCTCCAGGAG	AAGTTAGCTT	CAGAGTTCTT	TGTGGATGGA	120
CTTGATTCTG ATGAGAGGT	ACTACAATTG	CAAAGTAGAA	TTTGCTTTGA	CACCTGATGC	180
CAGGACAATA GTATGTTAC	ATCCTTCTAT	AGACATTCCA	TATGAACGCA	CAAAACCTAT	240
CCCTTGACCA GATCCTGTG	T ATAATAATGA	AGAAACACAT	GGTCAAGTGC	TGAAAACTAG	300
AGAAGAAAA AGTGAACAC	TGGAGCTCGA	G			331

- (2) INFORMATION FOR SEQ ID NO:607:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 632 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GAATTCGGCC TTC	CATGGCCT ACTGCCTCG	G CCTCCCGAGT	AGCTGGGACC	ACAGACGCCC	60
ACCACCATGC CCC	GCTAAAT TTTTGTATT	T TTAGTAGAGA	CGGGTTTCAC	CGTGTTAGCC	120
AGGATGGTCT CGT	ITCTCCCG ACCTCGTGA	T CCGCCCGCCT	CGGCCTCCCA	AAGTGCTGGG	180
ATTACAGGCG TGA	AGCCAACT CGCCCGGCC	A GGAATCCCTC	CTCTGTCTGA	CCTAACTGCC	240
CTCTGCCCTG GAG	SCTGCTCA GCCTCTATC	A ATTTTTCTGG	CTCTCAGCGA	ACGTTTTCAT	300
TCAGTTGCAA GAC	CACAGAAA CTCAAATTC	A AACCTGCTTA	CACAAAATAG	TGAATGTACT	360
GGCTCATGCA CTT	TTTTAAAG AGATGAGGT	C TGTTGTGCTG	CCCAGGCTGG	ATGTGAACTC	420
CCGGGCCCAA GAA	AATTCTCC TGCCTCAGT	C TCCTGAGTAG	CTGGGACCAC	AGGAGCATGA	480
CTGTAAGTCC TGC	STGTGAAT CAGGCTCCA	G AAACAGCTTG	ATCCTGGTTC	CCAACAGTAT	540
GGTCAAAACT CAT	TTCTCTCT TCTGTCTTC	T TCTCTATGAC	AGGTGCTCCC	TAAGAAGTGA	600
CAAAGAAGGC CAC	CTAACAGC TCTGGGCTC	G AG			632

- (2) INFORMATION FOR SEQ ID NO:608:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 531 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GTATNGNTGA	AAATAAGAAA	AAATATTTCT	GAAATTCGGG	AACTTGAGAA	CATAGAAGAA	60
CACCAGTCTG	TAGATATTGC	AACTTTGGAA	GATGAAGCTC	AGGAAAATAA	AAGCAAAATG	120
AAAATGGTTG	AGGAACATAT	GGAGCAACAA	AAAGAAAATA	TGGAGCATCT	TAAAAGTCTG	180
AAAATAGAAG	CAGAAAATAA	GTATGATGCA	ATTAAATTCA	AAATTAATCA	ACTATCGGAG	240
CTAGCAGACC	CACTTAAGGA	TGAATTAAAC	CTTGCTGATT	CTGAAGTGGA	TAACCAAAAA	300
CGAGGGAAAC	GACATTATGA	AGAAAAACAA	AAAGAACACT	TGGATACCTT	AAATAAAAAG	360
AAACGAGAAC	TGGATATGAA	AGAGAAAGAA	CTAGAGGAGA	AAATGTCACA	AGCAAGACAA	420
ATCTGCCCAG	AGCGTATAGA	AGTAGAAAAA	TCTGCATCAA	TTTTGGACAA	AGAAATTAAT	480
CGATTAAGGC	AGAAGATACA	GGTAGAACAT	GCTAGTCAAG	GAGACCTCGA	G	531

- (2) INFORMATION FOR SEQ ID NO:609:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GTGACTTTGG	AACCTTGAGA	GTTAGATGAA	TAAATCAGAA	AAATGGAATT	AAATGTATCT	60
ACTTTATTAT	TGGTAAATCT	${\tt GGTTAGGATG}$	TGCAGCCCTA	ATCAGGCTTC	CTTAATTCCT	120
TCTCCACTGA	GTCTGGACCA	GCACTCTCCA	GTAGAACTTT	CTATGATGAC	GGAAATCCTC	180
TGTGTCTGCG	CTGATCAGTG	TGGTAGTTAC	TGGCCACATG	TGGCTGTTGA	GTACTTGAAA	240
TGTGGCCAGT	GTGGTGATGG	AATTGTGTTT	TTAATCTTAT	TTAATTTAAA	TTTAAATAGC	300
CAAATGTGGC	TAGTGGCTGT	TGTACTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:610:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GTGGAGGCTT	TCTTGATCAT	GGATGGTGAA	GATATACCAG	ATTTTTCAAG	TTTAAAGGAG	60
GAAACTGCTT	ATTGGAAGGA	ACTTTCCTTG	AAGTATAAGC	AAAGCTTCCA	GGAAGCTCGG	120
GATGAGCTAG	TTGAATTCCA	GGAAGGAAGC	AGAGAATTAG	AAGCAGAGTT	GGAGGCACAA	180
TTAGTACAGG	CTGAACAAAG	AAATAGAGAC	TTGCAGGCTG	ATAACCAAAG	ACTGAAATAT	240
GAAGTGGAGG	CATTAAAGGA	GAAGCTAGAG	CATCAATATG	CACAGAGCTA	TAAGCAGGTC	300
TCAGTGTTAG	AAGATGATTT	AAGTCAGACT	CGGGCCGAAC	TCGAG		345

- (2) INFORMATION FOR SEQ ID NO:611:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

GAATTCGGCC	TTCATGGCCT	AAATGACCAN	ATCGAGAGGG	AGGACTATGA	GGACTTTGAG	60
TACATTCGGC	GCCAGAAGCA	ACCCAGGCCA	CCCCCAAGCA	GAAGGAGGAG	GCCCGAGCGG	120
GTCTGGCCAG	AGCCCCCTGA	GGAGAAGGCC	CCGGCCCCAG	CCCCGGAAGA	GAGGATTGAG	180
CCTCCTGTGA	ACCTCTGCTG	CCCCCGCTGC	CCCCTGACTA	TGGTGATGGT	TACGTGATCC	240
CCAACTACGA	TGACATGGAC	TATTACTTTG	GGCCTCCTCC	GCCCCAGAAG	CCCGATGCTG	300
AGCGCCAGAC	GGACGAAGAG	AAGGAGGAGC	TGAAGAAACC	CAAAAAGGAG	GACAGCAGCC	360
CCAAGGAGGA	GACCGACAAG	TGGGCAGTGG	AGAAGGGCAA	GGACCACAAA	GAGCCCCGAA	420
AGGGCGAGGA	GTTGGAGGAG	GAGTGGACGC	CTACGGAGAA	AGTCAAGTGT	CCCCCCATTG	480
GGATGGAGTC	ACACCGTATT	GAGGACAACC	AGATCCGAGC	CTCCTCCATG	CTGCGCCACG	540
GCCTGGGGGC	ACAGCGCGGC	CGGCTCAACA	TGCAGACCGG	TGCCACTGAG	GACGACTACT	600
ATGATGGTGC	GTGGTGTGCC	GAGGTCACTC	GAG			633

- (2) INFORMATION FOR SEQ ID NO:612:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

AAATACTAGA	GATAAAGTAG	ATTCATGGCT	TGGTAAGGAA	ATTTTAAGCA	TTCCTTCAAA	60
GATTGACGTG	${\tt CTAAAATAAG}$	CATTGATGTT	TTGAGTTTTT	TTACACCTAG	GATTTTTAGC	120
TTGGGTGTGT	AGGTGAAGGC	CAAGACTCTC	TGCAGGAAAA	AGCTTATTTT	CAAACTCAGA	180
AAATAAAATG	TCAATCATAA	AAATCTACTT	CAACTTTAGC	AAAAAGAAAA	AAAAAATCAA	240
CAAAAAGTAT	ACTCTGTATG	CTGGGATTCC	GAGGTTCCAA	CACACTGTTA	CTCGAG	296

- (2) INFORMATION FOR SEQ ID NO:613:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GATCCAGTGC	TGCAGCTTCC	TTACTATGAA	ATGACAGCTC	CACTTCCTAA	TAGTGCATCC	60
GTGTCTTCCT	CACTGAATCA	TGTTCCAGAT	CTTGAGGCTG	GACCCAGCTC	ATATAAATGG	120
ACTCACCAAC	AACCAAGTGA	CTCTGACCTT	TATCAGATGA	CAGCTCCACT	TCCTAATAGT	180
GCATCCGTGT	CTTCCTCACT	GAATCATGTT	CCAGATCTTG	AGGCTGGACC	CAGCTCATAT	240
ATAATGGACT	CGCCAACAAC	CCCTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:614:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

GGTGGAAACT .	ATCCAAGAGG	CCTTCTGAAT	TCCTCTGACA	TATATTTGAG	AAACTGGGCT	60
ACTGAAAGCC	CTAACCCCAC	TTGGCTGCAT	TTTATTTGGT	AACCAGTGAG	GCAAACACCC	120
TTGCCAGACC	CCTACCATCC	ATCTTGATGT	GGTTCCTGCA	CTGGACACTG	CTTGGGTACG	180
GGCCTGCCCA	GATCTTGGGA	ATGTGGGCAG	TGGCTCCTCT	GAAGCACCAG	TGGGCAGAGG	240
ATGAGTCATG	GTATCCTCCC	GGCACCCTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:615:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

GAATTCGGCC	TTCATGGCCT	AGTATTTTTG	TAGAGACGGG	GCTTCAGCAT	ATTGGCCAGG	60
CTGGTCATGA	ACTCCTGACC	TCAGGTGATC	CTCCTGCCTC	AGCCTCCCAA	AGTGCTGGGA	120
TTACAGGCAT	GAACCACTGC	ACCCAGTCAA	GGGTATAAAA	TTTCTACACA	GCACAGGCAG	180
ATTCTGGCTG						240
ATTATCTTCT						300
TAGTAAAGCA	AATTTAAGAT	AATTTTCTGC	TTTGAGATTT	AGGGATAGAT	TTTTTAACAT	360
AGTCTTGCTG	ATAATGATAG	ACATCCTGGG	ATGTTGGAAA	TTAGGAAACT	TGAACTTTTA	420
TTTGCACAGA	CTGAGAATTA	TGACTGAGGA	AAAGTTAGAG	GATCAGAAAA	AATAAATTTA	480
TAAATCACAA	GCTAGGCTTG	GCAATATGAG	TGGCGCTCGA	G		521

- (2) INFORMATION FOR SEQ ID NO:616:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 577 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GAATTCGGCC	TTCATGGCCT	AGATTGGAAG	GTGTGGTAGG	CAGAATTCTG	GCCCCCATGA	60
CTGCCCCTTC	CCCTCACACC	CCCCGGGTTG	CTCCAATGGT	TATGTCACGT	TGCTTGGCAA	120
AAGGGACTTT	GTAGATGTCA	TAAAAGGTGA	CTAATCAGCT	GACTTGAGAG	AGTTTATCCT	180
GGATTATCCA	AGGGGCCCAG	TGTAATTCCA	AGAGCCCTCA	AGAGCAGAGC	TGGAGAGATG	240
CCGCGCAGGA	GGCCTGGGTG	CCGTTTCGGA	GCAGGATGGA	AGGCGGTGAA	TCCCGCCTCC	300
AGCATGGAGC	TCGGGAGAGG	CCCTGACTGC	AGATGGAGAG	GCTGCCCTGG	CCGCAGCGCA	360
CGGGGCTCCT	GACCCACAAA	AATCGCGAGA	TAATGAGTTC	ATGTTGTTTG	AAAGTCCGTC	420

ATTTCTGGTA ATTTGCTATA TAAAACTATT GCTATACGAT TAAAAACTAA TACAGAAGAA TATTTCTTTA ACATTATGTT AAAAAGGAAA AAAGCTAACA TTTTCTTTAT AGCAAAACAC TGCCATGATT TACATTAAAA TTAGGAACAT ACTCGAG	480 540 577
(2) INFORMATION FOR SEQ ID NO:617:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 269 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:	*
GAATTCGGCC TTCATGGCCT AGCACATACA GTATAAAAAA TAATCACCCA CCATAATTAT ACCAAATTCC TCTTATCAAC TGCATACTAA GTGTTTTCAA TACAATTTTT TCCGTATAAA AATACTGGGA AAAATTGATA AATAACAGGT AAGAGAAAGA TATTTCTAGG CAATTACTAG GATCATTTGG AAAAAGTGAG TACTGTGGAT ATTTAAAATA TCACAGTAAC AAGATCATGC TTGTTCCTAC AGTATTGCGG GCCCTCGAG	60 120 180 240 269
(2) INFORMATION FOR SEQ ID NO:618:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 469 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:	
GAATTCGGCC TTCATGGATT CTGCTTTGAA TATAGCTACA GAAATAAAGG ATGGACTACA ATGTGGGACA GTGTCTTCTC AGAAACAACC AGCCTTGAAG GCTACAACTG ACGAGGAAGA TTCTGTTTCC AATATAGCCA CAGAAATAAA GGATGGAGA AAATCTGGGA CAGTGTCTTC TCAGAAACAA CCAGCCTTGA AGGCTACAAC TGACGAGGAA GATTCTGTTT TGAATATAGC CACAGAAATA AAGGATGGAG AAAAATCTGA GACAGTGTCT TCTCAGAAAC AACCAGCCTT GAAGGCTACA ACTGACGAGG AAGATTCTGT TTCGATTATA GCCACAGAAA TAAAGGACGG AGAAAAATCT GGGACAGTGT CTTCTCGGAA AAAACCAGCC TTGAAGGCTA CAAGTGATGA GAAAGATTCT TTTTCGAATA TAACCAGAGA AAAAAAGGAT GGACTCGAG	60 120 180 240 300 360 420 469
(2) INFORMATION FOR SEQ ID NO:619:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 448 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:	
GAATTCGGCC TTCATGGCCT AGTCCGTGTT GTGGTCAGTG TGTGAACTCC ACACTGGACA GTAGCTGAGT TTGGGCAGG ATGAGGAGTG GAGGGGTGAG GTCTAAGGTT CAGAAAAAGT TTGTGTTTAA GAACTTGGTT ACACTGGAGT CAGTTGCAGA CCAGAATGGA GAAAAGCACT CCTGACTTGA GTTGGGTGTG CTTGGGACTG GATCACCTTT GACCTTCTTT ATTTACCTAA	60 120 180 240

TIGGAGGAA GAGCAGGGA GGCAACACIA TITCICIIGG GIGIIAGAAG AAGAIICGAG	300
CTTATTTGGG CACTGGTCTC TATCTTTGCC TTCAGCTGAA TCAACATCTA AGATGTTTTA GATGCTTAGC TAATTCCTCT TAAAAAAAGA ATAAGCAGAG GCCGGACGTG GTGGCTCATA	360
GATGETTAGE TAATTEETET TAAAAAAGA ATAAGEAGAG GEEGGAEGIG GIGGETEATA GETGTAATEE CAGCAGTGTG GTCTCGAG	420
SCIGIAATCC CAGCAGIGIG GICICGAG	448
(2) INFORMATION FOR SEQ ID NO:620:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 457 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
,	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:	
GAATTCGGNC TTCATGGCCT ACTTAAATCC ATCAAGTTAC ACAATCGATC TGTTGTCAGC	60
TGAACAGAAC CACATTAAAT TTAAGCCAAA CACACCAATA GGAATGTTGG AGGTAGAGAA	120
GGTAATTTTA AAGCCAAAAA TGTTGGATAA GAAAAAACCT ACACCTATAA TACCAGAGAA	180
AACTGTGAGA GTAGTGATTA ATTTTAAGAA AACACAGAAG ACCATAGTGA GAGTGAGTCC	240
ACATGCATCG CTTCAAGAGC TTGCCCCTAT TATATGTAGC AAATGTGAGT TTGATCCGTT	300
GCATACACTA TIGITGAAAG ATTATCAATC GCAGGAGCCT CTTGACTTGA CAAAATCTCT	360
TAATGACCTG GGACTAAGAG AATTATATGC GATGGATGTC AACAGAGAGT CCTGCCAAAT	420
ATCACAAAAC CTAGATATTA TGAAGGAGGC CCTCGAG	457
	457
(2) INFORMATION FOR SEQ ID NO:621:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 287 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(II) Nobbeomb IIID. CDM	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:	
GAATTCGGCC TTCATGGCCT ACTCTCTGAT TTACAGATTG CTAATTAAAT GGCTATTATT	60
AGTTTGGÄTT AATTAGACTT AAGAAAACAA CTAACTGAGG GTTTTTTTTG TTTGTTTTTT	120
GAGGGTTTTC TTTGCATGAG AATTGTATGT AACCAGTGAT ATGATTATTC CTGAATGTAC	180
AGACAGAAGT AAGCCTGGAC ATTGTTAAAT AGTCCCTGCT TTAAGGGACT ACGATAATGT	240
GTACTATGAC AAACGTGCTT TATTCTTCTA ACGCAGTAAG TCTCGAG	287
(2) INFORMATION FOR SEQ ID NO:622:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 328 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) Torobodi. Hiteat	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:	
GAATTCGGCC TTCATGGCCT AGTAGGTGTA TCACAGATTT CTAATGTAGA ATGGTCAGTC	60
CAGGAGTAAT TGTAATTGTG GAAAAATGGA GAATTATAAA ACAAGAATGA TGTGCAAAAA	120
AGGACACAGT TGAATTCATC TGTGTTCCTC TAAACTATTT CATTTACTCA TTCATCCAAG	180

TTTTGAAAAA	TGTTGGGAGT	CTGAAAAATT	CCAGGCACTC	TGGATAAATG	AGTATGGAAG	240
AATCCTCCAA	AAGAACTTTT	AGTCTACAGG	${\tt GGAACATTAA}$	TAAGCAATCA	GGGACTTGAG	300
ACCTACAGTG	CTGTGGAAGA	TTCTCGAG				328

- (2) INFORMATION FOR SEQ ID NO:623:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GAATTCGGCC	TTCATGGCCT	AGGACGTTTG	GGTTGTTTCC	ATCTCAAATA	AATAAATAAA	60
TAAAAGTCTA	TAAAAACAGC	TGGGCCCAGG	CATTTAAAAA	AATGTTCGGT	CTTCTAGTTT	120
AGTCTTTTAT	TGTCTATGCA	AATTCTTTGG	CTATTGAACT	ATCCAAGCTT	TCTCTTTTTA	180
AGCTTTTGGG	${\tt GAATAGGTTG}$	CAATACATTT	CTTGTCTACT	GTTTCTCTTA	GTGTTTTCTA	240
ATTCTAACCC	ACTGTTTTTG	GAATTTCTAT	TAGATGGTTT	TGCAACTTCT	GCATCTATCC	300
TCCATGCACC	TTCACATTTC	CTTCACAGTT	TTCGTGCTGT	TTTCCTTGTG	TGCTACATTC	360
TGCACAGGAC	TCGAG					375

- (2) INFORMATION FOR SEQ ID NO:624:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 763 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GAATTCGGCC	AAAGAGGCCT	ACCTCAAAGG	ATTGGCTAAA	AGCAAGCAAC	TGGATTGAAC	60
ACCCTAAGAA	GAAAGATTCA	CACTGCACCA	GGAGACATCA	GAAAGAATGA	AAACTCTGCC	120
GCTGTTTGTG	TGCATCTGTG	CACTGAGTGC	TTGCTTCTCG	TTCAGTGAAG	GTCGAGAAAG	180
GGATCATGAA	CTACGTCACA	GAAGGCATCA	TCACCAATCA	CCCAAATCTC	ACTTTGAATT	240
ACCACATTAT	CCTGGACTGC	TAGCTCACCA	GAAGCCGTTC	ATTAGAAAGT	CCTATAAATG	300
TCTGCACAAA	CGCTGTAGGC	CTAAGCTTCC	ACCTTCACCT	AATAACCCCC	CCAAATTCCC	360
AAATCCTCAC	CAGCCACCTA	AACATCCAGA	TAAAAATAGC	AGTGTGGTCA	ACCCTACCTT	420
AGTGGCTACA	ACCCAAATTC	CATCTGTGAC	TTTCCCATCA	GCTTCCACCA	AAATTACTAC	480
CTTCCAAATG	TGACTTTTCT	TCCCCAGAAT	GCCACCACCA	TATCTTCAAG	AGAAAATGTT	540
AACACAAGCT	CTTCTGTAGC	TACATTAGCA	CCAGTGAATT	CCCCAGCTCC	ACAAGACANC	600
ACAGGTGCCC	CACCCACACC	TTGTGACAAC	TACACNAGCT	CCACCATCTT	CCTCAGCTCC	660
ACCAGAGACC	ACAGTNGCCC	CACCCACACC	TTTTGCAACT	ACACNAGCTC	CACCATCTTC	720
CTCAGCTCCA	CCAGAGACCA	CAGCTGCCCC	ACCCATCTTC	GAG		763

- (2) INFORMATION FOR SEQ ID NO:625:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GAATTCGGCC	AAAGAGGCCT	AGTAGTTTCT	ATGTGCGGTC	TGGGGTGGGG	GCAAGGCCCT	60
TGTGTTCCAC	TGGTTTCCAC	CACGTTGACA	GCAGTCGCTG	GCAGCAGAGA	GCCATTTCCT	120
GTCATGCTGG	TCTGTTCCAG	GACTCTGTGG	AAGATTCTCT	ATCTCCACTG	GCACAGGAGC	180
AGAGGAAATG	GAAGGACTCA	CAGGCAGAGC	AGATCTCATC	CCCCAAGCCT	GTTGGGAGCC	240
ATTACTTTGG	GTCGAAACAT	TATTGTGAAC	ACTAAGTTCT	TCAGGTTTTG	TAGCACATGC	300
TTTCATTTGT	AGAGTTCGTC	TAGAATATCG	TTTGCTGGGC	CTTCTTTCAA	AGGATGTTGA	360
TCTTCTTGCT	TTATTGGTTT	TTGTGGTCTG	ATACTCTGTT	TTCCCACTAT	ATCTAAATCG	420
TGATCCTAGT	CGAATAAATC	CTGATCGATG	AGAACTCTTT	TGGACGGGGC	CTCGAG	476

- (2) INFORMATION FOR SEQ ID NO:626:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GCGATTGAAT	TCTAGACCTG	CCTCAACTGT	CTGGTTTCCT	GTAAAATAAA	CACATTGTTT	60
${\tt TATATTTTA}$	GGGAACAAAA	AGTGCTGCTA	TAGGGTTCAA	AGTTTTCCTT	CTGAACACTT	120
TTCCGAAACA	AATTACCCCA	AAGACACATT	TTGAATATCC	TGGTCACATC	TTTGGATCTG	180
TAAAATATAC	CTTTTAGTAT	GGCACCTGTT	AAAATGCAAA	GCAAAAACCT	CGAG	234

- (2) INFORMATION FOR SEQ ID NO:627:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 583 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GAATTCGGCC	TTCATGGCCT	AGGCCTTGTG	AATCATTCAG	CATAAGGAAC	TGTCAATATT	60
TTTTTGAGCT	GTCAGAAATC	CATTTAGTGA	TTTTCGACAA	TTCAAAAAAA	TATTTCTGAC	120
CGCTTGATTC	AGTTCCTAGT	GAATTAGGGA	AGAAGAGGAA	TAAAAGAAAT	ATATCAATCT	180
AAATTATGAA	CCCAGAGTCT	AGCTTCCTGA	ATTCTTCTCT	GTGCTTAAAC	GAACAACAGG	240
ATGTTGAGGT	TCAAAAATAC	TCTCTTCTAT	TTCCCCCCCT	TCCTTCCCTT	TTCTTTCCTT	300
CTCTTCCATT	. CCTCGAAAAG	ATAATAAAAC	AGAATGTGCC	TAGAGCTTCT	GGAAAGAATA	360
CAGTCCTGCT	GATACTAGAA	CTCAGTGAAA	TTTGCACCAG	ATTTCTGAGC	TACAGAACTG	420
AAGATAATTC	ATTTATTTCA	AGCCACTGAG	TTTGTGGTAA	ATTTGTTACA	GTAGCAATAA	480
AAATCTAATA	CATGCCTTCT	ATACCAGAAG	TACACATCCA	CGTGACCATT	CCTGTCCTCA	540
CCCCACACAC	ACATACACAC	ACACACACAC	ACGCACACTC	GAG		583

- (2) INFORMATION FOR SEQ ID NO:628:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

GAATTCGGCC	TTCATGGCCT	ACCTGCCTCG	AGTTCCTACT	GCCCCGGGC	GGCCTGCACA	60
GAGCTGCTGC	CCTCCAGAGA	CTGTGAATCC	CAAGCCTGAC	TCAGTGGACT	GCTTCCTGTT	120
CCCCTCCCTC	CTCTTCCTCA	CCTTGTTCTG	CACCCTCAAG	CCTTTCTCCA	ATGCCTCCCA	180
GGAGGATTTG	GGGACTTTCT	CCCTGGGGCG	CCCAGATCCA	GCTCGGAGGC	CTCACTGGGA	240
CCTGGCAAGG	CCTGACCTCC	CGCCCAAACT	TGCTTCTGTA	GCCCCCCTAC	TCGAG	295

- (2) INFORMATION FOR SEQ ID NO:629:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

GAATTCGGCC	TTCATGGCCT	AACCTGTTGC	TTCCCCTGGG	ACTGAAGGCA	GAAGTGACTC	60
CCGAAATTCT	CTTTCTGGAC	TCAGAAGGAA	ACCAAAGCAA	TTGATGACAC	CGCATCCCAT	120
ACTAAAAGCT	ATGGAAGAGA	GAGCAATTCA	ACGAGCTGAA	TGTAGGCGGA	TCTTGGCAGA	180
GAAGNAGAAA	AAACAAGAAG	AAGANAAATT	GGCCCAGTTA	AAGGCCCAAG	AGGAGGAACG	240
TCAGAAAAGG	GAGGCAGAAG	AAAAGGAGGC	ACAGCTTGAA	AGAAAACGAG	AAGAGAAGAG	300
ACTGAAGAAA	ATGAAAGAAC	TTGAGAAGCA	GAAGAGAACT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:630:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

GAATTCGGCC	TTCATGGCCT	AGTTCTTCCT	TAGGAACAAG	GGCAGGACCT	CAAACAGTCC	60
AGAGGAGAAG	CCTGGGGTGG	TCAGGGAAGG	CTTCCTGGCT	GAGAGGACAG	GCTTAGGGGC	120
ACCTTGAAAG	TTCAGGCTGA	CTGGGGCTAG	GGGCATGTGG	GTAACAGGTT	AAAGGGGGGG	180
GGGCTGGAAA	ATGCAGACAC	CAAAGACCCT	TCAATATGAG	GCCAAGAAAG	GAAGGTTCAG	240
AACAGGGATC	ACTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:631:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

ACC AGCACAGGAG	CTACAGCAAA	TCATGGCACT	TCTGCAGTAG	60
TAC CTAGGACAAG	AAACTTTGAC	AGAAATCCAA	ACCTCACCAG	120
GTG AAAGCGGACG	GAGCTAGCAC	CCCCAGGTTA	AGAGAACAGG	180
TCG CCAGCAGCAT	CCATCTCCAG	ACTCTCTGGG	GAACAGGTCG	240
GGC AGTGTATCTG	AAAGTGCGCG	GAGTGAAGGA	AGGATTAGTC	300
GAG CTCGAG				326
	TAC CTAGGACAAG GGTG AAAGCGGACG TCG CCAGCAGCAT	TAC CTAGGACAAG AAACTTTGAC GGTG AAAGCGGACG GAGCTAGCAC TCG CCAGCAGCAT CCATCTCCAG AGGC AGTGTATCTG AAAGTGCGCG	TAC CTAGGACAAG AAACTTTGAC AGAAATCCAA GTG AAAGCGGACG GAGCTAGCAC CCCCAGGTTA TCG CCAGCAGCAT CCATCTCCAG ACTCTCTGGG AGC AGTGTATCTG AAAGTGCGCG GAGTGAAGGA	ACC AGCACAGGAG CTACAGCAAA TCATGGCACT TCTGCAGTAG TAC CTAGGACAAG AAACTTTGAC AGAAATCCAA ACCTCACCAG GGG AAAGCGGACG GAGCTAGCAC CCCCAGGTTA AGAGAACAGG TCG CCAGCAGCAT CCATCTCCAG ACTCTCTGGG GAACAGGTCG AGGC AGTGTATCTG AAAGTGCGCG GAGTGAAGGA AGGATTAGTC TGAG CTCGAG

- (2) INFORMATION FOR SEQ ID NO:632:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GAAAAAATGG AA	GAATTTGT TTGTAAGGT	A TGGGAAGGTC	GGTGGCGAGT	GATCCCTCAT	60
	GACTGGCT CAAGGATAA				120
ATGCCTTCTT TC	CGGGCCTG TTTTAAGAG	CATTTTCAGAA	TACACACAGA	AACAGGCAAC	180
ATTTGGACAC AT	CTCTTAGG TTGTGTATT	TTCCTGTGCC	TGGGGATCTT	TTATATGTTT	240
CGCCCAAATA TC	TCCTTTGT GGCCCCTCT	G CAAGAGAAGG	TGGTCTTTGG	ATTATTTTC	300
TTAGGAGCCA TT	CTCTGCCT TTCTTTTC:	A TGGCTCTTCC	ACACAGTCTA	CTGCCACTCA	360
GAGGGGGTCT CT	CGGCTCTT CTCTAAACT	GATTACTCTG	GTATTGCTCT	TCTGATTATG	420
GGAAGTTTTG TT	CCTTGGCT TTATTATTC	TTCTACTGTA	ATCCACAACC	TATTCTCGAG	480

- (2) INFORMATION FOR SEQ ID NO:633:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GAATTCGGCC TTCATGGCCT	AGCGGGATCG	TATCACTACG	CACGTGGCGT	CAATGACAAA	60
GACGCCTTCC CCACGGGACA	GGCCCTGGGA	ACTGCGGGGC	AAGGTGTGGG	CACGGCGGGT	120
CGCCTTCCAA CCCTCCAGGG	TCTCCGGTCC	TGCCCCCTCT	CCAAGACCCA	GAGATTCTCT	180
CCATCCGGTG CCTCCGGGAG	CCCAGGGTCT	GGGGAGTGTC	TGGCTATGGC	GGGGCGGCTG	240
CTTTTTAGGG GAGGGAATCC	AGCATTTGGG	AAACCAGATC	TGTTCTCCTT	CTTTCCCTTC	300
CCTCGAG					307

- (2) INFORMATION FOR SEQ ID NO:634:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

CCTCTGCAAG	AAATGCCTAA	GCGTATTATC	AGGAAGTGGA	TAAAATTA	GTTTCCAGAT	60
CAAATTAAGC	ATCTACAGGT	GAATTAATAT	AGAATTAAGC	TTAGAAAGCT	TAAGTAGAAG	120
TTGAATGAAT	TGTGTTCATT	CTTTGAAACC	CATTGATTTG	CAAAACCAAT	ATTCCACTGT	180
CTATAGGAGG	CAATTCAGAC	TGAAAATAAT	TTAGAAAAAA	AAATAGTCCA	GAAAAAAAA	240
TAGTTCTAGA	GATAAATAGG	TCATTTGAAG	ACTAACCTCT	GCCATTAGGG	GTTTCTAAAG	300
ATAGGCTGAC	TCTATCTATT	TAATAATTAT	TTTGTTCATT	AACTCCTTGC	ATATAGAATT	360
GTAACTGATA	CCAGCCAGGT	ACGGTGGCTC	ACGCCTGTAA	TCCCAGCACT	TTGGGAGGCC	420
AAGGCGGGCA	GATCACCTAA	GGTCGGGAGT	CTCTCGAG			458

- (2) INFORMATION FOR SEQ ID NO:635:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GAATTCGGCC	TTCATGGCCT	ACCCACTCTC	ACTTTGTACC	TCTGTCAGTT	ATCTCCTCTT	60
TACCCTTCTT	TCAACGAGCA	TACCACCGGC	CCTCCCAGCA	CCTATGGCCC	AAGCCAGTTG	120
TTTGCAAATT	${\tt TTATACTGTG}$	ACACAGGACA	ATTTACACAC	ACATACACAG	TTTCACTTGT	180
GACATACTTT	TTTTTTGAGA	TGGAGTCTCA	CTTCATTGCC	CAGGCTGGAG	TGCAGTGGTG	240
TGATCACACC	TTATTGCAGC	CTCAAACTCC	TGGGCTCAAG	TGGTCTTCCT	GCCTCAGCCC	300
CCCTAGTAGC	CAGGATTACA	GGCGTGCACC	ACCATTTCTC	GAG		343

- (2) INFORMATION FOR SEQ ID NO:636:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

GTGGATAACA	AACAAACAAA	TCTGATGCTC	CCTGAGTCAA	CTGTTTATGG	TGATGTGGAC	60
CTTAGTAACA	AAATCAATGA	GATGAAAACC	TTCAATAGCC	CAAATCTGAA	GGATGGGCGT	120
TTTGTCAATC	CATCAGGGCA	GCCTACTCCT	TACGCCACCA	CTCAGCTCAT	CCAGTCAAAC	180
CTCAGCAACA	ACATGAACAA	TGGCAGCGGG	GACTCTGGCG	AGAAGCACTG	GAAACCACTG	240
GGACAGCAGA	AACAAGAAGT	GGCACCAGTT	CAGTACAACA	TCGTGGAGCA	AAACAAGCTG	300
AACAAAGATT	ATCGAGCAAA	TGACACAGTT	CCTCCAACTA	TCCCATACAA	CCAATCATAC	360
GACCAGAACA	CAGGAGGATC	CTACAACAGC	ACAGAGCTCG	AG		402

- (2) INFORMATION FOR SEQ ID NO:637:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GCTTCCTCGC	AGCAAGCGGC	TGGAGATAGA	GAAGAGCTTA	CTGGTGCGAG	CGTCCGTCGA	60
CCCCGTCGCC	GCTGACCTAG	AGATGGCAGC	CGGTCTCACC	GACATATTTC	AGCATGATAC	120
ATACTGTGGT	GATGTCTGGA	ACACCAACAA	ACGCCAGAAT	GGCAGACTCA	TGTGGCTCTA	180
TCTCAAATAC	TGGGAACTCG	TTGTCGAACT	GAAGAAGTTT	AAGAGAGTAG	AGGAAGCCAT	240
ACTAGAAAAG	TAAGACAAGA	GTGAAATCAA	ACTGCTTTTA	GTGACTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:638:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

GTCGAGAAAA	TGGGGATAAT	GGAGAAATTG	TGGGCAAGCT	GGCTTCCTGG	GAAGGGACTA	60
ATTGAACAAG	ACAATGATTT	ATCTTTTCGG	GGTTCAGAGG	CAGCTTGTTA	ATTCGAATTA	120
TTTTCTTTAT	TTTTGCCCAC	AAGTGTTTGG	TTGTCCTTTT	CTCTGGCTTT	TTACCTGATC	180
AGGCTGCAAG	CTGCAAAGGT	GTGGCTTGTG	CTGCAGATTT	GTAATAAAAG	ATGACAGGTG	240
AGAGAGACAG	TGGTGGAACT	GGTAGAGCTT	GCACACCCAC	ACGGTGTGGC	TGCTCGGGAG	300
GCTGTCTAGT	GCACCTGCCA	ACAGAGCACA	GATATCCTCT	CTTCCTCATT	TCAGATTCCT	360
CCTTCCAGCT	GTTTACTAAA	CAGCAACAAA	AACACCCTCT	TGGCTGTAAC	TTGTCAAATA	420
AAGTCCCTGC	AAAGTGTATA	AGATTTTCCT	CCCCAACCTC	GAG		463

- (2) INFORMATION FOR SEQ ID NO:639:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GCGAGGGAGA	TGGCAGCCTG	GGCTTTAGCA	GCAGGGAGGA	AGGTGAANAA	AGAACCGGGG	60
CTTGCAGCAG	AGGTGGGTTC	TGCCTTAAAG	GCAGAGACCC	CCAACAACTG	GAATGCCACG	120
GAAGACCAGC	ATGAGCCTAC	CAAACCTTTG	${\tt GTTCGCAGGG}$	${\tt CTGGAGCTAA}$	TTCTCGCTCC	180
AGGAGAAAGA	AGCAGAAGAA	GAACTCCAGG	CAGGAAGCAG	TGCCCTGGAA	AAAACCCAAA	240
GGCATCAATT	CCAACAGCAC	AGCTAACTTG	GAGGATCCTG	AGGTGGGTGA	TGCTGAAAGC	300
ATGGCGATCT	CAGAGCCGAT	CAAGGGCAGC	AGAAAGCCCT	GTGTGAATAA	GGAGGAGTTG	360
GCTTTGAAGA	AGCCCATGGC	GAAATGTGCC	TGGAAGGGTC	CCAGAGAGCC	ACCTCAGGAT	420
GCCCGGGCAG	AAGCCGAGAG	CCCAGGAGGC	GCCTCTGAGT	CAGACCAAGA	TGGTGGCCAT	480
GAAAGCCCAC	CAAAGAAGAA	GGCCGAGCTC	GAG			513

- (2) INFORMATION FOR SEQ ID NO:640:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

GAATTCGGCC	TTCATGGCCT	ACACCTCAGC	CTCCAGAGCA	GCTGGGACTA	CAAACGTGTG	60
CCACCATGCC	GGGCTAATTT	TTGTATTTTC	AGCAGAGGTG	GGGTTTCACC	ATGCTGCTGG	120
CCAGGCTGGT	CTCGAACTCC	TGGCTTCAAG	TAATCTGCCC	ACCACAACCT	CCCAAAGTGC	180
TGGGATTACA	GGTGTGAGCC	ACTGCGCCCA	ACCAAGAGCT	CCTTTTTGTT	TTTCTTTTTT	240
TGTGAATTCG	GATTCTTTAT	ATTCAGGAGT	TTTACTTAAA	CTTTGAATCT	GAAAGAAACT	300
TTAGGAGGAG	CTCATAGATT	TGTGGGAAGA	AGCAAATCTA	CATTATTTTC	TCTCTTCTAA	360
AATCATATTC	CATGTATTTT	GATCTTTTAC	TGAATTTTAA	CACATTGTTT	CATCACTAAC	420
ATAAAGTGTT	TCAATAGTTT	TTGTAACTCA	CACACAAATA	CTGGATTTAA	AAGTTATATA	480
CCTGAGTATA	TTTTTATGGC	AGGTCTCGAG				510

- (2) INFORMATION FOR SEQ ID NO:641:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

GAATTCGGCC	TTCATGGCCT	AGTGTTCCCA	GCCAGTCTCT	ATTCTCTCAC	CTAACACTCT	60
CAAGGAGATA	GAAGCTTCAG	CTGAAGTCTC	ACCCACCACG	ATGACCTCCC	CCATCTCACC	120
CCACTTCACA	GTGACAGAAC	GCCAGACCTT	CCAGCCCTGG	CCTGAGAGGC	TCAGCAACAA	180
CGTGGAAGAG	CTCCTACAAT	CCTCCTTGTC	CCTGGGAGGC	CAGGAGCAAG	CGCCAGAGCA	240
CAAGCAGGAG	CAAGGAGTGG	AGCACAGGCA	GGAGCCGACA	CAAGAACACA	AGCAGGAAGA	300
GGCTCGAG						308

- (2) INFORMATION FOR SEQ ID NO:642:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

GAATTCGGCC	TTCATGGCCT	AGTTAGATGA	AAATCTAAAG	GATGAATACT	TTGAGGAAAT	60
CATGGAAGAA	TATGAAGATA	TTAGACAGGG	CCATTATGAG	TCTCTCAAGG	AGAGGAGATA	120
CTTACCCTTA	AGTCAAGCCA	GAAAAGTGG	TTTCCAAATG	GATTGGCTGT	CTGAACCTCA	180
CCCAGTGAAG	CCCACGTTTA	TTGGGACCCA	GGTCTTTGAA	GACTATGACC	TGCAGAAGCT	240
GGTGGACTAC	ATTGACTGGA	AGCCTTTCTT	TGATGTCTGG	CAGCTCCGGG	GCAACCCCAC	300
TCGAG						3.05

- (2) INFORMATION FOR SEQ ID NO:643:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

GCGATTGAAT	TCTAGACCTG	CACCCAGCCA	ACACTGAGAG	מסיים מיידידים	ር ጥ አ ር ጥጥጥጥ አ ጥ	60
CCACCTGACC	ACCATCATTA	CCTATCACCT	GTCATTCTTC	ATCCACCCTA	CATCCATCCT	120
TCATCCCCCC	ATCATCCACC	CATCTATCCT	TCATCCATCC	ATTCATCATG	GAACCATTAT	180
		CAGCCAGAAA				
						240
CTCTCTAAAC	CAGTTCTTAA	TCTGGGGCCA	AAGTCCTACC	CACACATCCC	TTAGTCTCGA	300
G						301
-						201

- (2) INFORMATION FOR SEQ ID NO:644:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GAATTCGGCC	TTCATGGCCT	AGATCCCCCG	TGGAGAAAGC	AGTGACACAT	TCACACAGCT	60
GTTCCCTCGC	ATGTTATTTC	ATGAACATGA	CCTGTTTTCG	TGCACTAGAC	ACACAGAGTG	120
GAACAGCCGT	ATGCTTAAAG	TACATGGGCC	AGTGGGACTG	GAAGTGACCT	GTACAAGTGA	180
TGCAAAGGAG	GGTTTCAAAG	AAAAAGGATT	TTGTTTAAAA	TACTTTAAAA	ATGTTATTTC	240
CTGCATCCCT	TGGCTGTGAT	GCCCCTCTCC	CGATTTCCCA	GGGGCTCTGG	GAGGGACCCT	300
TCTAAGAAGA	TTGGGCAGTT	GGGTTTCTGG	CTTGAGATGA	ATCCAAGCAG	CAGAATGAGC	360
CAGGAGTAGC	AGGAGATGGG	CAAAGAAAAC	TGGGGTGCAC	GCCTCGAG		408

- (2) INFORMATION FOR SEQ ID NO:645:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 364 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

GAATTCGGCC TTCATGGCCT AGTTATGTGA TTAGGAGTAG GGTTAGG	ATG ANTGGGAAGA 60
AGAAAGAGAG GAAGTAAAGT TTAATTATGC CTTTTTGGGT TTATTAT	CCC TGATGCATGT 120
GGCCCCCCAC TGCTGTGTCC TTCTCCTGTT GGCTAGGGTT AGACCAC	ACA GGCTAAACTA 180
ATTCCGATTG GCTAATTTAA AGAGAATGAC GAGGTAAGTG TTTTGGC	GGG AAAAATGGTT 240
ATGACAGAGC AGGTAATAGG AATGAGTTAG GGTGGAGTAG GTAATCG	GAA TGAGTCAGGG 300
TGGAGCAGGT AATTGGAATG AGTCAGGGTA GAGCAGGTAA TCGAAAA	AGG TTGCTTTGCT 360
CGAG	364

- (2) INFORMATION FOR SEQ ID NO:646:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

GCTGATGTGG CACTACTGCA CCATTTACCA CAACATTAGA ATATGTCTGA GTAACTGGTT GGCTTAGATT TTTTGCATTG AGTCCCACCC CATTTTCCAG AACTTTCATG GCTATTCTTA TATGTTTGTT TTCCGTAAGA TCTTTAGGAT CAATTTGTCT AGTTCTAAAG AGGAAATTCT GATATTATTG ATTTAGTAAC TTTCCATGAA AAAAACCTAC CATCACAGGA AAGATGCACA TTAATTACAG GTAGCTCGAG	120 180 240 300 320
(2) INFORMATION FOR SEQ ID NO:647: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:	
GAATTCGGCC TTCATGGCCT AGTCAGTGGC TAGATTGATT GATCCTCCAG AATTAGACAC CCACATGTTA ACACCAGTCT CAGTTGGAGG GCTGATAGTA AACCTTATTG GTATCTGTGC CTTTAGCCAT GCCCATAGCC ATGCCCATGG AGCTTCTCAA GGAAGCTGTC ACTCATCTGA CCACAGCCAT TCACACCATA TGCATGGACA CAGTGACCAT GGGCATGGTC ACAGCCACGG ATCTGCGGGT GGAGGCGAGG TCTCGAG (2) INFORMATION FOR SEQ ID NO:648:	60 120 180 240 267
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 321 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:	
GAATTCGGCT TCATGGCTAC TTTTGGTAAA GCATACCCAA CCTTCAGTTA GAATATCTCC GATAATAAA AAAGATCTA TTGAAATTTA TTAATTCTTT TGTGTCTAGT AGATAACTTG GATGGCACAC AGTGCTTTGA TTTTTACCTG CCCAGAATTT AACTCCTCAT CCTATCCTAC GTGATTTTCT TTTTCCTCTC CCCTTCCTC TTTTATTCCA TGTCACTGG AATGGCAGGT TTTGCACCAA GTAATGGCAG GTCTTGCACC AAGCAAGCCA GAAACCTGAG CTTTAGTCTT CATTCCTCCC CACTTCTCGA G	60 120 180 240 300 321
2) INFORMATION FOR SEQ ID NO:649: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 559 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:	
AATTCGGCC TTCATGGCCT AGAGGAAGTG AACGGATGGG GCCTCATCCT CCTGCCTCCC AAAGGGTGA GGGTGGAAGG ATGGGGCTGT GCCCTCTTAG GGCAGGGAAA AACAGCTTGG GGGGTTTCT GCCATCAGAG ATCCCATAGG AGGCAGGTCA GTCCTGCAGA ATTCTCCCC	60 120 180

AGTCTGGCCT CO	CAGCCTCCC	TGGCCCCTTT	CTAGAGGCCT	CCATCCCACT	GGCGGCTTGC	240
TCCTGCCACC GO						300
GTCTTGATAT T						360
CTCTCCTATA TO						420
AGATATACAC AG						480
TTAGCATACT GO		ACAGTGTGAT	ACAATAAATA	ATTTCATTCA	TGCTCTATCT	540
ACACATCATA T	IGCTCGAG					559

- (2) INFORMATION FOR SEQ ID NO:650:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GAATTCGGCC	TTCATGGCCT	AGGGAGACTG	AGGCAGGCAG	ATCACCTGGG	GTCGGGAGTT	60
CGAGACCAGC	CTGACCAGCA	GGGAGAAACC	CCGTCTCTAC	TAAGAATAGA	AAATTAGGTG	120
TGGCGGTGCA	TGCCTGTGGT	CCCAGCTACT	CGGGAGGCTG	AGGTAGGAGA	ATCGCTTGAA	180
CCCGGGAGGC	GGAGGTCATG	GTGGGCCGGG	ATTGCACCAT	TGCACTCCAG	CCTGGGCAAC	240
AAGAGTGAAA	CTCCATCTCA	AAAAAATAAA	AGCCTAGCCT	CCCAAAGTGC	CAGGATTACA	300
GGCATGAGCC	ACCGCGCCTG	TCTGTCCGCC	CGTCTTCTTT	TTTAAGAGCA	AGAAAAGGTT	360
TCCCAGAAGT	ACTCTGGTAG	ATTCTTATCA	CACACACATT	CCTAAACCAG	TTACTGGCAA	420
AGAAAATAGA	ATTATCATGA	TTAATTAGCA	TATTCTGAAG	NACATGCTTC	CCTCGAG	477

- (2) INFORMATION FOR SEQ ID NO:651:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

GTGTGAACCT	ACGGGAAGGC	GGCCGCCTGC	ACCTCTGTGC	GGAGACCAAG	GATGATGCCC	60
			ACTCCACCCC			120
ACCAAGACTA	CTACGAGGTG	GTGCCCCCCA	ATGCACACGA	GGCCACGTAT	GTCCGCAGCT	180
			TGACGCACGT			240
GCTACAGCGC	CGGCGCCCCT	CTGGCCATGG	GCATGCTTGC	GGGAGCCGCC	ACTGGGGCGG	300
CGCTGGGCTC	GCTCATGTGG	TCGCCCTGCT	GGTTCTGAGC	CCTGGGACTC	GGAGCACTGA	360
CCCCTGCGCT	TGGATTGCTA	GACTCCTCTT	CCTCCTGGAC	CCCATCCTCT	CGAG	414

- (2) INFORMATION FOR SEQ ID NO:652:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

CAACCAAAAC	A MOOOO O A A A	0001 mmmm m	0m0			
CAACCAAAAC	ATGGGCACAG	GGGATTTTAT	CTGCATTTCC	ATGACTGGAG	GGGCGCCCTG	60
GGGGTTCAGA	TTGCAAGGTG	GCAAGGAGCA	GAAGCAGCCC	TTACAAGTTG	CAAAGATTCG	120
AAATCAGAGC	AAAGCCTCTG	GGTCTGGGCT	CTGTGAGGGA	GATGAAGTGG	TTTCCATCAA	180
TGGCAACCCT	TGTGCAGATC	TCACCTACCC	TGAAGTCATC	AAGCTCATGG	AAAGCATAAC	240
AGACTCTCTC	CAAATGCTCA	TCAAAAGACC	ATCCAGTGGA	ATAAGTGAGG	CTTTGATATC	300
TGAAAATGAA	AACTCTAACC	TCGAG				325

- (2) INFORMATION FOR SEQ ID NO:653:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

GAATTCGGCC TTCATGGCCT	AGGTATTTAG	GCTTTTGTCT	TAACAGCAAA	TCCTGGCTGT	60
CTGGGGCCTG ATGACTGTGT	TCCATGGGTA	TCCACTCCCT	GTCCACAGTG	TGGGAGCCCC	120
TCAGCTGCTT ATTGCAGGGA	CACAGAGCCC	GGCATGGTCC	AGAAGGCGGG	CTTATGGGGC	180
CTGCAGCACA CAGGGAAAGT	GAGCCCACAC	TGTGATAGGA	GGGCAGACAC	ACAGGATGTG	240
TTCTGTGTTA CAGGGTTGCC	GTGAAGAATT	TCATTCTTTT	GCAAGGACTG	GAGAGAAAAT	300
TTTATGTGGA AGGTAGCCCT	TGGAAATGAC	CTCAAAGAAT	AGGTAGGATC	TTAGCCTGCG	360
TTTGAAAGCC TGGAAAAAA	CAGGATGACA	GGATGAAGAG	GCCACAGCAC	AGCTGCAGAC	420
AATGGGAGTG CGGAGATCTC	GAG				443

- (2) INFORMATION FOR SEQ ID NO:654:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

CCCXCCCCC cmccmmcxma	0mas agas ms				
GGGAGCGCCG GTGGTTCATC	CTGACCGATA	ACTGCCTCTA	TTACTTTGAA	TACACAACAG	60
ATAAGGAGCC CAGGGGAATC	ATCCCGTTGG	AAAACCTCAG	CATCAGGGAG	GTGGAGGACC	120
CCCGGAAACC CAACTGTTTT					180
CCTGTAAGAC GGAGGCCGAC					240
CAGCCCCGAG CCCGGAGGAG	AAGGAGGAGT	GGATGAAATC	CATCAAAGCC	AGTATCAGCA	300
GATCCCTCGA G					311

- (2) INFORMATION FOR SEQ ID NO:655:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

GGGGGATACG GATACCCAAA CTTCAATGTT CCTTGATAGT AGGAAGGAGG ACAGTTATAT AGACCATAAG GTGCCTTGCA CAGATTCACA AGTGCAGGTC AAGTTGGAGG ACCACAAAAT	60 120
AGTAACTGCC TGCTTGCCTG TGGAACATGT TAATCAGCTG ACTACTGAGC CAGCTACAGG	180
GCCCTTTCT GAAACTCAGT CATCTTTAAG GGATTCTGAG GAGGAAGTAG ATGTGGTGGG	
AGATAGCAGT GCCTCAAAAG AGCAGTGTAA AGAAAACACC AATAACGAAC TGGACACAAG	240
TCTTGAGAGT ATGCCAGCCT CCGGAGAACC TGAACCATCT CTCGAG	300
	346
(2) INFORMATION FOR SEQ ID NO:656:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 116 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:	
GAATTCGGCC AAAGAGGCCT ACTAAACCGT CGATTGAATT CTCGAGGCAG GTCTAGAATT	60
CAATCGACGG TTTAGGCTCC CTATAGTGAG TCGTATTAAT TTCAGAGGTG TATTTA	116
(2) INFORMATION FOR SEQ ID NO:657:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 482 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:	
BAATTCGGCC AAAGAGGCCT AGGGATGAGG GTGAAGAAGG GGAGAGGGTT GGTTAGAGAT	
	60
ACAGTGTGGG TGGTGGGGGT GGTAGGAAAT GCAGGTTGAA GGGAATTCTC TGGGGCTTTG	120
GGGAATTTAG TGCGTGGGTG AGCCAAGAAA ATACTAATTA ATAATAGTAA GTTGTTAGTG	180
PTGGTTAAGT TGTTGCTNGG AAGTGAGAAG TTGCTTAGAA ACTTTCCAAA GTGCTTAGAA	240
CTTTAAGTGC AAACAGACAA ACTAACAAAC AAAAATTGTT TTGCTTTGCT	300
GAAGACTGAA GAAGTGTTAA CTGAAAACAG GTGACACAGA GTCACCAGTT TTCCGAGAAC	360
CAAAGGAGG GGTGTGTGAT GCCATCTCAC AGGCAGGGGA AATGTCTTTA CCAGCTTCGG	420
RGCTGGCAC GTGTTACCAG GCCGAGTGGG ATGACTATGT GCCCAAACTG TACGAGCTCG	480
AG	482
(2) INFORMATION FOR SEQ ID NO:658:	
(i) CENTENCE CUADACTEDICATOR	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 430 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(D) IOPODOGI: IIIIEGI	
(ii) MOLECULE TYPE: cDNA	
(will destinate programment and to the	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:	
PATTERSON OF THE PROPERTY OF THE APPEARS TO THE APPEARS OF THE APP	60
CACGCAACT CCAGCTTGTA CCATGCCGGT CAAAGGAGT AGCAAGTGCA TCAAATACCT	60 120

ATGGCTCCGA TTCGACTCTC AGACCAAGAG CATCTTCGAG CAAGAGAATA ACCATTCCAG TTTCTACACA GGAGTGTACA TTCTGATTGG AGCCGGGGCC CTCATGATGC TGGTTGGTTT CCTGGGCTGC TGTGGAGCTG TACAAGAGTC CCAGTGCATG CTGGGATTGT TCTTCGGGTT CCTCTTGGTG ATATTCGCCA TTGAGATAGC CGCCGCCGTC TGGGGCTATA CCCACAAGAG TCGAGTCGAG	240 300 360 420 430
(2) INFORMATION FOR SEQ ID NO:659:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 290 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:	
GAATTCGGCC TTCATGGCCT AAGAGTACAG AGATTTCACT TCATCTTGTG CTAATGTTTA ATTNAAAGTA TATTGACACT AGTAAAGACA CTTTATTTTA ATTTGAGGTA TAAATGTCTA CCTAAAATAG ACTATTCCA TTGAGTCATA CATTTTAAAT GTGGTATATA TTCTTATATT TCAGAAAATG ATAACTATCA TAGAAATCTA ATACTCATTA ATTTGATTAA TAATTATTT TTTCCTCAAA TTTGGAAATA TCTTTTCCTA TGTAATGGTC ATGTCTCGAG	60 120 180 240 290
(2) INFORMATION FOR SEQ ID NO:660:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 406 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:	
GAATTCGGCC TTCATGGCCT AGTCAGAAGT CTTTGTGTCC CTGTTTTTGT GTCCATTTCA TGTACCTTGG CACTTTAAGG CTTGTCCTGC AAAATAAAAC ATTGCATCAT CACTTGTGAA GGCAGAGCTT GGGAGTTTGC ACCTGTCAGA TGAGGATAGG AAAGAAATTT ATGCCGCAGG GCCTTTGATG CTGCCCACTC ACCTGTCTGC ACAGCCAGG CACGGCCAGC GGGAGTGGAG AAGACGAGCG AGACCAAAAC CTTGCCGTGG GGAGGAGGGT GGCATAGCCA TTGATAAATC GGGCATGGAC TGATGCCTCA ACTCTAAAAA TATTTTTTAT CTGATTACAA AAGTAATAGA TGGCCAGGCA TGATGGCTCA TGCCTGTAAT CCCCAACACTC CTCGAG	60 120 180 240 300 360 406
(2) INFORMATION FOR SEQ ID NO:661:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 461 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:	
GAATTCGGCC TTCATGGCCT AGTGGAACTG AAAACTCAGA GGAGGCATCA AACCCAGGCT TGGGGGACAA AACTAAGTCT TGCCAGAGTC CTGAAGGATG AACAACAGTT AACCAAGCAA	60 120

GGGATACTGG AGGGCATGGA GGCTCTCTGG CCTGGAGTGC AGAGCATGGA GTGCTCAAAG

AGCTAGTTAG	CTCTGCAAAG	CTGAGTGTCA	GGAATGTAAA	GGGAGAGAAT	AGGAGTGAGA	240
GAAGAGTCTG	GCAAGGCAGA	CAGGGAAGGC	CTATATGCCT	TGATGGAGAA	CCACTGAAGG	300
ATTTAAAGAA	GGAGAGGGTT	AATTTTGTCC	AATAGAAAGA	TCACATTGTG	TGTAGTGTGG	360
AGGATGGGTT	GCAGAGAGAG	AAGCTAGAGA	CCAAAAGATG	AGACGGGAAC	AGCTGCAAAT	420
TTCGAGAGCT	CGTAAGATTA	TGTATGGCTG	GACCACTCGA	G	•	461

- (2) INFORMATION FOR SEQ ID NO:662:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

GAATTCGGCC	TTCATGGCCT	AGCCTGAGCT	CAGGAGTTCA	AGACCAGCCT	GGGCAACACA	60
GTGAAACTCC	ATCTCTACTA	AAATACATAA	AAATTAGCTG	GGCCTGGAGG	CATGCACCTG	120
TGGTCCCAGT	GCTACTGGGG	AGGCTGAGGC	AGGAGAATTG	CTTGGGCCCG	GGAGGCAGAG	180
GTTGCAGTGA	GCCAAGATCG	CGCCACTGCA	CTCCAGCCTG	GGCAACAGAG	CGAGACTCCA	240
TCTCAAACAA	ACAAACAAAC	AAACAAACAA	ACAAAACAAC	AGTTATTTTT	TTCTCACCAT	300
TCTAAAGAAT	GTTACATTTG	ATTCTTTTTC	AAAATTTGGT	CAGTTTTGAT	AGTCTTATTT	360
CTCCATACTT	TCATTCCCCC	TTTTTTTTTC	TGTAAATAAT	TGAACTTTAT	ATTCCTTATA	420
TGATAATTTT	AATATCCAAA	GTCATTGGTC	ATATTCTCCA	GTTCATGATT	TCTGCTGAGT	480
TTGTGGTGCT	GATTTTCTCG	AG				502

- (2) INFORMATION FOR SEQ ID NO:663:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GAATTCGGCC	TTCATGGCCT	ACAACCACCA	ACATTTGTGT	TTTTGCAGAT	GAACAGGTTG	60
ACAGAAGTCC	CACTGGCTCA	GGAGTGACAG	CCCGAATTGC	CTTACAGTAT	CACAAAGGGC	120
TTCTGGAACT	GAACCAGATG	AGAGCCTTCA	AAAGCAGTGC	AACTGGCTCA	GTATTCACAG	180
GGAAAGCTGT	GAGGGTAAGT	GGCACCCTTA	GCTTCTTATT	TATAAATGTG	TCACTCATGA	240
GACTGGAGAG	GCCTGAGTTG	GGTGTTTGAT	AAATTTCTTC	ACTCAGCTCT	CAGAAGAGAA	300
TTTTAAAGCA	GGCCTGTAAA	AACTTCTTTT	CAACTAGGAC	ATTGGTTATC	CAGTGTGGTC	360
TTGGGGCCCC	AGCGGGCCCC	TAAGGTCCTT	TCCATGGGTT	CAGAGGGTCA	AAACTGTGTT	420
CATAATAATG	ACATTATTTG	CTTTTCACTC	TCATTCTCTC	AAGAGTGTAC	AGTGGGTTAC	480
TCGAG						485

- (2) INFORMATION FOR SEQ ID NO:664:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GAATTCGGCC	TTCATGGCCT	AAAAATTATA	AAGTGTAAAA	TATCTTTGTA	TCTCTAGTTT	60
TTCTCCTTTC	CCCAGATAAG	AATAAAAGCA	GGCTGCAGGC	TCCTGGGGTG	ATAACCCACT	120
TGGGTCGAGT	TCCATCGCTG	TTGGCGATAA	ATCTTGTTGG	TGTTCACTTT	TTGGGTTCTC	180
ACTACCTTTA	TGAGCTATAA	CACTCACCCT	GAAGGTCTGC	AGCTTCACTC	CTGAAGCCAG	240
CGAGAGTACG	AACCCACAGG	CAGGAAGAAA	CTCTGAACAC	ATCCGAACAT	TGGAAAGAAC	300
AAACTCCAAA	CAAGCCGCTT	TTAAGAACTG	TAACACTCAC	AACTCGAG		348

- (2) INFORMATION FOR SEQ ID NO:665:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 571 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

GAATTCGGCC	TTCATGGCCT	AGTCGTTATC	AGAGGTGGAG	ACATTTAGAA	GTTGTTCTTA	60
ATCAGAGTGA	AGCTTGTGCT	TCGGAAAGTC	AACCTCACTC	CTCAGCACTC	ACAGCACCTA	120
GCTCTCCAGG	TTCCTCATGG	ATGAAGAAGG	ACCAGCCCAC	ATTTACCCTC	CGACAAGTTG	180
GCATAATATG	TGAGCGCCTC	TTAAAAGACT	ATGAAGATAA	AATTCGGGAG	GAGTATGAGC	240
AAATCCTCAA	TACCAAACTA	GCAGAACAAT	ATGAATCTTT	TGTGAAATTC	ACACATGATC	300
AGATTATGCG	ACGGTATGGG	ACAAGGCCAA	CAAGCTATGT	GTCATGAAGC	TTTGTCACAT	360
ATCTGGGTAC	CAGGTTTGAC	CTCAAGAGAT	GGCTGCTGTA	CACTTTTTGC	AACTGGTTTG	420
ATGTCACATT	TCAGCTCCAA	CTTTGCATCC	TGAGAACACT	TAAACGTTTC	TGCAGGTCCA	480
TTTTATACAA	CTTGAAAGAC	CGTAAAACTT	TCTGGTTGCC	ACAAGCATAT	CTTTCTTTTC	540
TGCTCATCCA	ATAAACAGCT	GAGCCCTCGA	G			571

- (2) INFORMATION FOR SEQ ID NO:666:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GGGATCATTA	TTATTCAGCT	ACTGAGAACT	AGAATATTAA	GAGACTGCTG	GCAAGGCAAG	60
CAGTTAATTT	TCAGTTGAAA	TTGCATTAAA	TAAAAAGTAT	TTTCTTGCTT	TGTGGAAGCA	120
CGTGAATTTT	TGTAAAAAGC	TGCTTGTTTT	CCCCATTTAC	AGGTTCTGTA	CAGAGTAATG	180
AGATGTGTGA	CGGCTGCAAA	CCAGGTGTTT	TTTTCTGAGG	CTGTGTTGAC	AGCTGCTAAT	240
GAGTGTGTTG	GTGTTTTGCT	CGGCAGCTTG	AATCCTAGCA	TGACTATACA	TTGTGACATG	300
GTCATTACAT	ATGGATTAGA	CCAACTGGAG	AATTGCCAGA	CTTGTGGTAC	CAATTATATC	360
ATCTCAGTCT	TGAATTTACT	CACGCTGGTA	TGTGAATTAT	TCTTTTCCTT	TTTAATGTGT	420
TGGTTTATTC	AGGCCCATCT	CGAG				444

- (2) INFORMATION FOR SEQ ID NO:667:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GGGAACTGAC	AAGCAATTAA	CTGGAGAATA	AGTGAGGGGA	ATGGAGCAGT	AGTATTCTTT	60
AACTTAATTT	GCCATTTAAG	AGAGCACTTG	GAATCTGAAG	AAAGTCTATC	CCTACCAAGG	120
AAACGGAGTC	AAATTGCAAT	TAAGATTAAC	TTTGGTTATA	TGGAAGCAAG	AATCATGCTT	180
CTCATCATCA	ATTGCGTCTC	TTTGGTAGCC	AATAATTCCA	TCTGTAATCA	TGGCAGCAAC	240
TTAAGTATTG	CCAATGTTTT	CAAATGTGTT	ACAGCATTAA	GGCATCCACA	TCTAAAGAGG	300
CAGTTTTAAA	CAAGAGGAAA	ACGGAACTGA	AATGTGCCAA	GAAGTGAACA	CGGACATGGC	360
CTCTCCTGGA	ATACTGCCCA	CCATGCCAGC	AAGCTCTTCC	TCCAGTCAAG	AAGGCCTGTG	420
CCACGCTGCT	TGGTTCCCTG	CTGCCTGAAG	ATGCATTTGA	GCCCTATGAG	ATTAGTATGG	480
		GGAGAGAAAT				524

- (2) INFORMATION FOR SEQ ID NO:668:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 554 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GAATTCGGCC	AAAGAGGCCT	ACACAGAGGG	ATAATTGGCA	TTGGTATCAA	CTGACATATT	60
CACAACTTTG	AATAAAACTT	TCCACATTTG	GAAAATCACC	ATGCCTGGCC	CCTAGGCTAT	120
ACTTTGAAAA	CCACTGCTTT	AGTGTTTTAG	AAATTGTTAC	CCTCATACTA	ATATTTACTA	180
CACCCCCCAC	CTTGACAATA	CATACAAAAG	AGGAGTAACA	GTTTCCCATA	ACCTTTCTAA	240
ATTTGAGTCT	TATTAAACCA	GACTCATAGC	CCTTGTTGAC	TTTTCTTCCT	GATCTGTGCC	300
TTATCCCTAG	GGCGGTGATC	ATGCGGGTAT	CTGCTAATTG	GCAGATGTGA	GTGGTTATAC	360
CTATTTACAA	GCAACTCATT	GCAAAAATAA	TTTTAGCTAA	AGAAAACATC	CATGGCCAGA	420
			GAGCTTTATG			480
ATATTTACCA	TTCATGGATT	ACCTTTTTTC	AGAAAGTAAG	AATATATAA	TTACATTTAA	540
TCTTGAAGCT	CGAG					554

- (2) INFORMATION FOR SEQ ID NO:669:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GAATTCGGCC	TTCATGGCCT	AATCGTATTC	CATCTACTGC	ATACTTTTCA	TAGATGTCCT	60
CCATCAGAAG	CACCTATGGT	TGTTTGTTAA	ACGTGTTATT	TCCTGATCCC	ACCCCAGGAT	120
TTCTGAGTAT	TCTAAGAATT	TCTAAGTGTA	AGGCCTGGAA	ATATGCATTT	TACAACCCCC	180
TAGAACATTC	TTATGTGCAC	TAAAATTTGA	GAACCACTAA	TCTGGTGTAT	ATACTGTTGT	240
			GGATGATTTT	TGACTTTATT	ATTATTATAA	300
GCAATGTTGT	AAACATCACA	CAGGCCAAG				329

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 267 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:
GGCGTATGAT ACCTAAAGTG GAGTGGTCGG CGTTCCTGGA GGCGGCCGAT AACTTGCGTC
TGATCCAGGT GCCGAAAGGG CCGGTTGAGG GATATGAGGA GAATGAGGAG TTTCTGAGGA
                                                                      120
CCATGCACCA CCTGCTGCTG GAGGTGGAAG TGATAGAGGG CACCCTGCAG TGCCCGGAAT
                                                                      180
CTGGACGTAT GTTCCCCATC AGCCGCGGGA TCCCCAACAT GCTGCTGAGT GAAGAGGAAA
                                                                      240
CTGAGAGTTG ATTGCACCAG ACTCGAG
                                                                      267
(2) INFORMATION FOR SEQ ID NO:671:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 429 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:
GAATTCGGCC TTCATGGCCT ATTATCTCTC AAAAACAAAG CAATAAGTAC CAAGAAATAG
CAACAAAAAT TAGCTTGTAA GGTTGGTTTC TGAGGGTAGA AATGGCTCTT GATGCCATGT
GGAGCAATGG GAAGGAGGCT TTCTAGTTAC ACAGACTCTT GGTCCTGCCA CTTATTCATT
                                                                      180
TTATTTTATT TTATATTTTA CTTTAAATTT TTTGAGATAG GGTTTCACCC TGTCGCCCAG
                                                                      240
GCTGGTGGGC AGTGGCTCAC TGCAGCCTCG AACTACCAGG CTGAAGTGAT GCTCTTACCT
CAGCCTTTCG AGTAGTTGGG ACAACAGGTG CACACCACCA TTCCTGGCTA ATTAAAAAAA
                                                                      360
TTTTTTGTG GGAACATGGC AAGACCTTGT CTCTATTAAC AACAACAGCA ACAGCAACAA
                                                                      420
CAACTCGAG
                                                                      429
(2) INFORMATION FOR SEQ ID NO:672:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 357 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:
GTAAAATCGT TCTTGAGAGG AACGTCTCTG TGCGAAGAGA TAATGAGTTT AGCTCTGAGA
AGTGAGCTTG TAGTGGACAA AACAAAGAG AAAAAAAGAA GAGAACTGTC TGAGGAACAG
                                                                      120
AAACAAGAAA TTAAAGATGC TTTTGAACTA TTTGATACAG ACAAAGATGA AGCAATAGAT
TATCATGAAT TAAAGGTGGC AATGAGAGCC TTGGGGTTTG ATGTAAAAAA AGCTGATGTA
                                                                      240
CTGAAGATTC TTAAAGATTA TGACAGAGAA GCCACAGGGA AAATCACCTT TGAAGATTTT
                                                                      300
AATGAAGTTG TGACAGACTG GATATTGGAA AGAGATCCCC ATGAAGAAAT ACTCGAG
                                                                      357
(2) INFORMATION FOR SEQ ID NO:673:
      (i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 292 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

GGTAGATACT	GGTTTTTCGT	ATCCTGCTTC	TCTTAAGGGC	AGCTCTTTTT	AGCATACTCC	60
CATGCAGCAA	CAGAAATTTG	TATCTTTTTT	TTCTTTTTTG	AGATGGAGTC	TCGCTCTATC	120
ACTAGGCTGG	AGTGCAGTGG	CACAATCTCG	GCTCACTGCA	ACCTCTGCCT	CCTGGTTCAA	180
GCGATTCTCC	TGCCCTAGCC	TCCTGAGTAC	CTGGGACTAC	AGGTGCGCGC	CACCACACCC	240
AGCTAATTTT	TATATTTTA	GTAGAGACGG	GGTTTTACCA	TGTGGCCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:674:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GGATGGACAT	CAGCACTTTA	CGGCGCCAGC	TGAGACCCAC	AGGCCAGCTC	CGTGGAGGGC	60
TCAAGGGCTC	CAAGAGTGAG	GATTCGGAGC	TGCCCCCGCA	GACGGCCTCC	GAGGCTCCCA	120
${\tt GTGAGGGGTC}$	TAGGAGAAGC	TCATCCGACC	TCATCACCCT	CCCAGCCACC	ACTCCCCCAT	180
GTCCCACCAA	GAAGGAATGG	GAAGGGCCAG	CCACCTCGTA	CATGACATGC	AGCGCCTACC	240
AGAAGGTCCA	GGACTCGGAG	ATCAGCTTCC	CCGCGGGCGT	GGAGGTGCAG	GTGCTGGAGA	300
AGCAGGAGAG	CGGGTGGTGG	TATGTGAGGT	TTGGGGAGCT	GGAGGGCTGG	GCCCCTTCCC	360
ACTATTTGGT	GCTGGATGAG	AACGAGCAAC	CTGACCCCTC	TGGCAAAGAG	CTGGACACAG	420
TGCCCGCCAA	GGGCAGGCAG	AACGAAGGCA	AGTCAGACAT	CCAACTCGAG		470

- (2) INFORMATION FOR SEQ ID NO:675:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 637 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GAATTCGGCC	AAAGAGGCCT	AGTCGCTCTT	GCTGAAACCT	TCAATGCAGT	GAGCGCCCAT	60
CTCATTGGGA	CCTACAGGCT	GAAGTTCTTC	CTCTGATGGA	CATGACCCCC	GTGTTGTCTC	120
TAATAACCTC	ACTTTCACTC	TGTTCCAGCC	ACACGGGGTT	TCTGTCTTTC	TCGGGTCATG	180
TCGGGCTTAT	GTGCCTCGGG	CCCTTTGCTC	ATGCTGTTCT	CTGCCTGGGA	TGCGCTTTAC	240
TGGGTGCCAG	GATGGTCAGT	GATTCCATTT	CTCTCAGAGT	CTATTCACAG	GTCCCCTTCT	300
CGGTCACGCC	TTCTCTGGCT	CCACTGTCTA	AAATTTCAAC	AGCTGCCTCT	GCCCCCGAA	360
CTTCATATCC	CCCTTATCTG	CCTTTTTTCC	TTCAGCTCTT	ACTTCCATCA	AATACAGTAT	420
GTATTTTTAA	AAGTCTTATC	TTGTTCACGG	TCATTTTCTT	CCACAGGTAA	TTTTGGTAAA	480
CTTTGTAAGA	TTGATGATGT	TTAATACTGT	TTTGTTTAAT	ACAGTACCCC	CAGTTTAGCA	540
CACAGCTTTT	GAATGAATGA	CCAGTTTTTA	TTCCCCTCTG	AAGCGCTAAG	AGCTGCCGCT	600
GAGGTGGCAT	CTGTAGCNGC	TCCCGCTCCA	ACTCGAG			637

- (2) INFORMATION FOR SEQ ID NO:676:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

GAACACGTCA	TGAGGAAGGA	GCAGCGCAAG	GAGGAGAAGG	AGAAGCGGCG	CCTCGACCAG	60
CTGGAACGTA	AGAAGGAGAC	GCAGCGCCTA	CTGGAGGAGG	AGGACTCCAA	GCTCAAGGGC	120
GGCAAGGCGC	CGCGGGTGGC	CACGTCCAGC	AAGGTCACCC	GGGCCCAGAT	CGAGGACACG	180
CTGCGCCGAG	ACCATCAGCT	CAGGGAGGCC	CCGGACACAG	CCGAGAAAGC	CAAGAGCCAT	240
CTGGAGGTGC	CGCTGGAGGA	GAACGTGAAC	CGCCGCGTGC	TGGAGGAGGG	CAGCGTGGAG	300
GCGCGCACCA	TCGAGGACGC	CATTGCAGTG	CTCAGCGTGG	CGGAGGAGGC	GGCCGACCGG	360
CACCCAGAAA	GACGCATGCG	GGCAGCCTTC	ACAGCCTTTG	AGGAAGCCCA	GCTGCCGCGG	420
				AACAGCTGCT	CAAGAAGGAG	480
TGGCTCCGCT	CTCCTGACAA	CCCCAAACTC	GAG			513

- (2) INFORMATION FOR SEQ ID NO:677:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

GTCCATCCTG	AGCTCCATGG	AGAAGCCACC	CAGCCTCGGT	GACCAGGAGA	CTCGGCGCAA	60
GGCCCGAGAA	CAGGCCGCCC	GCCTGAAGAA	ACTACAAGAG	CAAGAGAAAC	AACAGAAAGT	120
GGAGTTTCGT	AAAAGGATGG	AGAAGGAGGT	GTCAGATTTC	ATTCAAGACA	GTGGGCAGAT	180
CAAGAAAAAG	TTTCAGCCAA	TGAACAAGAT	CGAGAGGAGC	ATACTACATG	ATGTGGTGGA	240
AGTGGCTGGC	CTGACATCCT	TCTCCTTTGG	GGAAGATGAT	GACTGTCGCT	ATGTCATGAT	300
CTTCAAAAAG	GAGTTTGCAC	CCTCAGATGA	AGAGCTAGAC	TCTTACCGTC	GTGGAGAGGA	360
ATGGGCCCCC	CTCGAG					376

- (2) INFORMATION FOR SEQ ID NO:678:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

GAATTCGGCC	TTCATGCCTA	GCAGGAGGTT	TTATTGTAAA	GAGGCCGATT	GTACAGAGCA	60
					TGGGTGAAGG	120
ATGAGGGGTG	GCATCGCCCC	ATCCAGGCAG	TGGGCAGGGC	AGGGAGGACT	AAACGGCTGC	180
			TGGGTAAGAG			240
GATCCAGGAG	AATATAGCAG	GAGACCCTCA	CCACCCCACA	CCATGCCCCA	AGGATACGGG	300

AGGTGCCCCA GTCTGGCTTT TGCAGTCGGC CAGCTCCCAG CCTCCTCGAG

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:	
GAATTCGGCC TTCATGGCCT AGTTCTCACC GGGGAAAAAC CCACTGTTAG GATGGCATGA ACATTTCCTT AGATCGTGGT CAGCTCCGAG GAATGTGGCG TCCAGGCTCT TTGAGAGCCA TGGGCTGCAC CCGGCCGTAG GCTAGTGTAA CTCGCATCCC ATTGCAGTGC CGTTTCTTGA CTGTGTTGCT GTCTCTTA^A TTAACCGTGC TGAGGCTCCA CATAGCTCCT GGACCTGTGT CTAGTACATA CTGAAGCGAT GGTCAGAGTG TGTAGAGTGA AGTTGCTGTG CTGAACTCGC GTACCCCGTA GATACATTGT GCAACGTTCT TCTGTTATTC CCTCGAG	60 120 180 240 300 357
(2) INFORMATION FOR SEQ ID NO:680:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 250 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:	
GGGGGTGGAA GGCGTAGTGC TTGAAATGCA GGGATCTGGC AGTCAGCAGA AGGATCTGAG ACCCAGTGTC GAGGTTAAAA AAAAAACAAA AAACCAAAAA CCAATGCAGG AATCCAGTGG FTGGAGTGAG GGGATCTGGG ATCCAGTGAT GGGGGCCCCA GGATCCAGGC ATTGTGGTTG FCAGGATCCA GTGGTGAGGT TTGTTGACAT CCAGAATCCA GCAGCTGAGC TTGGAGATCC AGGGCTCGAG	
(2) INFORMATION FOR SEQ ID NO:681:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 406 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:	
GGATTCCTAC AAAAATTGAG GCAGAAGATC AAAATCGAG TGGTAGGCGG ATCGGACTTT AAGAAAGTGC AGGAGCAACT GGGAAATGAT GAATATTCAA AGTCATCTGG GTGAGGCCCT AATCCAAGAT TTAATCAACT ACTGTCTGAG CTACATTGCG AAAATTAAAC TCCCGAAGAA GAGGGGTACT TTCATTGAAT TCCGAAATGG GATGTTAAAC GTGTCCCCTA TTGGAAGAAG CTGCAGCCAA GAAGAACGCA TTGAGTTCTA CGAACTCGAT AAAAAAGAAA ATATAAGACA AAAGTTTGTA GCAGATCTAC GGAAAGAGTT TGCTGGAAAA GGCCTCACGT TTTCCATAGG AGGCCAGATC AGCTTTGATG TCTTTCCTGA TGGATGGAAA CTCGAG	60 120 180 240 300 360 406
317	

- (2) INFORMATION FOR SEQ ID NO:682:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

			GTGTCATCTC			60
			GCCTGACTTA			120
GGAGGGGCCC	TGGCCCCCAC	TGACCCAGCA	TTGCTATCCA	CAGGAGGAGC	AGCCCCCACA	180
ACATCGATCC	AAGAGGGGG	GCTCAGTGGG	CGGCGTGTGC	TACCTGTCGA	TGGGCATGGT	240
CGTGCTGCTC	ATGGGCCTCG	TGTTCGCCTC	TGTCTACATC	TACAGATACT	TCTTCCTTGC	300
GCAGCTGTCC	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:683:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

			TAGACCTGCC			60
GATTACAGGT	${\tt GTGAGCTAGC}$	ACTCCCAGCC	GACAGGTGCT	TCTTAAATGT	TTTCTTTGAG	120
			TTAGAAGGAA			180
			GTTATTAGGA			240
			TGTGTAAATA			300
GACAAACACG	TGTATGCACA	TTTCACAATG	GAGGAAGAAG	GGATATGGTG	TGCACTGAGG	360
TAAAGTGAGC	AGGGATACAG	AAGAGAAACT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:684:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

GTCCTAACCT	TGGGTCCAAG	TTTCGTTATA	GTGGCAGGAC	ACAAGCGCAA	ACGAGAAGAG	60
CCAGTGCGTT	GATAGATCGC	CCAGCACCTT	ACTTTGAACG	CTCATCCAGC	AAACGTTATA	120
			TGAATGAAAA			180
ATTCTATGTC	TGCTGCAGAG	GTTGGTACTG	GCCAGTACGC	CACAACAAAA	GGCATCTCTC	240
AGACCAACTT	GATCACCACT	GTGACTCCGG	AGAAGAAGGC	TGAGGAGGAG	CGGGACGAGG	300
AAGAGGACAA	ACGGAGGAAG	GGGGAAGAAG	TCACGCCCAT	CTCGGCCATC	CGGCACGAGG	360
			CAGCCGACGG			420
CGGACCAGGA	GGAAGATGCA	GAGCTCAAGG	CACAGGAGCT	AGAAAAAACT	CAAGATGACC	480

TGATGAAACA TCAAACCAAC ATTCTCGAG

(2) INFORMATION FOR SEQ ID NO:685:

(i) S	SEQUENCE CHARACTERISTICS: (A) LENGTH: 441 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:685:	
GCCTCTTTCT 1 TTATATGATT 1 TTGGGTGCTG C TTATTTTCAT # CCTTTTCTGC # GAAGGAATGG # CCTTTNACCC C	TTCATGGCCT ACCAAAGTGC TAGGATTACA GGCGTGAGCC ACTGCGCCTG TCTTTCTTGA ATTCTCTTCT TTTTATGTTC CTGGGAAAAT CCTACTCATT TGGCTGATGT AAAGCCACCA TTGTCTTCCT AAGCAGAGAG GGTCTTGCTT CACAACTTTG TGCAATTTTT CTGTTACATC ATTTATCTTT TGGGGATTGT ACTTATCTCT CTTCCAGGAC CATGTTAGGG AGAGGTGTTT TTAATTTTTA AGCACTTAGC ACAGTGCCTA ATCATAGTAA ATATCACGTA AAAGTTGAAT ATGTTTGATA TAGAGTTAGG ACACCTGTGT CCAGGTCTGG CTTTGCTTTT CCCCACCTCGA G	60 120 180 240 300 360 420 441
(2) INFORMAT	FION FOR SEQ ID NO:686:	
(i) S	EQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:686:	
GTGCTGAAAT G AGGAGAGAAA T GGATAGTGCC A	TTCATGGCCT AGTTGGTTTA TGTTATGTAA AGTTATGTAG TTATGTAAAG STCACTCTG TGATTATGTT TTATTATATA AGGCTCTATC TTAGCAAACC STCTCCTGAT GGCCTTGAAG AAGCAAACAG CCACCTGGTT AAGCCCCTGT AAGTGGCAGG AAAGTGGGAG CCACCTCTAG GACCTGAGGA TTAAAGTCAG BACCTCACTC ATGCAGACTC GAG	60 120 180 240 273
(2) INFORMAT	TION FOR SEQ ID NO:687:	
(i) S	EQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:687:	
	AAAGAGGCCT AGGGCTCTGG ATTTTGAGTT TCGGGCTCTA GATGGAATTG ACTTGCTCAG AGGGCCCTGG AGGCTCATCT GACTTCACCC GGATTTTCCT	60 120 124
(2) INFORMAT	TION FOR SEQ ID NO:688:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:	
GAATTCGGCC AAAGAGGCCT ATGCCATCTT AGTCCCTCTT CCCAACCCCA TTTTTTAGTT ACTTTCCTTT CATTAAAATA TCCTTATGCA CTTACAAATA AAACTAAGTC CCAAGAGGGC AACAAAATAT AAGATCTTT ATGATACAAA AACAAATCTT TCTGATACTA GATCTTTAT ACTAGAAAAA TAAATTCTTG TGCTTGAACA TCATTTTTAA GCACTTAGTG AATTGAGAAT CTGAACTGCC ACTTGAAATA TTCCCGGGAA AGAAACATTA TGAACCAAAT GAAGGAACAT AGCTATTCAA AGGGACATAT TTTTGTACTT GTTTTGCTCC AATTTCTGCT ACATAGACTG CTCCAGTCTT TCTGTCGACT CTAGGAGATG CCTAAAACCGT CGATTGAATT CTAGACCTGC	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:689:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:	
GAATTCGGCC AAAGAGGCCT ATAGTTTTT CATGTTACAT CTTTTAGATT ATTTTCTTTT TAATCTATCT GTGACTATAT TTAAAGTCAA TTCTTGTTTT TTCCTTTTCC TTTTTGTGGG TAACGGGGTC TCGCTGTGTT GCCCAGGCAG ATCTCAAACT CCTGGGCTCA AGCTGTCCTC CCACCTCTGC CACCCTAGGC TCGAG	60 120 180 205
(2) INFORMATION FOR SEQ ID NO:690:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:	
GAATTCGGCC AAAGAGGCCT ACGTTGATTG AGCACTGAGC CCTTACTACG TGCTAGGCAT GGTACATGCA TGGCCTTATT TAATCCTATC AACCCTCGAG	60 100
(2) INFORMATION FOR SEQ ID NO:691:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 302 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
320	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

GAATTCGGCC	AAAGAGGCCT	ACATCATACA	AGTCGTCGTA	AAGCAAATCT	GAGCTGTTGT	60
CATTGGAAGG	CACTTTAGTT	TTGATGCAGT	ATTCCGCCAG	GGTTGTGGGG	ACCTTCACTC	120
CATCCTTTTC	TGCTTCGGCC	TTAGTGGCTG	AAACTTGTTT	CCTAATAATT	TCAGCATATT	180
CTTTGTCTTT	TCCTTTACTG	TCTCTCCATT	TCCTGAACAT	AACTGAAGCA	TCGACATTGG	240
	GGTGTTGGGC	TCATTAAGCA	GTGAGATTAC	ACTTAATAGG	ATAGTCCTCG	300
AG						302

- (2) INFORMATION FOR SEQ ID NO:692:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 662 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

GAATTCGGCC	AAAGAGGCCT	ACCAAATACC	AGGCTACCAT	GGTCTACAAG	ACTCTCTTCG	60
CTCTTTGCAT	CTTAACTGCA	GGATGGAGGG	TACAGAGTCT	GCCTACATCA	GCTCCTTTGT	120
CTGTTTCTCT	TCCGACAAAC	ATTGTACCAC	CGACCACCAT	CTGGACTAGC	TCTCCACAAA	180
ACACTGATGC	AGACACTGCC	TCCCCATCCA	ACGGCACTCA	CAACAACTCG	GTGCTCCCAG	240
TTACAGCATC	AGCCCCAACA	TCTCTGCTTC	CTAAGAACAT	TTCCATAGAG	TCCAGAGAAG	300
			AAGGCACAAA			360
			TAACAACCAC			420
			TGTCGCAGTC			480
			CCTCATCCCT			540
			GCTCCACTGT			600
GAGCTCCAAC	TGCACCAGAG	TCCCCGACAG	AGGAGTCCAG	CTCTGACCAC	ACGACCCTCG	660
AG						662

- (2) INFORMATION FOR SEQ ID NO:693:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

GAATTCGGCC	AAAGAGGCCT	AAGCCCCCAA	AACACGCTCT	TTTGTGCCTC	CCCTCAAATC	60
CTTCACAGTG	TTCTTCCATA	TCCACTCCTT	CCAGGAAGCA	TGTTCTCACT	ACCCCAGTTC	120
ATGTGGGTTT	CTTCCCTCTC	AGAATTTCTA	TCATGCCCCT	ATAAGTTTAG	CAAATTGTCC	180
TTCTCTAATT	GTTTCACATC	TGTCCATCCG	ATATCCCAGG	AGGACTGTCA	GCTCTATGAA	240
GGCAGGGGTT	GTCTTTCCTT	TACCATGCCT	ACCATGCCTT	ATAGTGTTAA	TAAATTAACC	300
TACCCAGAAA	TGTTTCTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:694:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 357 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

GCGATTGAAT	TCTAGACCTG	CCTCAATCCC	CTCCCTACTT	GCTTTTTCTT	AGCATATAAA	60
AGTCCACAAG	TTTTACTCAT	CTTTTTAAAA	AACGAAAACA	TCCTTAGACC	GTGTCCTCCA	120
TTAGTTGCTA	TCCTGCCTTC	TTCTCTCAGC	TGAGCTGTCT	GAAACATGCT	AACATGCTTA	180
TACAATACTT	GCTGTCCTGC	CTTCTGCTCT	CAGCTGAGCT	CTCTGAAACA	TGCTAACATG	240
CTTATACAAT	ACTTGCTGTC	CTGCCTTCTC	CTCTCAGCTG	AGCTCTCTGG	AACATGCTTT	300
TTATACAATA	CTTGCTGTCC	TGCCTTCTTC	TCTCAGCTGA	GCTCTCTGGA	ACTCGAG	357

- (2) INFORMATION FOR SEQ ID NO:695:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GAATTCGGCC	AAAGAGGCCT	ATGGGTTTTT	AAAAATTTTG	TTTTTATTTT	TTCCTTTGAT	60
GTGCAGAGGC	TGTTTACTTT	GATGCAGTCT	${\tt CACTTGTTTA}$	TATTTTATTT	TGTTGCTGGC	120
CTAGGCCTCT	TTGGCCGAAT	TCGGCCAAAG	AGGCCTAGTC	GGGTGTGGCA	GTGCCATTCT	180
GCAGTCCCAG	CCACCGGGAA	GACCGAAGCG	GGAGGATCAC	TCGAG		225

- (2) INFORMATION FOR SEQ ID NO:696:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3:14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - ,,,
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

GAATTCGGCC AAAGAGGCCT	ATCCGCTTCT	GTTGCAGCTG	GCGGTGCTCG	GCGCGGCGCT	60
GGCGGCCGCA GCCCTCGTAC	TGATTTCCAT	CGTTGCATTT	ACAACTGCTA	CAAAAATGCC	120
AGCACTCCAT CGACATGAAG	AAGAGAAATT	CTTCTTAAAT	GCCAAAGGCC	AGAAAGAAAC	180
TTTACCCAGC ATGGGACTCA	CCTACCAAAC	AACTTTCTGT	CGTTGTGCCT	TCAAACAATG	240
AAGAAAACG GTTGCCTGTG	ATGATGGATG	AAGCTCTGAG	CTATGTAGAG	AAGAGACAGA	300
AACGAGACCT CGAG					314

- (2) INFORMATION FOR SEQ ID NO:697:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

CCCGTCACAG GGCTGGAGGT GTGGCCGGCC CACTGGGTTG TGCTTTCTGC CGTACGTCCC 120 TTCCCATGAG GATGAGATGA CCCATCTGTT GCATCCCGGC TGCTGATAAA ACAAGACCCT 180 CGGAGCCAAG AAACAACACT GAGTTCCAGA TTTCGGAAGG TTCACGAGTG TTGCCGACAC 240 GCCCTCCCAA CTGCAGACAT CCTCCCTGGA GGACCTGCTG TGCTCACATG CCCCCCTGTC 300							
TTCCCATGAG GATGAGATGA CCCATCTGTT GCATCCCGGC TGCTGATAAA ACAAGACCCT 180 CGGAGCCAAG AAACAACACT GAGTTCCAGA TTTCGGAAGG TTCACGAGTG TTGCCGACAC GCCCTCCCAA CTGCAGACAT CCTCCCTGGA GGACCTGCTG TGCTCACATG CCCCCCTGTC 300	GAATTCGGCC	TTCATGGCCT	ACAGAGTGTG	GACGGCCCAC	TGGGTTGGTG	GTGGTGGGTG	60
CGGAGCCAAG AAACAACACT GAGTTCCAGA TTTCGGAAGG TTCACGAGTG TTGCCGACAC GCCCTCCCAA CTGCAGACAT CCTCCCTGGA GGACCTGCTG TGCTCACATG CCCCCCTGTC 300	CCCGTCACAG	GGCTGGAGGT	GTGGCCGGCC	CACTGGGTTG	TGCTTTCTGC	CGTACGTCCC	120
GCCCTCCCAA CTGCAGACAT CCTCCCTGGA GGACCTGCTG TGCTCACATG CCCCCCTGTC 300	TTCCCATGAG	GATGAGATGA	CCCATCTGTT	GCATCCCGGC	TGCTGATAAA	ACAAGACCCT	180
	CGGAGCCAAG	AAACAACACT	GAGTTCCAGA	TTTCGGAAGG	TTCACGAGTG	TTGCCGACAC	240
CAGCGAGGAC GACACCTCCC CGGGCTGTGC AGCCCCCTCC CAGGCCCCTC GAG 353	GCCCTCCCAA	CTGCAGACAT	CCTCCCTGGA	GGACCTGCTG	TGCTCACATG	CCCCCCTGTC	300
	CAGCGAGGAC	GACACCTCCC	CGGGCTGTGC	AGCCCCCTCC	CAGGCCCCTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:698:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

GAATTCGGCC	TTCATGGCCT	AGATTGACAG	AGGTCAGTTG	TCACTTCTTG	CCTCTCTCCC	60
CTTCCAGCAA	CATGTATAAT	CCTGTGAGTG	TTTCTTCAGC	ACCCTTCTCT	GTTGTTTACA	120
CTACTGCAAG	AGCCTCCCTA	AGTGGTCTGC	CTGTTTCCAC	CCTGTTGTCT	TGGAATTTAG	180
TTTTCTCGCA	AAAGCCAGAG	AATGTTTTCA	GAAGGTAGCT	CTTGAGCAAC	TTCCCACTTT	240
CTTGGAGGGG	AGATCCAGCT	TCCCCAACAA	GACCAGCAGG	CCCCTGTGCG	GCCTGGCTCC	300
TGTTCACCCT	ACCAGTCTTG	GCTCAGGCTC	ACGGCTGGAA	TATGCCGAGC	TCTTTCTTGT	360
CCTGGGGCCT	TTGCACTTGG	CTTCCCTCTG	TCCAAAATCA	TCTTCCTGTA	GCTTTGTGCT	420
TGCCTAGCTC	ATCATCATAG	CAGCTCGAG		•		449
TGCCTAGCTC	ATCATCATAG	CAGCTCGAG				449

- (2) INFORMATION FOR SEQ ID NO:699:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GAATTCCCCC	TTCATGGCCT	ACAGAGAACT	CACCAAAACC	N N CTIN COTTOC	ስር እስጥርጥር አ ል	60
						00
AGAAAAAAGC	GAGGGAGAAG	CTTCACTGTA	TGAAGATAGA	ATAATAACAA	GAGAGAAGGA	120
CATGAGGAGA	GTGAGAGATG	AGCCCGAGAA	GGTGGTGAAG	CAGTGGGACC	ATAGTGAGGA	180
TGAGAAAGAG	ACAGATGAGG	ACGATGAGGC	TTTTGGGGAA	GCTCTGCAGA	GCCCAGCAAG	240
CGGAAAGCAG	AGTGTGGAAG	CAGGAAAAGC	CAGAAGCGAT	TTGGGAGCAG	TTGCCAAGGG	300
CCTGTCAGGA	GAATTAGGCA	CAAGATCAAG	AGGGCTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:700:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GAATTCGGCC	TTCATGGCCT	AAGCCAAGCA	AGGCTGTACC	TTTAATTACT	GCTGCCCTCA	60
TTTGCATCTG	GCTGCCCTCA	TTATAGTGCT	ATTAGCAGAG	TGCAGGGGTC	CTCCTGCTGG	120
CCCATCGGGA	GTGGTGCGTG	CACAGTTGTG	GGGCCTTGCT	TTGGTGGTCT	TTGCTGCCTT	180
CTGGGCAAAA	TGAAGGATTT	GGAGTAGACA	GCAAGCAGGC	ATACATCCTG	GGCCAGAAGC	240
AGCCTGCGGA	GCTCATCGTG	GCTTGCCTTA	AATTGTTTCT	CAACAATAAA	GTTGTTGAAA	300
AACAATTTGT	GTTTTCTTTC	TCCTTATTAA	AAACCCAAAA	TTATATTCAT	TATAGAAAAT	360
TAAAGAAGAT	AGCTCTCGAG					380

- (2) INFORMATION FOR SEQ ID NO:701:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GAATTC	GCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCAGCCTCCC	AAAGTGCTGG	60
GATTATA	AGGC	GTGAGCCACC	GCGCCCAGCC	GAAAATCTAA	AGATATTGAA	AAGATACAAA	120
GGAGCA	CATT	ATGAACATTT	TTTTCGTATC	ACTGAGTATT	TTATAACTGC	ATCATTGATT	180
TTAAAA	TAAE	TCATGACTTT	GAAAACTAAT	ATTCTACAAA	GTAGCTTTTG	ATTTAACATG	240
AGATTT:	ATAT	TATGTGCTTA	TCTTGGTTCT	CTATGAAACC	CCATTGAAAT	AAGAAAATGT	300
AAACAC	CAGC	CAACTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:702:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GAATTCGGCC	AAAGAGGCCT	AATAGTCAAG	ACCTTTGCAG	TTTTGATCAC	AGAAATATGA	60
AAGATTACAC	AGCTACAGCT	ATATGAATGA	TAAAAGTGAC	AGCTATGGAT	TTTTAAAGTT	120
		TATGTAATGT				180
TATATTTATA	CACACACTAT	ACATGTATTT	TAAAATATTG	AAAATCCAGA	ATTATTTAT	240
GGTAAAAATT	ACTAAAATTG	ACTTCACATG	CTGAATGAAG	AGAGCCTGAG	TAGACCAACA	300
		GGTTAGAAGA				360
		CCTACTCTCC				420
GAACCTAATT	TTTTACAAGT	AAAATCTTTG	AAGAATTGGT	AATTGCTAAA	TTTTTCCAAC	480
ATACTATTCT	ACAAGACTAA	CCTAAAACTG	ATTATAAGAA	CTAGGTGAGG	AGGGCCGGCA	540
AAACTCGAG						549

- (2) INFORMATION FOR SEQ ID NO:703:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 758 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GAATTCGGCC AAAGAGGC	CT ATCGAGCCAC	TGCACCTGGC	CGATGTGTTC	TGTTTGAAAT	60
CTTACTCAAA AGTATTTG	AA GAGTTGTGTA	TAGTTGTATG	GATATGTCTG	TAGTAAACAG	120
AAACAAATTG CTTCAGTT	TC TCTTTACTTA	TTTTCTAGGT	TACAGTACCT	TTACCAGCAT	180
CCCAGCTTTC CTTGCCTA	AT TTTGGATCTA	CAGGGCAACC	TCTAATTGCT	TTGCCTCAGA	240
CTCTTCAGCC CCCATTAC	AG CATACCACTC	CCCAAGCACA	GGCTCAGAGT	CTGAGTCGTC	300
CTGCACAAGT AAGCCAGC	CT TTCAGAGGAT	TAATTCCTGC	TGGAACACAG	CATAGCATGA	360
TTGCAACCAC CGGAAAAG	TA AGTAAAGAGA	CATTTGCACA	GGTTATTTGA	GAATTTAAGG	420
TAGTGTGTTC AGATATAT	GC ATCTGTGTTA	TCTAAAAAAC	TAAAATGCGT	CAGTTTTTAC	480
CACCCTGCAA AAATCTCA	AA CCCCAGTATA	TTTACATTTT	ATCTATTTAC	TTTTAATGTG	540
TTTGGCCCCA TCTAGTTT	тт асстаатаас	AAAGAATTCA	CAAATTTATT	GGAAGAATTG	600
GATTTATAGT GTCTCTTC	GG CTTATTTAAT	TATAAGTCTG	TTTGGTCAGG	TAATTCCATA	660
ATACTTGAAG CCTAACTA	TA GGAGTTTTGT	ACTAAGGTTC	TTTGCCCTTT	CCTAGATTAC	720
GTCTTCACGT ATAGGACA	TG TAAACACAGC	AACTCGAG	•		758

- (2) INFORMATION FOR SEQ ID NO:704:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 663 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

GAATTCGGCC AA	AGAGGCCT AAGA:	GGCCT TCCCAT	GTTA TGGCTAC	ATG GCTGTGATA	4 60
CAAGTAGAGT TA	TGTGTCTG CGCT	CTAAAC TCACTO	SAGTC TTGCAGG	ATG TAAACATCC	120
AGCTCAGCCT AT	CCTTGACC AAAG	ACANT CATGCT	CCTT ACAAACT	CCA ACCAGCCTG	180
ACACTGGGAG GA	GCGCGTGC TGGG	TAGAG CCACAG	SAATT TTGTACCO	GTT GGCAGCAGG	240
AGGAGCCTGG CC	CCTCCTTT CCTA	GTAGA ATCTG	BAATT CAATCTG	rga ggtgggaag	300
ATATACTAGG AG	GACTTTCA CTCT	SCTGAG TCCCTC	STTCC CGCTCCC	TTT TTTTTCCTT	r 360
TTGCCCAATA AA	CCCCTTTA TTCT	CACACT TCAAA	TTGTC TGTGAGA	CTA ATCTTTTGT	420
GCCATGTGAC AT	GGACCCTG TCTG	PAGCTG AAACTA	AAGAA AAAGCCC	CTC CCGCACAGT	480
TGATGTTTCC TC	AGTCAGAC ACTG	CAAGCT GTGAT	STTGG GGTGAGT	ACA GGATATITG	540
CAATATTTGC AG	ACAGTTTT GGCT	etcaga gagga	AGATG CTGTATG	CAG ACACACTTG	\$ 600
CAGCAATAAC TT	AAGCCCAC CCTG	GACTG ACTCT	CATG GTGATGC	ACC TGAAGGCCT	660
GAG					663

- (2) INFORMATION FOR SEQ ID NO:705:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

325

GTGGTGGAAT	TACAGGCGTA	AGCCACTGCG	CCTGGCCCCA	AGTGTCCATT	TTTTAATTTA	120
					TTACATGAAA	180
					CAATCTGAGC	240
				_	ACAAAAATAT	300
		GAAACTGGCT				
	TI DIE CASTOIN	Oranic rooc r	COAG			334

- (2) INFORMATION FOR SEQ ID NO:706:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

GAATTCGGCC TT	CATGGCCT A	CCGAGCTTC	AGAGCATCAG	CAGTGTTCCT	CCTTCACTGT	60
GACGCTTGTC CT	CACTTCCC A	GGTGAGGAG	TCTAAGAAAA	CAGCCTTTCC	ATCAGCCCCT	120
GTCGTGACAG AC	CCTCCAGT G	GGATGGTAG	TGGCTGCCTC	ACCCATTTAC	AGGGCAACCC	180
AGTTTTGCTC CT	TCTGCCTT G	AAATTTGTT	CCTCCCAGAA	ACTGTCCCTC	ACAAGGCATG	240
AACAATCAAT AG	AAGATATA C	GTGGTCTTC	CCAGCACTAC	AGCTGCAGAA	TGAGCTGTGG	300
AGTGCCCCGT CC	GGAGTCCT G	AACAGCTTC	AAACTTTTCC	CCTTTAGAAA	TGCCTAACAC	360
GCCCTCGAG						369

- (2) INFORMATION FOR SEQ ID NO:707:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GAATTCGGCC	TTCATGGCCT	AGGCATCCTT	GGTGCGGCAT	CCTTGGTGCA	TTATATCAGG	60
AGGCAAATGA	TGTGGGTTTG	TCCCATTGTT	TGTAATGGTA	ACATTGGTTG	CTTGGTTAAG	120
GTGAAGGGTG	CCAAGCTTCT	CCACTGTAAA	GTTCCTATTT	TTTTCTCTGT	AATTAATAAG	180
TAATTTGTAT	GATACTTTGA	GATAACAAAG	TAGACTGTTC	ATCAAACTTT	CATCAATGAA	240
TTTAACATCC	AAAGACGCCT	CAAGAATGAT	CATCAAAAGC	AGCCTACTAA	TGACTGTCAT	300
TTACCATTTA	ATACATTTCA	AACAGTGCAC	GTGCTCTGTG	ACATATTCTG	GGAAGGAATC	360
TCGAG						365

- (2) INFORMATION FOR SEQ ID NO:708:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

GAGCAAAGAG	CATGAGAAGC	TGATGGAGGG	AGAACTTGAA	GCTTTGCGGC	AGGAATTTAA	120
AAAGAAAGAC	AAGACGTTGA	AAGAGAATTC	CAGAAAGTTG	GAGGAAGAAA	ATGAGAATCT	180
CCGAGCAGAG	CTACAGTGTT	GTTCTACACA	ACTGGAATCC	TCTCTCAACA	AATACAACAC	240
CAGCCAGCAA	GTCATCCAAG	ACTTGAATAA	AGAGATAGCC	CTTCAGAAGG	AGTCCTTAAT	300
GAGCCTGCAG	GCCCAGCTGG	ACAAAGCTCT	GCAGAAGGAG	AAGCACTATC	TCCAGACTAC	360
CATCACCAAA	GAAGCCTATG	ATGCATTATC	CCGGAAGTCA	GCCGCCTGCC	AGGATGACCT	420
GACACAAGCC	CTCGAG					436

- (2) INFORMATION FOR SEQ ID NO:709:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

GCTGCTCTAT ATCTTAGAC	SA AAATAAAAGA	ACCACATGTT	GCTTCCCTGC	CTGCAAGCTC	60
TTCTGAATTC ATCACCAT	C ATGTTCCTTC	CTTCAGGGGA	AATGAAGGCA	GATTGTTCTG	120
TTGGTGCTCA CAGATCTC	TT TCTGTTCTGA	TACCCTCCTC	TTCCTCTCCT	GCTTCTTTCC	180
CTTCATCATG TGCTCCTAT	TA CAAGTCTCTC	CCAACTTTAA	AACAAAAACA	AACCCTTCCC	240
TAAATCTTGT GTTTGTTC	CA GCCATTAGAC	TGTATCGTCC	TTGCCATCCA	CGTTATTGGA	300
AGAAGGCCAG CTCACCTC	TA CTCCCTTTCT	GCCCTTTCCC	TCTTAATCTG	CTGTCCTCTG	360
ATTTCTGCCC CCACAAAC	CC GAG				383

- (2) INFORMATION FOR SEQ ID NO:710:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

GAATTCGGCC	TTCATGGCCT	AGGGGCCTGA	AGATCTTCGG	GTATTTGGCT	CCCAGAATCT	60
GACCACAGTG	AAGCTAAAAG	GGGTGGGTGA	CAGCTTCAAG	AAGTATCCTG	ACTACGAGTC	120
CAAGGGCATC	AAGGCTCACT	TCAACCTGGA	TGAGAGTGGC	GTGCTCAGTC	TAGACAGGGT	180
GGAGTCTGTA	TTTGAGACAC	TGGTAGAGGA	CAGCGCAGAA	GAGGAATCTA	CTCTCACCAA	240
ACTTGGCAAC	ACCATTTCCA	GCCTGTTTGG	AGGCGGTACC	ACACCAGATG	CCAAGGAGAA	300
TGGTACTGAT	ACTGTCCAGG	AGGAAGAGGA	GAGCCCTGCA	GAGGGGAGCA	AGGACGAGCC	360
			TGAGGCCCCA			420
CCCACCCCCT	GAACCTAAGG	GAGATGCAAC	CCCTGAGGGA	GAAAAGGCCA	CAGAAAAAGA	480
AAATGGGGAA	CTCGAG					496

- (2) INFORMATION FOR SEQ ID NO:711:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

	${\tt GAATTCGGCC}$	TTCATGGCCT	AGTATGGAAG	GTGGAACTAA	AACTGAAATG	ATCAGTTCAC	60
	ATATTTGTAA	ACTGCGTATT	TTATATCAGT	CGCTGGATTA	GGCCCCTAGA	GACAGTGGTG	120
	GCTAAGTGAT	AAAGTCTTTG	CGCTTGTGGC	ATTTTATAGT	GTAGTGGGAA	GACAGAAAGC	180
	AAACAAGTAG	AGAATCATAT	ATGTAATGTG	ACCTCAGGTC	CAGCTAAGCG	CCAGACAGAA	240
	GAAAAAAGTA	AGGTGAAGGT	${\tt AGAGGGGTTG}$	GAGCAGGAGG	AAGGTGTTAT	TTTAGGTAAA	300
	GTGGCCAGGG	AAGGCCTTTT	GAAGAATTGA	TATCGATTCC	AAAATGATGA	GAAGGTGCAA	360
	TTGTGCCACC	ATGGAGGAGA	AGAGCTTTCT	AGGCAGAGGG	CAGGTGCAAA	GATGGTAGGA	420
•	ACAAACACGG	CTTGTTGAAA	GAACAGCAAT	GTTTGAGGAA	TGAGCCAGAC	TCGAG	475

- (2) INFORMATION FOR SEQ ID NO:712:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 608 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

GAATTCGGCC	TTCATGGCCT	AATTTTGCAT	AAAACCTCAT	CAATCTCTGC	CAATCACTGA	60
		TGTTTTAGGT				120
		GGTTCAGGCT				180
TTTTAAATAA	CGGAATGCAC	ATCTCACAGT	TCTGGAGGCT	GGAAGTCCAA	CAGCAGAGTG	240
CCAGCATAAT	TGGGTTCTGG	TGAGAGAGCT	CTCTTGGGTT	TCAGACTGCT	GCCTTCTCAA	300
TGCAGCTTCA	CATGGTGGAC	AGAAAGAGCT	CTCAAGAGTC	ATTTTTAAGG	GCACCAATCT	360
AATTTATGAA	GCCTCCACCA	TAATAAGCTA	ATTACTTCCC	AAAGTGCTGA	GATTACAGCT	420
GTCAGCCACC	GTACCTGCCT	GGGAATTTTT	TTAAAGCTCA	AATTGGATAA	GAGGGTTATA	480
GGAATATATT	CATCTATCAT	ATAGAAAAGA	ATATGTGCTC	AGTCCCAGGA	AATAGAAAAT	540
ATATTACCTT	ATTTATACTG	TTTTAATTAA	TGCTTTTTAA	AATCTGATTA	ACTCTGGGAG	600
AGCTCGAG						608

- (2) INFORMATION FOR SEQ ID NO:713:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 531 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

GAATTCGGCC TTCTTGGC	CT AGTGCACTCC	TGTAATCCCA	GCTACTCGGG	AGGCTGAGGC	60
AGGAGAATCA CTTGAACC	CA GGAGGTGGAG	GTTGCAGTGA	CCCAAGATCA	TGCCACTGCA	120
CTCCAGCCTG GGTGACAG	AG CGAGAACGTC	TTTAAAAAAA	TTAAAAAAAA	AAAAAAAAGA	180
TTGCACAAAT CAGACAGT	GA CCCAGAGCTC	AGCCTTGAGG	AAAGTCAGTG	TTGGGGAGGG	240
GAGGGCAAAG AAGCAAGT	AA AGGTTTAGCA	GACATGGCAC	CTCAGTCTGG	ACTTGAAGGA	300
GGGCTAGGCA CAAAGGAAG	GG GGAACATGTC	AGATGAGAAA	CACGTGAAGG	TTCAGCCAGA	360
TGAGCAAGGA AGGTTGGT					420
GATAGGGCAC GATAGAGT					480
ATAGGTAAGT AGGGGAACT	TT GAGGATGTTT	AATCAGAAAT	GAGATCTCGA	G	531

(2) INFORMATION FOR SEQ ID NO:714:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

GAATTCGGCC	TTCATGGCCT	AATTTATCCC	ATCCTTATCC	CATCCTTATA	AGGAATAATG	60
TATTGAATAA	AGATTGTATC	AGTATTTGTA	ATTCAATAAA	CCAGAACTTG	TGGAAATAAA	120
TATGTAGGAG	ACATAAATAT	GGTGTCCTCA	AATTGAATTA	TGTGGGAAAA	AAGTGGGGTG	180
GAGTTAAAGT	CCAAGCCAAT	AAAGTTGTAA	CATTAAAGAA	AGACAGGTAT	GGGATGCAAG	240
GTGCAAAGAA	AAGGTCATCA	TATCTCATAC	TGGGGTGAGA	TAGAAGACTT	CCTGAAGTAG	300
GCGATGCCTA	TATTGAATCT	ATAAGGACAA	ACTGGCATCA	ATATGTCAGG	GAAGACAGGT	360
TGAAGGTGGT	CCTGCCAGAG	AAAGGAGCAA	GGATAAAGGC	AAGGAAGCAT	GTAACGTAAT	420
TGTTTGTGGA	GAAACCTCAA	ATCGGCTGAG	GAAAAACGAC	TCAGGTATGT	AGTAGGGCAC	480
AGTATAAGTA	GGTCTCGAG					499

- (2) INFORMATION FOR SEQ ID NO:715:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

G	AATTCGGCT	TCATGGCCTA	GAGATTTAAT	GTTCCCTTAC	CTTGCTGGAG	GAACATCAAT	60
G	TTGGAGGAA	ACAACTTTTC	TTTTTTGCTC	AAGGAGACAG	ATGGAGCGAG	TGTTTTCTTT	120
1	TCATGGTCA	AGGATCCGGC	TGGCTTTTTT	GGTGTCTGCT	GTTTTCACAT	CTTCCTCCAT	180
G	GCCAAGGAA	AACACGTGTT	GATGAGACAT	TTTTTTACCA	CAGTCACGTT	TTAAGTCCTC	240
1	GACTGAAAT	GTGAAGGTCA	TTTCCCGCTT	AATGCTCCCC	ACCTGTGAAA	TGAAACACAG	300
A	AATTCTTAC	TCACATAAAA	CATCACCTTT	GTACGACTAC	TGCAGATGGC	GGTGAGGAGA	360
G	ATTACAGAC	ACTGTCCTTC	CTGTTCATCT	GAAAGATTGT	ATAATTTTAA	TAAGAAAAAT	420
G	CAACTCGAG						430

- (2) INFORMATION FOR SEQ ID NO:716:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

GAATTCGGCC TTCATGGCCT	AGACCTTCTG	GGTGAACGAG	GGCAAGCACG	CCAAGTTCCG	60
CTGCTACGTG ATGGGCAAGC	CCGAGCCCGA	GATCGAATGG	CACTGGGAGG	GCCGCCCGCT	120
GCTCCCGGAC CGCCGCCGCC	TCATGTACCG	CGACCGCGAC	GGCGGCTTCG	TGCTCAAGGT	180
GCTCTACTGC CAGGCCAAGG	ATCGTGGGCT	CTACGTCTGC	GCCGCGCGCA	ACTCGGCGGG	240
CCAGACGCTC AGTGCCGTGC	AGCTGCACGT	GAAAGAGCCC	CGCCTCCGGT	TCACACGGCC	300
CCTGCAGGAC GTGGAGGGCC	GTGAGCACGG	GATTGCCGTG	CTGGAATGTA	AAGTACCCAA	360

CGAGCAGATC GAAGAGGGCA CTGTCCGGCG CCTCATCATC ACAGGCTCGA G	420 471
(2) INFORMATION FOR SEQ ID NO:717:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 397 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:	
GAATTCGGCC TTCATGGCCT AGCACTCTT AGCAACACAG ATTTTCTTCC AAATTATGCC TTGAAGCTGC TCCCGGAGCC ACCCGCTCAT CAGCACCCTG CTCCTGTGGT CCTTCTCGTG AAAGGCAGAG GGGAGATGCC TGTTGCCCGC AGTCTTCTCT GCAGCTGCCG TGGGAACAGG CACCTTCCCG GCTGCTGGGG ACACAAGGAG GGGAGTCAC CGTGGCTTGC TCACTTTCCA GATCAGCCAA CTGCAGAACA TTTGTTGTTG TTTAGATCCC ACGTCTGACG GTTTAGAACA GCTTTTATAA CATGGTTAAA CATGTTTACA AAGCAAGGGA GACATCTCTT ACCTTGACAA CACGAGGCTC CCACAGACCG CCTTCCCCCCA GCTCCGAG (2) INFORMATION FOR SEQ ID NO:718:	60 120 180 240 300 360 397
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 539 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718: GAATTCGGCC TTCATGGCCT AGAAGGAAAG AAATTTTATG TGAGAGAGCA TCTTGTATGG CAAATCTTG TCCTAAAGTA GAATGACTAG GAAAGAGCAA AATATAGGAC AAGTCAGAAA GTCATAAGAT GGGAAAGAAA AACTTACAAC TGCTAGATCT TCTCCTGTCT AGAAGTGTTG TGTGTGTGTA GCTTATATAA AAGTACTAT ATTAATTGGA TTAAGAGAAA ATGAAACCCC ATCTCTACTA AAAATACAGA ATTAGCCGGG TGTAGTGACA CATGCCTGTA GTCGCAGCTA CTCAGCAGGC TGAGACAGGA AGATAACTTT AACCCAGGAG TTGGAGGCTG CAGTGAGCCA AGATCGCGCC ACTGCACTCT AGCCTGGAGG AGACAGAGGC AGACTCCGTC TCAAAAATGA AAAAGTAGAG CCTGGTAGAG TGAAGCCACT TGCAGGAGTC GTTTAGTTAG GGCTGTGTTG CCTTACAGTG CTGGTGTCCT CACAGATGAT AATAGTAATA AAAAACACCA CAACTCGAG	60 120 180 240 300 360 420 480 539
GAATTCGGCC TTCATGGCCT AGAAGGAAAG AAATTTTATG TGAGAGAGCA TCTTGTATGG CAAATTCTTG TCCTAAAGTA GAATGACTAG GAAAGAGCAA AATATAGGAC AAGTCAGAAA GTCATAAGAT GGGAAAGAAA AACTTACAACA TGCTAGATCT TCTCCTGTCT AGAAGTGTTG TGTGTGTGT GCTTATATGA AGGTACTCTA ATTAATTGGA TTAAGAGAAA ATGAAACCCC ATCTCTACTA AAAATACAGA ATTAGCCGGG TGTAGATGA CATGCCTGTA GTCGCAGCTA CTCAGCAGGC TGAGACAGGA AGATAACTTT AACCCCAGGAG TTGGAGGCTG CAGTGAGCCA AGATCGCGCC ACTGCACTCT AGCCTGGAGG AGACAGAGGC AGACTCCGTC TCAAAAATGA AAAAGTAGAG CCTGGTAGAG TGAAGCCACT TGCAGGAGCC GTTTAGTTAG GGCTGTGTTG	120 180 240 300 360 420 480
GAATTCGGCC TTCATGGCCT AGAAGGAAAG AAATTTTATG TGAGAGAGCA TCTTGTATGG CAAATTCTTG TCCTAAAGTA GAATGACTAG GAAAGAGCAA AATATAGGAC AAGTCAGAAA GTCATAAGAT GGGAAAGAAA AACTTACAAC TGCTAGATCT TCTCCTGTCT AGAAGTGTTG TGTGTGTGAT GCTTATATGA AGGTACTCTA ATTAATTGGA TTAAAGAGAAA ATTGAAACCCC ATCTCTACTA AAAATACAGA ATTAGCCGGG TGTGAGACA CATGCCTGTA GTCGCAGCTA CCTCAGCAGGC TGAGACAGGA AGATAACTTT AACCCAGGAG TTGGAGGCTG CAGTGAGCCA AGATCGCGCC ACTGCACTCT AGCCTGGAGG AGACAGAGGC AGACTCCGTC TCAAAAATGA AAAAGTAGAG CCTGGTAGAG TGAAGCCACT TGCAGGAGTC GTTTAGTTAG GGCTGTGTTG CCTTACAGTG CTGGTGTCCT CACAGATGAT AATAGTAATA AAAAACACCA CAACTCGAG	120 180 240 300 360 420 480
GAATTCGGCC TTCATGGCCT AGAAGGAAAG AAATTTTATG TGAGAGAGCA TCTTGTATGG CAAATTCTTG TCCTAAAGTA GAATGACTAG GAAAGAGCAA AATATAGGAC AAGTCAGAAA GTCATAAGAT GGGAAAGAAA AACTTACAAC TGCTAGATCT TCTCCTGTCT AGAAGTTTG TGTGTGTGAT GCTTATATGA AGGTACTCTA ATTAATTGGA TTAAGAGAAA ATGAAACCCC ATCTCTACTA AAAATACAGA ATTAGCCGGG TGTAGTGACAC CATGCCTGTA GTCGCAGCTA CTCAGCAGGC TGAGACAGGA AGATAACTTT AACCCAGGAG TTGGAGGCTG CAGTGAGCCA AGATCGCGCC ACTGCACTCT AGCCTGGGAG AGACAGAGCG AGACTCCGTC TCAAAAATGA AAAAGTAGAG CCTGGTAGAG TGAAGCCACT TGCAGGAGTC GTTTAGTTAG GGCTGTGTTG CCTTACAGTG CTGGTGTCCT CACAGATGAT AATAGTAATA AAAAACACCA CAACTCGAG (2) INFORMATION FOR SEQ ID NO:719: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 387 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180 240 300 360 420 480
GAATTCGGCC TTCATGGCCT AGAAGGAAAG AAATTTTATG TGAGAGAGCA TCTTGTATGG CAAATTCTTG TCCTAAAGTA GAATGACTAG GAAAGAGCAA AATATAGGAC AAGTCAGAAA GTCATAAGAT GGGAAAGAAA AACTTACAAC TGCTAGATCT TCTCCTGTCT AGAAGTGTTG TGTGTGTGAT GCTTATATGA AGGTACTCTA ATTAATTGGA TTAAGAGAAA ATGAAACCCC ATCTCTACTA AAAATACAGA ATTAGCCGGG TGTAGTGACA CATGCCTGTA GTCGCAGCTA CCTCAGCAGGC TGAGACAGGA AGATAACTTT AACCCAGGAG TTGGAGGCTG CAGTGAGCCA AGATCGCGCC ACTGCACTCT AGCCTGGGAG AGACAGAGGG AGACTCCGTC TCAAAAATGA AAAAGTAGAG CCTGGTAGAG TGAAGCCACT TGCAGGAGTC GTTTAGTTAG GGCTGTGTTG CCTTACAGTG CTGGTGTCCT CACAGATGAT AATAGTAATA AAAAACACCA CAACTCGAG (2) INFORMATION FOR SEQ ID NO:719: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 387 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	120 180 240 300 360 420 480

AGTAAGCAGT TCTGTTATAC ACTCTTTATA TGCTTTTCCT CCTTTCCTCT CTCAGTCTCT CTGATCCTTC CACCTGTGCT CTGGGTTCAC CTCTCAAGTA AACCACCTGC ACACAAGTCC CTGTCTCAGG CTCCATTTGG GGAAACCAAA CTAAGACACC ACCTCAAAAC ACAGAATTTC ACGAGGCTCC AAATGCCTCA GAAAAGTAAT GTAAATATAA AATGACCAAT TTTTTGAAGT ATATTAATCC TAGTTATTTA ACTCGAG 180 240 360 360 360 360 360	0
(2) INFORMATION FOR SEQ ID NO:720:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 239 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:	
CCCGTGTATA GTTTGCAAAT ATTTTCTCCT CTTCTGTAGG CTGTTTACTC TTGTTGATAG TTTCTTTTGC CATGCACAAG CTTTTTGGTT TAATTAGATC CCATTTGCA ATTTTTGCTT TTGTTGCAAT TGTTTTTGGC GTCTTCATCA CGATATCTTT GCCAGTTCCT ATGTTCAAAA TGGTATTACC TAGGTTGCCT TCCAGAGTTT TTATAGTTTT GGGTTTTAT TTACTCGAG 23	0
(2) INFORMATION FOR SEQ ID NO:721:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:	
CTCGAGCACT ACCCTAGACG GTCTCATCAC TATACTGGCT CCTCCTTACC CCCGTAAATC TCCCAGGTAC ACTTCCTGAT CACCCTCCGG ATACCTCATC CCTATCTATT CCTTTATAA ATAATTCCCT GCTCCTCCTT CTCACCCACA ATCCACTCGC AGTTCAAGGC CTCACTGCCA TCGACTCCAC TGTCTGTAGG TGCTTCCCAA TATGCCCCAG GACCCCTCT GGTGTCACGC TCTGTATCCT GACACCCCTT GTAGACGAGT CCCGAAATTC CCGCCCCGTC CCTGGAGCTC CCTAGGCCAT GAAGGCCGAA TTC 300	0
(2) INFORMATION FOR SEQ ID NO:722:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 275 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:	
GAATTCGGCC TTCATGGCCT AGGCCTGTGG AGCCCCAGCT CTGGGTCCCT AGCCCGGGTC CAGGCAGCCA GGCTCCCTCC TGAGCTGAGA AACGGAACCT CGCGAACCAC TGGTGGCACA TCCTTCTCCT CCCCCGCCCC TGATCACCG CCCCCGGATC AGAAATATAT CTATATTCTC GACTAAAGTC TCATCAGGAA ATATTTCCTG TCTTTTATTT TAAGCATCAA ATTGTTTTAG 24	0

TTGATTTAAA AAGGAAAAAA TACAGACGAC TCGAG

- (2) INFORMATION FOR SEQ ID NO:723:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GAATTCGGCC	TTCATGGCCT	AAGAAGCAAC	AATCATATTA	GCTGGGGGAG	GAGGATAGTT	60
TGGTATTTTT	GTAGTTTGCA	CAGTGACCTT	TTTAAAAATC	TGGTTAGGCA	AAAATAGTGT	120
GATCTTGTTT	GTTGTCTCAC	TTCATTATGA	TCACAGAATG	ACCTGGTATG	ATGTTAGTGT	180
TTTATGAGAG	TGTTATGTTT	TAACAGGGGA	ACACCGCAGT	CAATTCCTAA	CAACACTAAA	240
GTGTCAGTTC	TGTTCGTGAC	ACCAAGGGCT	GTTTTTCTTT	TTCTCATATA	ATGTTGAGGC	300
AACCAGGAAG	ACTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:724:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

GGCCTCAGCA	GGTGTGAAGC	GTGTGCTTTA	GTTTCGTGGG	AGGCCTGGCA	TCCCCGAGAG	60
${\tt GGAGGGGAAA}$	${\tt GGTAACCACT}$	CCTTTGTGGA	${\tt GGTCGCCAGG}$	GTCATTGTCG	TGGATTTGCA	120
CAGTCGGCTG	GGCGGTGCAA	TGGCGGAAAG	AAAAGGAACA	GCCAAAGTGG	ACTTTTTGAA	180
GAAGATTGAG	AAAGAAATCC	AACAGAAATG	GGATACTGAG	AGAGTGTTTG	AGGTCAATGC	240
ATCTAATTTA	GAGAAAGCAG	ACTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:725:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

GAATTCGGCC	TTCATGGCCT	AAGTCAGTGG	TAAGCCGCAG	CAGTTTCCTG	CCACTCGTAA	60
TATGGCAATT	AAAAATTTTA	AATTTGTGGC	TGCTTGGGGT	CTGGGAGGTG	ACCTGCTCCT	120
CAGCAAATTT	TGACTGATAA	ATTAATGCCT	GGGTCTTCAG	CCTGGTTCTT	TGCTGGCCAG	180
TGTGACAACA	GTCTGTCACG	TCTCTGGGGG	CACATTATAA	TTAACAGATG	TAATCTTTCT	240
CCGGTTCAGG	GTCATCTGTG	AATCAGGGGT	ACTGCCCCAG	TAGAACTAGG	AACATCCAGC	300
AAAAGACTGT	TTTCAAAATA	TACAATTAAG	TGAAAAAAGC	ATGAAGAACT	CGAG	354

- (2) INFORMATION FOR SEQ ID NO:726:
 - (i) SEQUENCE CHARACTERISTICS:

Sound of the State

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:	
GAATTCGGCC AAAGAGGCCT AGAGGTTGAC CTGAAAAACA ATGAAACACA TGAACACACT TCCGATTTTC TCCTCGCTGA TTAGCTTCCT GCCTGCTGTC AGTGCTGGAC GAAGTGCTAT AACTACTTTA TGTAACATTA CAGAACAGCT CGAG	60 120 154
(2) INFORMATION FOR SEQ ID NO:727:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 338 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:	
GAATTCGGCC TTCATGGCCT AGTGGGAAGA TGTGGATGAT GAGAAGGGAG ATAGCAATGA TGACTATGAC TCTGCAGGCC TATTGTCAGA TGAAGACTGT ATGTCTGTGC CCGGAAAAAC TCACAGAGCT ATAGCAGATC ACTTGTTCTG GAGTGAGGAA ACAAAGAGTC GCTTCACGGA GTATTCGATG ACTTCCTCAG TCATGAGGAG AAATGAACAG CTGACCCTAC ATGATGAGAG GTTTGAGAAG TTTTATGAGC AATATGATGA TGATGAAATT GGAGCTCTGG ATAATGCAGA ATTGGAAGGT TCTATTCAAG TAGACAGCAC GACTCGAG	60 120 180 240 300 338
(2) INFORMATION FOR SEQ ID NO:728:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 433 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:	
GAATTCGGCC TTCATGGCCT AATTGAATTC TAGAACTCTC CCAGAGAAAC CAGGCAGATA CTGCTCCACA CCGGTGAGCT GCTTCTCACC TGGGTAGTCT AGGGTGGTTT GCTCCAGAAT TGTATTTCTG CTTTTTCTTT TTTTAACTTG GCAGTGGTTA ACCATTCCCT GGAGCAGCAC CAGGTAACTC AGCTTGTATC AGAGTCATCT GCTTTACCTG ACATGAGCAC ACGTTGTCAT ATATTTGCAC ATGCAGATAT CATATGTTAA ACAATATCAC ATTGTTGAAG AAAATTACAC TGGAAAGCGT AAAATATAGT TTGGATGCCA TATTGAGTGT AACTTAATCC ACCCGATTCA GAACTTTTGT AGAGTGCCTC GGAGTTCCTA TTTGGAAATA TCAGTTAGCA GTTTTAGTCA GTAGAGACTC GAG	60 120 180 240 300 360 420 433
(2) INFORMATION FOR SEQ ID NO:729:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 315 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

(A) LENGTH: 154 base pairs

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

GAATTCGGCC	TTCATGGCCT	AACAAGAAAC	ACCAAGTACC	TCGACCTCAA	GAATTCACAA	60
GAGATGCTCC	GCTACAAAGA	${\tt GGTCTGCTAC}$	TACATGCTCT	TTGCCCTGGC	TGCCTACGGG	120
TGGCCCATGT	ACCTGATGCG	GAAGCCCGCC	TGCGGCCTCT	GCCAACTGGC	TCGGTCCTGC	180
TCGTGTTGCC	TGTGTCCTGC	${\tt GAGGCCGCGG}$	TTCGCCCCTG	GAGTCACCAT	CGAGGAAGAC	240
AACTGCTGTG	GCTGTAATGC	CATTGCCATC	CGGCGCCACT	TCCTGGACGA	GAACATGACT	300
$\tt GCGGTGGGAC$	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:730:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GAGTTGTCTC	TCTGAATTAA	CTTTCTCACC	AATAGCTCCT	CTTTAAGATC	AATAACTCTT	60
ATGTTTGCAC	TTTTTAGGCT	ATTTTCTAGA	TCTTGTATGT	GTGTCTTATT	ATTTTTTATT	120
CTTTTTGTCT	CCTCTGTGAA	TTTTCAAATA	GTCGAG			156

- (2) INFORMATION FOR SEQ ID NO:731:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

GAATTCGGCC	TTCATGGCCT	ACTTGAACCT	AGATCTCACC	CCCAGGATGT	TGCGGAGGCT	60
GCTGGAGCGG	CCTTGCACGC	TGGCCCTGCT	TGTGGGCTCC	CAGCTGGCTG	TCATGATGTA	120
CCTGTCACTG	GGGGGCTTCC	GAAGTCTCAG	TGCCCTATTT	GGCCGAGATC	AGGGACCGAC	180
ATTTGACTAT	TCTCACCCTC	GTGATGTCTA	CAGTAACCTC	GAG .		223

- (2) INFORMATION FOR SEQ ID NO:732:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

GGAAGAGGCA TGTGAATCCT	GTTTTTCATG ACGGTTAAAA GTGCA GGCTGTGGCA CTAACTATCT GTGTGG	GGATT TGGAGTCCCA ACTGG CTGTGAACCT	TGGTCCTGGG CTCGTGCCTC	120
	TCTGCAAAAT GGGTAGTTGT ATAGC: TTGGAAGCAC TCAGTAAATG TTAAT			240 300 309
(2) INFORMA	TION FOR SEQ ID NO:733:			
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 275 base pair (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	s		
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ I	D NO:733:		
TTGCCACCAT GGAACTCTTA CTCCAGACAT	TTCATGGCCT AGATTAATTC TAGACCAACCAACCAATT GGTCAACAACAACCA AGACCATTCCACATGC AGACCACCACACACACCACAC	CCACG TGTCTTCTTC GGAGC ATGCACCCTA	CTTTGTGGCA GTGTCTCAAT	60 120 180 240 275
(2) INFORMA	TION FOR SEQ ID NO:734:			
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 250 base pair (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	S		
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ 1	D NO:734:		
ATTTTGGGGT GCAAGTCCTG	GGCACGTTTC CCACAACTGC GAAGA TTTGGAAAAG AAGCTATGGA AAACG CTTTTCTTTG TTTTGCTGGG AATGT ATGGAGGAAT TGCAGAGCGG GAGCT	GAGGG GCAGGCACTC	TGCAGATAAG AAACTGGGAA	60 120 180 240 250
(2) INFORMA	ATION FOR SEQ ID NO:735:			
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 324 base pair (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	·s		
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:735:		
GCTCTTGGGT ATCACCCCGT	TTCATGGCCT ACACAGACTG GGCAA CCAGAGGCTA GGAAGTCCAA GACCA GGTAGAAGAT GGAAGGCACA ACTCA	TGGTG TCAAGCATCA GCGTG TGAGACAGAG	GGTGAGGATC AGGGAGAATT	60 120 180

TGGAGTTTTG CTCTTGAGCT CGAG

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:

ATAATGGCAT TAATCCATTC ATGAGGCCCC TACCTCTTTT TCTCCCCCCG CCCCCGAGA

300

	(A) LENGTH: 259 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(b) Toroboot. Timear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:736:	
GAATTCGGCC	TTCATGGCCT AAACACATAC CAGATTCTTA GATTCATTTG GTGAAGGAAG	60
CCTCTGAATT	AAAACTTTTA AATATTTCTG ATTTGCAACC AGACGAAAAA GAAGAAAATT	120
GACAACTTTT	TTGATGCAAC TTTGTGAAAT CATGGTGTTC CTGGTTTTTC TGGTCTGGTT	180
TCCACTTCAG	TTTTGTTTTG TTTTGCCACA GTTTAGTTCC TCACCTGATC TTTCCTTGTA	240
ICCACIICAG	AGICICGAG	259
(2) INFORM	ATION FOR SEQ ID NO:737:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 409 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:737:	
CTCGAGGGGG	TGCCAGACAC GGGTCTCCTC CGACTGGGCG GTGCGTGGGA TGCCGCCAGC	
GTCCAGGTAC	TGCGTGATGC GGATGTAGGC GATGCAGGCT GACTCGTCGC CCATCAGGTG	60
GATGTGGGGA	TTCAGGATGG TGGTGTGCAC GGGCTTGCTG TTCCGGGACC ACAGGTTTTC	120 180
AAAATAGAAT	CGATGGAAGT CCAGGCCCTC AACCAGGTTC CCCAGGGCCT CAGGTTCGAA	240
GGCTGTCATG	CCAGGGTCGC ACATCTTCGT GTAGGACTCA AAATCTCCAT TGCTTATGGC	300
TTCAATCAGC	TGCTCTGTCA CTTTTATAAT TTCCTGTTTC CGCACTTTGG TGTCTTCATC	360
	GTGTTGGTGC TCTCTGAGTA GGCCATGAAG GCCGAATTC	409
(2) INFORMA	ATION FOR SEQ ID NO:738:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 466 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(::)	MOLECTIVE MUDEL - DVA	
(11)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:738:	
	,	
GAATTCGGCC	TTCATGGCCT ACTTTCCCCT CCTTCCTTCC TTCCTTCCTC CCTCCCTCCT	60
CTCTCCTCTC	TTTCTTCCTT CCTTGCCTCC TTCCATCCTT CCCTCCCTCT CTCTCTTTCT	120
TTCTTTCTTT	CTCTCTCTCT CTCTTTCTTT CTTTCTCTCT CTCTGTCTTT CTTTCTCTCT	180
TICITICITI	CCATCTTCTT TTCTTTCTAT CTTTCTTACT TTTGATGTAG CTGTCACGAC	240
CTAATGAAAA	TACTGGCATG AGTGATGCCA CCTTTAGATT CTCCACCTTC CTGTTCCTGT AACATGAATT GGTTTGTGGC TGTAAGTACT TGGTGGGTTA TTGCTCATAG	300
	THE TRANSPORT OF THE TR	360
	227	
	336	
	·	

AGTAAACCTA ACTCTGAAAA ATAGAGACTC TCCAGAAACA CTCGAG

ATTCAGTTGC ATTTTTGCTG AGATAGTGCT GTTACCAAAA GCAGGGGTGC TGCTTGAAGA

420

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 367 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:	
GAATTCGGCC TTCATGGCCT ACATTCTGCA AACTATTTTG TTATTAGCTT TTTCACTTAA AAATAGCCCT GCTTGCAAGC AGGCTCTGTG GTGCAATGGA TAGCGCATTG GACTTCTAGC CTAAATCAAG AGATTCAAAA ATAGCCCTGC TAAATATTTG CAATCTTTCC TACGCTCCTT TTTCCCCCAA AGTGACTTTG GATATCCAGA GTTACCAAAT CTAGTATTTG AAGTCCTTAG GTTTGAGGGT TGAAAGTGAA AGGCAAGCTG TTTTAATGAA AATTCCTAAC TGAAGAGAGC GGAGACTTAA GATGCTTAAA TTTTGGTCAC ACCTGAGCGG TATTTGTTTG CATGGCAGGA GCTCGAG	60 120 180 240 300 360 367
(2) INFORMATION FOR SEQ ID NO:740:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 264 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:	
GTGATGGACA AAGACAGGGA AGGCCTCATC AGCAGGGATG AGATCACAGC CTACTTCATG AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT GTGTTTGAGT GTAAGAAGCT CGAG	60 120 180 240 264
AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT	120 180 240
AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT GTGTTTGAGT GTAAGAAGCT CGAG	120 180 240
AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT GTGTTTGAGT GTAAGAAGCT CGAG (2) INFORMATION FOR SEQ ID NO:741: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180 240
AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT GTGTTTGAGT GTAAGAAGCT CGAG (2) INFORMATION FOR SEQ ID NO:741: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	120 180 240
AGAGCCAGCT CAATCTATTC CAAGCTGGGC CTGGGCTTTC CTCACAACTT CCAAGAGACC ACCTACCTGA AGCCCACTTT TTGTGACAAC TGTGCTGGAT TTCTCTGGGG AGTGATCAAA CAAGGATATC GATGTAAAGA CTGCGGGATG AACTGTCACA AACAATGCAA AGATCTGGTT GTGTTTGAGT GTAAGAAGCT CGAG (2) INFORMATION FOR SEQ ID NO:741: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	120 180 240

- (2) INFORMATION FOR SEQ ID NO:742:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GAATTCGGCC TTCATG	GCCT AAGAAATGAA	AAAGATTATT	GAAACTATGC	CAATGACTGA	60
GAAAGTTGAA GAATTG	CTGC GTGTCATAGG	TCCATTTTAT	GAAATTGTCG	AGGACAAAAA	120
GAGTGGCAGG AGTTCT	GATA TAACCTCAGT	CCGACTGGAG	AAAATCTCTA	AATGTTTAGA	180
AGCTGAAAGC AGTGAC	AGTG GAGCCGAGTC	TGAGGAAGAA	GAGGCCCAAG	AAGAAGTGAA	240
AGGAGCAGCC CTCGAG					256

- (2) INFORMATION FOR SEQ ID NO:743:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GAATTCGGCC TTCATGGCCT	ATGTTTTTAT	AGCACCGATG	GTACTGTTTT	ATTTATTGCC	60
AATAGACCAC AACATTCACA	TCTGTTTTTC	CTCAAGGGAA	CCGTATTTGC	TTTTGGTTGA	120
AGGATTTATC TATTTGATAC	TATCCAGAAT	ATTGTGAAGC	TATAATTTCC	TGGGTTATAT	180
TTTAGATGGG TTGTCTGCAT	GGTGGTAAAA	TAAGCTTTTT	CCTCTCGCCT	ACGTCCTTTG	240
GAAGATCTCC TGATCATACA					300
CCAGCTCTAG ACTGTTTCTT					360
GCGCTCAGAA ATAGGGCTTG					420
GCTCTCTCTA CCGCACGATC					480
AGAGCTTGAA GGAACCCACG	TCCCCAGATT	AGCAACCCTA	GAGTTCATCT	GCTCAGGCCG	540
GGAAATGTGT AAGCTTCCTT	GATCAACTCC	AGGCCTCGAG			580

- (2) INFORMATION FOR SEQ ID NO:744:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

GAATTCGGCC	TTCATGGCCT	ACCCAGAGAC	TCCCCCACCC	TONOCHTANO	CARCCACCAC	60
777777777		. recording	rededonede	ICACGAIAAC	CHMOGMCGMC	• •
CGCGAACCAA	GGGCAAAATA	ACATGGCAGC	CAGACGAATT	ACACAGGAGA	CTTTTGATGC	120
TGTATTACAA	GAAAAAGCCA	AACGATATCA	CATGGATGCC	AGTGGTGAGG	CTGTAAGCGA	180
AACTCTTCAG	TTTAAAGCTC	AAGATCTCTT	AAGGGCAGTC	CCAAGATCCA	GAGCAGAGAT	240
GTATGATGAC	GTCCACAGCG	ATGGCAGATA	CTCCCTCAGT	GGATCTGTAG	CTCACTCTAG	. 300
AGATGCCGGA	AGAGAAGGCC	TGAGAAGTGA	CGTATTTCCA	GGGCCTTCCT	TCAGATCAAG	360

CAACCCCTCT CGAG

CAACCCTCT CGAG	37
(2) INFORMATION	FOR SEQ ID NO:745:
(A) (B) (C)	ENCE CHARACTERISTICS: 1) LENGTH: 323 base pairs 1) TYPE: nucleic acid 2) STRANDEDNESS: double 1) TOPOLOGY: linear
(ii) MOLE	CCULE TYPE: cDNA
(xi) SEQU	JENCE DESCRIPTION: SEQ ID NO:745:
TTCTCCAAAA AATAI TCCAGTGGCT TCCC; GGGGCCTGTG TGATG	AGGCCT ATTGGTTTCC CTGCTTCCAT TCTTACTCCC CTACACTCTG ACCATT GTGATCCTTT AAAATCCTGA CTCTCTCTG CTCAGAGTCA ATATCA CGTAAAATGA AACCCCAATC GCTCCTTACT CTGGCCTGCA BGGCCT TCTCCAGCTT CGTTCTTCCT TTCCTTCTGT TCTCCCCTCT CCTCCA GGGCTTCTTT CCAGCTCAAG CCCTTTCCTG TTGAGAGCAT GCACTC GAG 32:
(2) INFORMATION	FOR SEQ ID NO:746:
(A (B (C	NCE CHARACTERISTICS:) LENGTH: 273 base pairs) TYPE: nucleic acid) STRANDEDNESS: double) TOPOLOGY: linear
(ii) MOLE	CULE TYPE: cDNA
(xi) SEQU	ENCE DESCRIPTION: SEQ ID NO:746:
TCTAGACTTC GCAGO GAGATTCTGA TGGAA ATGCGTAAAA AGGAT	CAAAGA AAAGGACATG TTCAATTTCA AACGAGCCCA GGAGGACATC AAAGCT GGAGACCACA AAGAAACCAG ACAATGTACC CAAGTGTGAT AGAGAT TAAGGATTAC AAGGCACGCT TGACCTGTCC ATGCTGTAAC AGCTGT TCTTACTAAG TGTTTTCATG TCTTCTGCTT TGAGTGTGTG CACCCC CCCCGCGCTC GAG 273
(2) INFORMATION	FOR SEQ ID NO:747:
(A (B (C	NGE CHARACTERISTICS:) LENGTH: 666 base pairs) TYPE: nucleic acid) STRANDEDNESS: double) TOPOLOGY: linear
(ii) MOLE	CULE TYPE: cDNA
(xi) SEQU	ENCE DESCRIPTION: SEQ ID NO:747:
CACATCGTGC TGCAC TCCAAATACT TGCAC GATGAGAGCC TCCAC CTCTGCTACT ATGAC	CCTCT CTGCCTCTAT CACACCAAAT ACAAGCGCAA CATGATTGAC CGGAGA AGAGCGTGTT GTCCCCATTG AAGTTTGCCG GTCCAAACTG GGGAGT AGTTTTCCGC TGTGATAAGT GTACCTTCAC CTGCTCCAGT CAAACA TATAGAAAAG CACAATGAAC TGAAACCTTA CAAATGCCAG GACCAA GCACACGGAG GAACTGGACA GCCACCTTCG GGATGAGCAT CTTTGA GCTGGTTGGA CGGGTTAACT TGGATCAGCT GGAACAGATG 360
AAGGAGAAAA TGGAG	AGCTC CAGCAGCGAT GATGAGGACA AGGAAGAAGA AATGAACAGC 420
AAGGCTGAAG ACAGA	GAGCT GATGAGATTT TCTGACCACG GGGCTGCTCT TAACACTGAG 480

AAGCGTTTTC CATGTGAATT TTGTGGACGG GCGTTTTCAC AGGGCTCTGA GTGGGAAAGA CATGTGCTGA GACACGGCAT GGCATTGAAT GACACCAAGC AGGTGAGCAG AGAAGAAATC CACCCAAAAG AGATCATGGA GAACAGTGTT AAAATGCCCT CCATAGAGGA AAAGGAAAGT CTCGAG	540 600 660 666
(2) INFORMATION FOR SEQ ID NO:748:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:	
GAATTCGGCC AAAGAGGCCT AACAACCGAA TATAGTACAC GACCTTCCTG CAGCAGTTCT AAGCTACTGT CAAGTATGGA AAATCCCGGC AATTCTGTAC TTGTGTTATA CTGATGTGAT GAAATTAGAC CTAATCACAG TGGAAGCTTT TAAGCCTATA CTTTCTACCA GAAGCTTGAA GGGTTTGGTT AAGAATATTC CCCAAAGCAC TGAGATACTA AAGAAATTGA TGACAACNAA TGAGATTCAG AGTAACATTT ATACATGATC TTAAACATTG TTTTGTAGTG TATATTACTT GTCCATTCCT TTAAGGGGAG CAGCCTGCAC TCTTTTGTAG ATTACTTTTG GGGGATATAT TTTGAGAATG ATGAAACGG	60 120 180 240 300 360 379
(2) INFORMATION FOR SEQ ID NO:749:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 335 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:	
GAATTCGGCC TTCATGGCCT AGGCGCAAGG CCGAGCGTTC CCAGCAGGGG GAGAAACCCT TCACACCCCA GGCCTTCAG GAACTGGGGC CTTGCCTTGC	60 120 180 240 300 335
(2) INFORMATION FOR SEQ ID NO:750:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 648 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:	
GCAAAGACCC AAGAACTGAA TATGCTCCGG GAACAGACCA CTGGGCTGGC AGCTGAGTTG CAGCAGCAGC AGGCTGAGTA CGAGGACCTT ATGGGACAGA AAGATGACCT CAACTCCCAG CTCCAGGAGT CATTACGGGC CAATAGTCGA CTGCTGGAAC AACTTCAAGA AATAGGGCAG	60 120 180

GAGAAGGAGC AGTTGACCCA GGAATTACAG GAGGCTCGGA AGAGTGCGGA GAAGCGGAAG GCCATGCTGG ATGAGCTAGC AATGGAAACG CTGCAAGAGA AGTCCCAGCA CAAGGAAGAG CTGGGAGCAG TTCGTCTACG GCATGAGAAG GAGGTGCTGG GGGTGCGTGC CCGCTATGAG CAGGAGCTCC GAGAGCTGCA TGAAGACAAG AAGCGTCAGG AGGAGGAGCT CCGTGGGCAG ATCCGGGAGG AGAAGGCCCG GACACGGGAG CTGGAGACTC TCCAGCAGAC AGTGGAAGAA CTTCAAGCTC AGGTACATTC CATGGATGGA GCCCAAGGGCT GGTTTGAACG GCGCTTGAAG GAAGCCCGAGG AATCCCTGCA GCAGCAGCAG CAGGAACAAG AGGAAGCCCT CAAGCAGTGT CGGGAGCAGC ACGCTGCAG GCTGAAGGCC ACGCTGCAG CAGGAACAAG AGGAAGCCCT CAAGCAGTGT CGGGAGCAGC ACGCTGCCGA GCTGAAGGGC CGCTTCGAG CGGGAGCAGC ACGCTGCCGA GCTGAAGGGC CGCTTCGAG CGGGAGCAGC ACGCTGCCGA CCGCTGAAGGCC CCGCTCGAG CCCCCCGCTCGAG CCGCTCGAG CCGCTCGAG CCCCCCCGCCCCCCCGCCCCCCCCCC	240 300 360 420 480 540 600 648
(2) INFORMATION FOR SEQ ID NO:751:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 266 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:	
GGAAAGAATC TAAAAGAAGA GAAGCGACCG GTGCTTTTAA GGGTGTCTAA TTTTCAAAAG AGACGTCTGG GAGTATTTTG CTCTGGGCGT TTGGGTGAGC AGGACCGGGG CGTTGGAGGG TGCGGCGGGC TTGGGAGCAG GGAAGGTTCC GAGTCCTAGG GAGGCGGCAG CGCTCGGCTA TGCCCTCTGG AGACTGGCGG GGCTGCGGGG CCGAGGGGAC CCGCGAGGGA GCCGCGCTGC GGACGCGCTG AGCGCGGAG CTCGAG	60 120 180 240 266
(2) INFORMATION FOR SEQ ID NO:752:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 288 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:	
GAATTCGGCC TTCATGGCCT AGGATGTTT AAGGCTAGGC CTGAGCGAGG AGGAGGCAGG GGAGACCTGG CAGGTATTGA AGTACCTGGG AAGAAAGGCA ATGGGGATGG TGGTCCTGCT CCAAGATGAT AAGTGGAGGC TGAGCGTCAC TGGTACTGGG GGCCATGATC CCCAGGGCCA CCCTGGCACC AGGGTGCAGG GGATGCGGGG CCTGAGCAGG AAGAACAGAG ATCTGCGGGC TGCACCGACC CATCCCTGCC CCTAGGCTGA AGAACGGCAT CACTCGAG	60 120 180 240 288
(2) INFORMATION FOR SEQ ID NO:753:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 487 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:	
GAATTCGGCC TTCATGGCCT ACTGAATTTG CTTTTCTTGC CTCTCTTTAG TCACCTGTCA CAGGAGGTTC CTGCTCAGTA ATGATATTGT GAGTTAGGAT AATAACTTTT TTTTTTTTGT	60 120

GCTTCAGATT	TAGAAGAAAA	GATCCTGTTT	CCATTTGAAA	GGAACTGTAA	GCTTTTATCT	180
TTTAACCAAC	TGAACAATAC	ACCAAAAGCA	GCCTAGGGAT	GAGCATTTCT	TTGAAAGCAA	240
TTAGGTTATT	CACCTGGTAT	TAAAACTATT	TACTGTTAAA	AAATCTGTGA	CTTCATGAAG	300
TTGATTTTTA	AAGGCAGCAT	CAAAAACTGA	AAAGGAAGGG	AAAAAATAGG	CAGCTTCTCT	360
GCACTTGTTT	GGAGCTCCCC	AAAACAGGAG	CCATGGAGAA	GTGGCATCAA	GACCGGGCTG	420
CCCTTTCGAG	AACACCCTGT	GGCAGTTCAG	AGACACGCTT	TTCCTACACT	GCATGCAGCC	480
GCTCGAG						487

- (2) INFORMATION FOR SEQ ID NO:754:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

GCTGGGTTTA	GGCGATCCTC	TTGCTTCAGC	CTCCCAAGAA	GCTGGAGCCA	CAGGCATGCA	60
CCACCACGCC	CAGTTAATTT	TTGTATTTTT	TGTGGGGACG	${\tt GGGTCTCACT}$	TTGTTGCCCA	120
GGCTTATCTG	GAACTCCTGG	TTTCAGGCAG	TTCTCCTTCC	TTAACCTCCC	AAAGTGCTGA	180
GATTATAGGT	GTGTGTGAGC	TATCACACCT	GGCCTAGAAA	ATTATAAGAA	AATATTAATC	240
ACATAATCTC	ACTACCCATT	GATGATTTAA	CATCTAGTAT	ATACATATGT	ATATATAATT	300
TTAAAAGTAG	GGTTATATTA	TATAATTACT	TCATTATTCT	TGTTTTCCAC	TTAATATACT	360
TAAGATATCT	TTCAAAATCA	CTAAATACAG	GAACATAGTA	TATCATCTTT	CAGTAGCCTC	420
ATTGTATAGC	TAACCCCCTC	GAG				443

- (2) INFORMATION FOR SEQ ID NO:755:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 584 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

GAATTCGGCC	TTCATGGCCT	ATTGATTTCC	TGGGCTCAGG	AGAGGATGGG	GAAGGGGCTC	60
CAGACCCTCG	GCGGTGCACT	GTGGATGGGA	GCCCCCATGA	GCTGGAAAGC	CGTCGGGTCA	120
AACTCCAAGG	CATTCTGGCT	GACCTGCGGG	ATGTGGATGG	GCTGCCCCCA	AAAGTGACTG	180
GCCCGCCTCC	TGGCACACCC	CAGCCCCGGC	CACATGAAGG	TTCCTTTGGC	TTCTCCTCAG	240
ACGTCTTCAT	CATGGACACT	ATCGGGGGGG	GGGAGGTGAG	CCTGGGGGAC	TTGGCAGATC	300
TCACCGTCAC	CAACGACAAC	GACCTCAGCT	GCGATCTGTC	TGACAGCAAA	GATGCTTTTA	360
AGAAGACGTĠ	GAACCCCAAG	TTCACCCTGC	GCTCGCACTA	CGACGGCATT	CGTTCCCTGG	420
CCTTCCACCA	CAGCCAGTCG	GCTCTGCTCA	CCGCCTCCGA	GGACGGCACG	CTCAAGCTCT	480
GGAACCTGCA	${\tt GAAGGCGGTC}$	ACGGCCAAGA	AGAATGCGGC	GCTAGATGTG	GAACCTATAC	540
ATGCTTTCCG	GGCTCACAGG	GGCCCAGTGT	TGGCTGGACT	CGAG	•	584

- (2) INFORMATION FOR SEQ ID NO:756:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

					ATTTTTTCTT	60
CTCAGTGGAA	TTTGCTGAGT	AAAAAATTAT	AGGCTCAAAA	ACTGAGAACT	TTGAAGATAT	120
TGCACCATAT	TCTTTTTGTA	TTGAGTGTTG	CTGATGAGAA	GTCTGAGGTC	AGTCTGTTGC	180
					TTTTGAGAAT	240
TTACTCCTTA	TCCATGTTAT	TCTTAAATTT	CACCACATTC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:757:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

		TTCATGGCCT					60
GAAAT	ACAGA	ACTACACCTG	TAATTACAGA	GGGCATATGA	ACCCTAGTTT	GATAAGCCTT	120
GCTTT	'AAAGG	ATGCAGTGTG	TTCTATTAAA	TGTATTTAAT	ACAATTGCAG	AAATGGAAAA	180
		CATTAAACAA					240
ATTCC	TCTTG	TTTTAGTGCT	CAAAAATAGT	TTCATTTTTA	GGTATTTATG	CTTTAGTGGC	300
CTTTC	TCGAG						310

- (2) INFORMATION FOR SEQ ID NO:758:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

GAATTCGGCC AAAGAGGCCT	AAGAAAAGAA	AGCAAGAACA	GAAAACGAAG	CCACAGGAAG	60
GGAAGTAGAC ATTGTATGCT	ጥልጥርርጥጥጥርጥ	(アスカウスカウスカウス)	amaan aamma	ma oca ocaman	120
GTACGGATGT GCTTTGAAGT	TO A TO COME A TO A TO COME		~~~~~		
GIWCGGWIGI GCIIIGWWGI	IAIGIAIAII	ACATATAACA	GGAAAAAATA	TTAAAATAAA	180
CAGTGCTGGT CTCGAG					196

- (2) INFORMATION FOR SEQ ID NO:759:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

AAGTCAGATA (GATGCTATTT (AGACCTGACT (TICATGGCT ACAGCAAATC TGCCT GAGGTAAGTA CGAAGACCAC AAAGC; TAGACAAGGT GGTCAGGGCA AGCCTC GAAGTGAGAG TGAGCTATTG ACACGG GGCAGGCTTT GGAGGGAGAG CTTGT;	AGGTT AAAAAGTAAG CTCAG AAGAGGGGAT GAGAA GGGCATTTCA	GTGGGAAAGG AAGTGCTCAG GACTCTGAAG	60 120 180 240
GTCTTGTGGA	IAAAGCAGAA TGAACAAGAG TAAATO			300 360
	SEQUENCE CHARACTERISTICS: (A) LENGTH: 192 base pair (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	s		
	MOLECULE TYPE: cDNA			
(X1)	SEQUENCE DESCRIPTION: SEQ I	D NO:760:		
AGAAGGTTGA A	AGTCAAAAGT AGGTGCCCAT ATATAT ATGGAAACAT TATGGCATGC TTTAGA ATCTTTTAGG TCTATCCATT GGTAAA AG	CGTT CTGTTTTGGT	TTTCTTATTC CACATCAACT	60 120 180 192
(2) INFORMAT	TION FOR SEQ ID NO:761:			
(i) S	EQUENCE CHARACTERISTICS: (A) LENGTH: 326 base pair: (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	5 .		
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ I	D NO:761:		
GCATGTTACG G ATAAAATGAA A IGTGGGAAAT A AACTCCACAC	TCATGGCCT AGTTTATTGC TCCCAA GTGGTTAGG TTCCAGGATT ATTGAG ATCTATCGTC ACCTTAATTG CCTGTG ATTCAGCCTG GTATGTGAGT GACTGA ATTCATCCCC TTGGTAACTC AGCACA CATTTGGCTT CTCGAG	ATCT ATTTCTACTC CCTA AAAATATAGC AATG CAACTCCGTG	ACAATTGCTT ATGCTTGTCT GAAACACCCC AGAAGTAAAA	60 120 180 240 300 326
(2) INFORMAT	TION FOR SEQ ID NO:762:			
(i) S	EQUENCE CHARACTERISTICS: (A) LENGTH: 205 base pair: (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	3		
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ I	D NO:762:		
CCTTTAGCTA C AATAGCTTTG C	TCATGGCCT ACTGGCCCAA GTGAAA AATCCAAAAA TTCATCAGGT ATATTI TAATATATA ATACTAGTTG CCTTGI AGTGCCCAC TCGAG	TCTG TTTTCCAAGT	TCATGCAGGC CAGTTTCATC	60 120 180 205

•	(2) INFORMATION FOR SEQ ID NO:763:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 285 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:	
	GAATTCGGCC TTCATGGCCT AAAAATGAAT ATATTCCTAT CCTATATTAA GACACTTTCC CTAACCTAAA AGTTTATTCT GTTTTTAAAA TAAATGAAAG TATTTGTATG GGCCCTGGGC CTGACGGAGA TATGCCCTGC CCCCTCTCTA GAGTGCTGGG AATTCTCAGG TGACCCAGTC CCACAGGCAG CCAAGTGCCC ACACATTTCC AGGCTGCCCT CCACCAGGGC AGCGACCTCG GGTCACCAGG GACACGCACA CCTAGAAAGC CGTGGGCTCC TCGAG	60 120 180 240 285
	(2) INFORMATION FOR SEQ ID NO:764:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 345 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:	
	AATTCTTTAT CATTTCAGAT ATTAAGGATT TCAGATTTTA AGAGTTATCA GTGAAACTGT GTTACAAGAA TATTTTGTTC CTGAGACATC TCAGTATTAT AGGTGGCTTC AGACTAACAG GCACAGAATA GGATAGTGG AAGTATCTGA TTAGCTTTAC TGTACTTGGT ACCTTTAGGA ACCATATCTC CTTTAGTGCC TGCTTTTGAA CTTATATAA ACAGAATGAT GCTGCCTGTT TATCTCTATA ATTTTCTTCT TTCCCTTAGC ACGTGCTCAC TCGAG	60 120 180 240 300 345
	(2) INFORMATION FOR SEQ ID NO:765:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 100 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:	
	GAATTCGGCC TTCATGGCCT AGAGAATGTT TTCATGTTAC TTATACTAAC ATTAGTTCTT CTATAGGGTG ATAGATTGGT CCAATTGGGT GTATCTCGAG	60 100
	(2) INFORMATION FOR SEQ ID NO:766:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

(GATTGAATT	CTAGACCCTG	CCTCGTCATT	GTGGAACCCA	TGGAGCAGTT	TGATGATGAA	60
(SATGGCTTGC	CAGAGAAGCT	GATGCAGAAA	ACTCAACAAT	ATCATAAGGA	AAGAGAACAA	120
(CACCACGTT	TTGCTCAACC	TGGGACATTT	${\tt GAATTTGAGT}$	ATGCATCTCG	ATGGAAGGCT	180
(TTGATGAAA	TGGAAAAGCA	${\tt GCAGCGTGAG}$	CAGGTTGATA	GAAACATCAG	AGAAGCCAAA	240
C	BAGAAACTGG	AGGCAGAAAT	GGAAGCAGCT	AGGCATGAAC	ACCAATTAAT	GCTAATGAGG	300
(CAAGATCTAA	TGAGGCGTCA	AGAAGAACTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:767:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

GAATTCGGCC	TTCATGGCCT	AGATAATATT	TTATGTTCAT	TGTGTGTTAG	ACTGTGTTGA	60
AGTGGAAACT	TTGGAACATT	GTTGGAACCA	GTAAGAATCC	CATTCCTCAG	GTATCAGGTC	120
GTTAAAGTAG	TTTAAAATAA	CGTATTCCTT	AATTTTCCTC	AGCAGGTTCC	CCCTCCCTTT	180
AACTTGTGTG	TATAAATATA	TGTGTGTGAT	GTTTTCTCTT	ACAAAGATAG	TACTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:768:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

GAATTCGGCC	TTCATGGCCT	AGGGATCCCA	CCTTTTACAT	CCTAGGTGTG	AACAGATTCA	60
AATCCACTAT	TCCTCCAGAT	TTTATAGATG	AGGAAACCAA	GGTGCACAAG	AGGGATTTTT	120
TTGTTTTGTT	TTTTGTTTTT	GTTTGTTTTT	GAGACAGGAT	TTTGCTTTGT	TGCCCAGGCT	180
GGAATGCAGT	GGCACAAACA	TGGCTCGCTG	CAGTCTCGAA	CTCCTACGCT	CGAG	234

- (2) INFORMATION FOR SEQ ID NO:769:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

	GGACACAGAC TGCAATATCG GTAGTTGAAG AGGATCTAAA GCTTTTACAG	
CITAAGCIAA	GAGCCTCCGT GTCCACTAAA TGTAACCTGG AAGACCAGGT AAAGAAATTG	
GAAGATGACC	GCAACTCACT ACAAGCTGCC AAAGCTGGAC TGGAAGATGA ATGCAAAACC	240
TTGAGGCAGA	AAGTGGAGAT TCTGAATGAG CTCTATCAGC AGAATCTCGA G	291
(2) INFORM	ATION FOR SEQ ID NO:770:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 432 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)) MOLECULE TYPE: cDNA	
(aci)	CECUENCE DECORIDATION, CHO ID NO 220	
(XI)	SEQUENCE DESCRIPTION: SEQ ID NO:770:	
CGCTGCGTGC	TTGTGAGACT GCCTGTTCTG GGACCAGCCC CTGGGCTCTT CCACCAAGAT	60
TTGGTGAGGG	TCCCCCTCTG CCTCTCACAG AAGCCCCTGG CCCTGGACTG TCCTGGGGGC	120
AGGGACACCT	GTGGCTGGGG AAGGATGGC CAACAGCGGG AAGCAGTTTG CGCCTGGTGC	180
CTGATGATGG	TGAACCACGA GACAGATGGA GACGGGAGTC AGGGGACCCTT	240
	TGACCTTTTC CCAGACAGGC ACTCTCCAGG CCTAGGACAG ACAGGGCCCC	300
	CACCCCATGA CTTGGCCTGG AGGAACCTGG GGTGGGAAAC AAGTAGTCCC	360
	AGGCCAGAAC CACAGGTGGG GGACAGGGAC CTCGACAGAG CTGTGCCTGC	420
TCAACGCTCG		432
(2) INDODM	AMTON BOD OBO TO NO BEL	
(2) INFORM	ATION FOR SEQ ID NO:771:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 399 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
/aci)	SEQUENCE DESCRIPTION: SEO ID NO:771:	
(XI)	SEQUENCE DESCRIPTION: SEQ ID NO: //I:	
	<u></u>	
	TGCCCCGTAC GAGCGCGCG CCATGGAGTT ACTGAAGGTC TCCAAGGACA	60
	CAAATTTATC AAGAAAAGGG TGGGGACGCA CATCCGCGCC AAGAGGAAGC	120
	GAGCAACGTA CTGGCCGCCA TGAGGAAAGC TGCTGCCAAG AAAGACTGAG	180
	GCCCTCTCCC TGAAATAAAG AACAGCTTGA CAGAAGCCCT GGCTCTCCTG	240
	GTGGGTGTGG GTGTCGGG GGCCCGCAGT CCCCTGTCTG GTGCCCGCTC	300
	CCTCTCCGGG TGCTGCCTGG TCGTGAATCA AAAGCCGTGG CCCGCCCACC	360
CTTCCCGGGG	CAGCAGGTGA GGAAGCCGCT GTACTCGAG	399
(2) INFORM	ATION FOR SEQ ID NO:772:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 520 base pairs	
	(B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

AGTTGAATCT AAACCGGATA AACCATCGGG AAAGTCAGGC ATGGATGCTG CTTTGGATGA CTTAATAGAT ACTTTAGGAG GACCTGAAGA AACTGAAGAA GAAAATACAA CGTATACTGG ACCAGAAGTT TCAGATCCAA TGAGTTCCAC CTACATAGAG GAATTGGGTA AAAGAGAAGT CACAATTCCT CCAAAATATA GGGAACTATT GGCTAAAAAG GAAGGGATCA CAGGGCCTCC TGCAGACTCT TCGAAACCCA TAGGGCCAGA TGATGCTATA GACGCCTTGT CATCTGACTT CACCTGTGGG TCGCCTACAG CTGCTGGAAA GAAAACTGAA AAAGAGGAAT CTACAGAAGT TTTAAAAAGCT CAGTCAGCAG GGACAGTCAG AAGTGGTGCT CCACCCCAAG AGAAGAAAAG AAAGGTGGAG AAGGATACAA TGAGTGATCA AGCACTCGAG	120 180 240 300 360 420 480 520
(2) INFORMATION FOR SEQ ID NO:773:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:	
GAATTCGGCC AAAGAGGCCT AGTTTATTGT TTGCATATAT TTTATAGTGT AGAGATTAGG CATTTTAATA AAATTTTAAA ATTTCCAGGA TCTTACAGAA TGCTTTTATG TTACAGCTTA CTCCTCGAG	60 120 129
(2) INFORMATION FOR SEQ ID NO:774:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 337 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:	
GAATTCGGCC TTCATGGCCT ACACAACGGA AAGCTGTTTT TCTGATCGAG GCTCTCTGAA GAGCATAATG CAGTCCAACA CATTAACCAA AGATGAGGAT GTGCAGCGGG ACCTGGAGCA CAGCCTGCAG ATGGAAGCTT ACGAGAGGAG GATTCGGAGG CTGGAACAGG AGAAGCTGGA GCTGAGCAGG AAGCTGCAAG AGTCCACCCA GACCGTGCAG TCCCTCCACG GCTCATCTCG GGCCCTCAGC AATTCAAACC GAGATAAAGA AATCAAAAAG CTAAATGAAG AAATCGAACG CTTGAAGAAT AAAATAGCAG ATTCAAACAG GCTCGAG	60 120 180 240 300 337
(2) INFORMATION FOR SEQ ID NO:775:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:	
SAATTCGGCC AAAGAGGCCT AGTGAGCGCG ACCATCATGT CCATGCTCGT GGTCTTTCTC PTGCTGTGGG GTGTCACCTG GGGCCCAGTG ACAGAAGCAG CCATATTTTA TGAGACGCAG	60 120

TGCCAGGCCC CCTGTGCACC	GCCTGGAGAC TCCAGACTTC CAGCTGTTCA AGAATGGGGT GGCCCAGGAG TTGACTCACC TGCCATCAAG CACCAG	24 27
(2) INFORM	ATION FOR SEQ ID NO:776:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 586 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:776:	
CAGTTCAGAG CACTGAGTCA AAAGGCTTTA GAAAAAAGAA CACTGAACCT TAAAGAAGAA TCCAAAGGAA CTTGAATTTA ACAAGAAACA (2) INFORM	AAAGAGGCCT ATGAAATAGA AGAAGGTAAA AATAAGGAAC AAGCAATAAA AACATAATGA ACATCAATGA GGAACCAGGA ACAACTGAAG GTGAAGAAAT AGTAGCACTG AAGAAATGAA GGTCAGAAGT GTGGTGGCTG ATACTGACCA GGAAGTGAAG TTCCAGGATGC TTCTAAAAGC ACTACTCAGA TAGATAAAGA ATTCCAGTTC CAATTAAAAAA AGAGCCTGAA GTTACTGTAG TTCACAGCC CAGCCTGTTC TAATACCCAG TATTAATATC AACTCTGACA GTGGAGAAAA ATAGGTTCTT TATCAAAAAC TGAAACTATT CTGCCACCAG AATCTGAGAA AATGATAATG ATTCAGGCAC TGGTTCCACT GCTGATACTA GCAGTATTGA TCCATCTCTA GCTTTCTAAG TAAAACTAAA GACAGTGGAT CGATATCTT AGAAGACAAA AGAAAACATT GAAGAAAACA CTCGAG ATION FOR SEQ ÎD NO:777: SEQUENCE CHARACTERISTICS:	60 120 180 240 300 420 480 540 586
(1)	(A) LENGTH: 463 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:777:	
CTGAGATTTC AGCTTCAAAC AGTATTCTAC GGGCCACAAG ACTCTCAATC CCACAACTGT TTTATCCTCA	TTCATGGCCT AGTTTATATA GAGTAGGTTT ACATAGAAAA GGAAAGTTCA TAGGTACAAG ATCTANCAAC ATGCACAAAC CAATATTGTT TATGTATAAC AATTAGAAAT TGTAATAACC ATTATGAAAG TGATGAAAAT TGTATTGCTT CAAAATTATT AAGTAATTTT TTTTTTTTT TTTNANACGG AGTCCCGCCT NGCNAAAATT TGTTTCNAAA AAAAAAAAGA AAAGAAAGAA AAAAAATTGA CCTAGATGTA AAATCAACCT CGTGTTCTTG ATTTCACCAG TAATTCATAA TGTGTCTTGA ACACTTACTA TGCTTGGCAT ACTTATAATT TTTATTTCAC AATTTAAGAT GAAGTTTCTC CTACTAACTC GAG	60 120 180 240 300 360 420 463
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 466 base pairs	
	"" mandin. 400 pase batts	

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

GAATTCGGCC	TTCATGGCCT	AGCTGGGAGT	TACCTGNTAT	CCTGATGGTG	CCATGTGCTA	60
GCTGGGTGAC	AATAACCCAG	CCACCTAACA	TCTCAAAGAT	TGTTCCTTTT	TGTGTGAAAT	120
AGGGATAGAG	TTGTCTACTT	CCCAGAGCCA	GATAGAGAAC	TTAAGAGATG	AATCTGAAAA	180
TACAATAGCC	TAAATAAATT	CAAGGAAACA	CTATTATCTT	ACTGGATCTT	TCCAGCAACC	240
ATGTTACTTT	TGGCTGGATT	TTGTATTTTC	CAATTTGTGA	ATGACACAAC	AAAGAGCTAG	300
GTAGGTTAAG	TAAATGGTTT	CAGATAATAA	GCCCAGTTAG	CCCAGACGTT	TATTTTCCAT	360
		TTATGCATAC				420
			AGAATACAAC			466

- (2) INFORMATION FOR SEQ ID NO:779:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

GAATTCGGCC	TTCATGGCCT	AATTCCACAG	GGAAATGGGC	AGACTGAACC	AGTCCAGGTG	60
GTGAATTTTC	CAAGAACATA	GTTTAAGTTG	${\tt ATTAAAAATG}$	CTTTTAGAAT	GCAGGAGCCT	120
ACTTCTAGCT	GTATTTTTTG	TATGCTTAAA	TAAAAATAAA	AATTCATAAC	CAAAGAGAAT	180
CCCACATTAG	CTTGTTAGTA	ATGCTCTGAC	CAAGCCGAGA	TGCCCATTCT	CTTAGTGATG	240
GCGGCGTTAG	GGTTTGAGAG	AAGGGAATTT	GGCTCAACTT	CAGTTGAGAG	GGTGCAGTCC	300
AGACAGCTTG	ACTGCTTTTA	AATGACCAAA	GATGACCTGT	GGTAAGCAAC	CTGGGCATCT	360
TAGGAAGCAG	TCCCTGGAGA	AGGCATGTTC	CCAGAAAGGT	CTCTGGAGGG	ACAAACTCAC	420
TCAGTAAAAC	ATAATGTATC	ATGAAGAAAA	CTGATTCTCT	ATGACATGAA	ATGAAAATTT	480
TAATGCATTG	TTATAATTAC	TAATGTACGC	AGACTCGAG			519

- (2) INFORMATION FOR SEQ ID NO:780:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

GAATTCGGCC TTCATGGCCT	ACTAGACCCC	CGCCACAGCA	GCCTCTGAAG	TTGGACAGCA	60
AAACCATTGC TTCACTACCC	ATCGGTGTCC	ATTTATAGAA	TAATGTGGGA	AGAAACAAAC	120
CCGTTTTATG ATTTACTCAT	TATCGCCTTT	TGACAGCTGT	GCTGTAACAC	AAGTAGATGC	180
CTGAACTTGA ATTAATCCAC	ACATCAGTAA	TGTATTCTAT	CTCTCTTTAC	ATTTTGGTCT	240
CTATACTACA TTATTAATGG	GTTTTGTGTA	CTGTAAAGAA	TTTAGCTGTA	TCAAACTAGT	300
GCATGAATAG ATTCTCTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:781:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 560 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

GAATTCGGCC	TTCATGGCCT	AAATGGGAAT	CATCATTGCA	TAACAAACCT	AAAGAGAAAA	60
TGAGAACATT	TACGAAGAAG	AAACAGAGTT	ACTGTACCAA	GGGCAAAAAG	AAAAGAAGGG	120
GGAAAAAAAA	TAAGTCCATA	AAAGAAAAAC	AAAAGGAATC	CATGAGCCTG	GACGACAAGC	180
CGTGGGGGAT	GTAAGAAGGT	TTGGAACCCA	AAAGGCAAGT	CTAATCAGCT	GGGGTAACAT	240
GGCGAGGCAG	TTCCACATGC	TGAGACTTGT	GGCTACCACA	TTAAAAAAGA	CTGTGCATAT	300
TCTAAATGAC	AGCAGTCCTG	CAGTGACGTG	GATATTCACT	CTAGAAGCTA	TGCAGGCAGG	360
CGTGGGAAAA	GCGAAGAGAT	GTTGCACCAT	GCAGCTGCAA	TCTTTATGTC	TCTACTGGCA	420
CAACCGAAAA	GAGTAATGTG	GAAATTATCC	AGAGAATTTA	GGTGAGAAAA	ACAGAAGCCA	480
	TCCTTTAAAT	CTTCAGAGGG	GTATACACTC	CCCTGGAAAA	CCAAGTTGCC	540
TCTCTGCTCA	CATCCTCGAG					560

(2) INFORMATION FOR SEQ ID NO:782:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

GAATTCGGCC	TTCATGGCCT	AGGGGAGTCC	TCATTCTGAC	CTCAAAGAAA	GGACTGTATT	60
GTCTGGCTCC	ATAATGCAGG	GGACACCAAG	AGCAACAACT	GAAAGCTTTG	AAGATGGCCT	120
			TCCTCCCATA			180
			CACCATCAAA			240
			${\tt GGAAAGTCGG}$			300
			TTCCCAGGGC			360
			TGTCAAATCC			420
			TGTGCCAGAG			480
			GACCGTGCGT			540
AAGCTCTGGC	CCCTCCGTTC	TTAGGTCCAC	ACTGCATGAA	GCTCCCAAAG	CACAACTGAG	600
CCCTGGGATT	TATGATGACA	CCAGTGTCTC	GAG			633

- (2) INFORMATION FOR SEQ ID NO:783:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

AAATGACACT G	AATGACACG	TTAGCCAAAA	CTAACAGAGA	ATTATTAGAT	GTGAAGAAAA	60
AATTTGAAGA T						120
GAAACCTGGA A	AACACTCAG	AACCAAATAA	AAGCTGAGTA	CATCAGCCTG	GCAGAGCACG	180
AGGCAAAGAT G	AGCTCGCTA	AGTCAGAGCA	TGAGAAAGGT	GCAGGATAGT	AATGCTGAAA	240
TCTTGGCCAA C						300
CCCAGAAGAA G	GAGCTCGAC	ACAATACAAG	AATGCATTAA	GGTAAAATAT	GCCCCAATTG	360
TCAGCTTTGA G	GAGTGCGAG	AGAAAATTTA	AAGCAACAGA	GCTCGAG		407

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 342 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:784: GCAGAAAAGT CAGAACAATT TGAGGAGCTT CAAAGCATCC TTAAGAAAGG GAAACTAACT 60 TTTGAGAATA TTATGGAAAA ACTGCGAATC AAGTATTCCG AAATGTACAC CATAGTCCCT 120 GCAGAGATTG AATCCCAGGT GGAAGAATGC AGAAAAGCTT TAGAAGACAT AGATGAGAAG 180 ATTAGCAATG AAGTCTTAAA AAGCTCACCA TCATATGCAA TGAGGAGAAA AATAGAAGAA 240 ATTAACAATG GGCTTCATAA TGTTGAAAAG ATGTTGCAGC AGAAAAGCAA AAATATTGAG 300 AAAGCTCAAG AAATTCAAAA GAAAATGTGG GACTCACTCG AG 342 (2) INFORMATION FOR SEQ ID NO:785: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 456 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:785: GAGATAATGG ATGAAAGGAT TCAGAGGAAA GTAGAGAAAC TAGAGCAACA ATGTCAGAAA 60 GAAGCCAAGG AATTTGCCAA GAAGGTACAA GAGCTGCAGA AAAGCAATCA GGTTGCCTTC 120 CAACATTTCC AAGAACTAGA TGAGCACATT AGCTATGTAG CAACTAAAGT CTGTCACCTT 180 GGAGACCAGT TAGAGGGGGT AAACACACCC AGACAACGGG CAGTGGAGGC TCAGAAATTG 240 ATGAAATACT TTAATGAGTT TCTAGATGGA GAATTGAAAT CTGATGTTTT AACAAATTCT 300 GAAAAGATAA AGGAAGCAGC AGACATCATT CAGAAGTTGC ACCTAATTGC CCAAGAGTTA 360 CCTTTTGATA GATTTTCAGA AGTTAAATCC AAAATTGCAA GTAAATACCA TGATTTAGAA 420 TGCCAGCNGA TTCAGGAGTA TACCAGTGCT CTCGAG 456 (2) INFORMATION FOR SEQ ID NO:786: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 488 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEO ID NO:786:

GAATTCGGCC	TTCATGGCCT	AGGGGTGAGA	GTGTAGACGG	CTTTCCCAGT	TGTATCCAAG	60
GCAGTCAGAC	AGGGGGATTT	GGGCTGTGTT	GTGCCCCAGC	GCTGCAAGGT	GGCCAACAGC	120
GACGGCGGTC	GGGGGACACC	TGCAGTGAGA	GGCTCCCCTC	TCAGCACACT	CGTCTCGCTT	180
		TGGATCTGGT				240
TCCACAAAGA	ACTCCTTCAG	TGGAGGGCGC	TTTGGCCTCT	TCAGGGTGTT	CAGAAGCTGC	300
TGGATTTTGG	AGGACACTCT	GCTGTTCACA	GGGACACCAT	CTGCTGTTTC	CAGCATGCTC	360
		ACTTCTCACA				420
TGCTCCACGA	GGCCCGTGGT	GACATCAGGA	GGGGCAGAAT	GCAGATCTAT	GTGGGTGTGG	480
GCCTCGAG						488

- (2) INFORMATION FOR SEQ ID NO:787:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

GAATTCGCCT TO	CA TO CO COTTA	ACTOTOTOTO A	A CA MA MOMOS	E		
GAATICGCCI IC	CAIGGCCIA	AGIGICCGGA	ACATATGTCA	TGATTCTATG	TCCAAACAAC	60
AGGCCAACCC TO	CAGGACAGA	CCCCGCCACC	CCCCTTCTCT	GCAGCTCCTG	GCAGGGACGG	120
TGCACAGTGG TG	GCCGTGTGC	AGGGGGCCAG	CGCAGCCACT	GGGCATCTGG	GGCAGCGCTG	180
GTCGCCTGGC CA	ACCTCCTTG	CTGGGGCCGC	TGGGCCTCCG	GCCTAGAAGG	ACAGGAAGCC	240
ATCCACCTCA AG	GCCCACGA	AGGGGTCCAG	CAGGGCCCGG	AGCTTCCAGA	TGGTGGCACG	300
GCTCAGCAGG GG	GCGGCACCA	GCCCCTCGAA	GGGCCTGGGG	TTCACCATGT	ACACGTAGGC	360
GACCAGCAGG GT						420
GTCCTCCATC TO						452

- (2) INFORMATION FOR SEQ ID NO:788:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

GAATTCGGCC GCATAATTAA						60 120
CTGTGTCAAA	TTCTCAAATT	GAAACTGAAA	TTGAAGTTCC	ATCGTCCGCA	GTTCCAGAAC	180
ACAGAATGTA	TGAAAATCAA	AGTCAGGTGG	TTCTTGTAGA	AAACCTTCAT	GTTAACAAAA	240
CAAATGAAAC	AATCAGACAT	GAAAATAAAC	CGTATGTTCC	TAGTTCAGCA	CAAATGACAA	300
GAAGGAAATT	CCAAAAGGCT	AAGCCAAATT	TGGGAAGAGC	ACACAGTAAG	AAAGAGGAAC	360
CAGTTTTAGA	AAAAGTCACA	AACTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:789:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

GCCTGAAGAC	ATCAAAAAGG	AGGCAGCCCG	GGCTTCTAGG	AAGATCTGCT	ттататась в	60
				1010111 01001	1101010011	
GAAAAAGGGA	GCTGCTATCA	ACTGCCAGAA	GGATCAGTGC	CTCAGAAACT	TCCATCTGCC	120
TTGTGGCCAA	GAAAGGGGTT	GCCTTTCACA	ATTTTTTCCA	GAGTACAAAT	$C\Delta$ T	180
						+40
CAAACATCGC	CCAACACAGA	ACATCCAACA	TGGGCATGTG	GGGGAGGAAA	GCTGCATCTT	240
T. C.	~ · · · · · · · · · · · · · · · · · · ·					
ATGTTGTGAA	GACTTATCCC	AACAGAGTGT	TGAGAACATC	CAGAGCCCGT	GTTGTAGTCA	300
AGCCATCTAC	CACCGCAAGT	GCATACAGAA	ATTATOCCCAC	N CATCACON N	N C C N COMM COMM	360
		~~~~~~	VIVIOCCCA	MUMICAGUAA	AGCALITCIT	200

	CAGTGTAACA ATCGAAAAGA GTTTCCTCAA GAAATGCT	rga gaatgggaat	420
TCATATTCCA	GACAGAGATG CTGCCTGGGA ACTCGAG		457
(2) INFORM	ATION FOR SEQ ID NO:790:	-	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 582 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double		
	(D) TOPOLOGY: linear		
(ii)	) MOLECULE TYPE: cDNA		
(xi)	) SEQUENCE DESCRIPTION: SEQ ID NO:790:		
GAATTCGGCC	TTCATGGCCT AGCGGCAGCG GCTCTTCAAA GCGGAGCC	CG GAGTTTTTCC	60
	GCCACCATGA GTCGCAGCTA TAATGATGAG CTGCAGTT		120
	TGCTGGAGGA TCAAGAAGGG CTTCGTGCCC AACATGCA		180
	AATGATGCTC TGGAGAAATT GATGTTTGAG GAATTAAG		240
	GTTGGTGGCT TCCTGCCAGC CATGAAACAG ATTGGCAA		300
	GTTCATCGAT CTATTGGGCT TCCTGATGTC CATTCAGG		360
	ATGGCAGCCT TTGATATGAA TGACCCTGAA GCAGTAGT		420
	GACATCAACT GTGGTGTCCG CTTGCTAAGA ACCAATTT		480
	GTGAAGGAGC AACTTGCCCA AGCTATGTTT GACCACAT	the state of the s	540
	GGTGTCATCC CAATGAATGA CAAAGACTCG AG	.10 0,01,00001	582
(2) INFORM	ATION FOR SEQ ID NO:791:		
(:)	OPOLITINOS CUADA OPERA CO		
(1)	SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 468 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: double		
	(D) TOPOLOGY: linear		
(ii)	) MOLECULE TYPE: cDNA		
(xi)	) SEQUENCE DESCRIPTION: SEQ ID NO:791:		
GAATTCGGCC	TTCATGGCCT ACATTTCTG AGAAAGGTTT GGATGACT	rga aatattteet	60
	GGACTTTGGC ATGTGGTGGC TGAAACTGAG CTTTTTTC		120
	TCTGCAATGC TCATGGCAAG TTGAATGGTG AGCTAGCT		180
	TGTATTCAGA CCGACTGGGT ATCTAGCTTA CTGTTTT		240
	CTGTAGTCCA GTGGTGCTGC CCTGTTGTGC AAACTGC		300
	AGAGCTTCCA TCTGGGCTGG ACCCAGTTCT TGCACATA		360
	AGGACCTTTC CGCCATGTAT TCTATTCTGT AGTAAAG		420
	TGTATCTGTT ATTTTTGGTT TAACACACAC TGCTCGA		468

- (2) INFORMATION FOR SEQ ID NO:792:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 519 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

GAATTCGGCC	TTCATGGCCT	ACGTGGCTAT	AACTGGAAAA	CTGGATCCGA	AATCGACCAG	60
TAAACTGGGT	AGCTCGGTCT	ACGCCCCGCC	CACCACCCTT	GCTAGCCAAT	AGCCTTCACA	120
ACTCTTCTGC	CACTCCCGCC	CATTCCAGTG	CTGTGCCGCT	GCTTTTTCTT	CCACTCGGAT	180
CTCTTGAGCG	CCCTTAGCCC.	GCTGTATACG	CGCCCCTCCT	CGGCTTCAGT	AGGCAAGAGG	240
GCCATCTGCC	CTTCCTTCCT	GAAGGTAGAG	GGGACAACAC	CAGCTACGAC	GGGGACTCCA	300
GAAGTCCATC	TCCCGAACAG	CAGCGGGGCG	AAAAGAAAGA	AAAAGGGTTT	CCGAAGACTC	360
CTACTCACAC	CCACGCTTTC	CCTTAACCCG	GAAGTGATTT	CCGCCCCTCC	TCTCCCTCTT	420
CGGTTGATAC	TGGAGGAGAA	GGACGGCCAG	GTCTGGCCCG	GCATGCCCTG	GGCTTCCGGT	480
GACCTCTGGC	CCTTTTCTGT	CGTCCACTCT	CCGCTCGAG			519

- (2) INFORMATION FOR SEQ ID NO:793:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 338 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

60
120
180
240
300
338

- (2) INFORMATION FOR SEQ ID NO:794:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 756 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

GAATTCGGCC	AAAGAGGCCT	ACCAGGATGG	TCTCAATCTC	CTGACCTCAT	GATCTGCCTG	60
CCTCGGCCTC	CCAAAGTGCT	GGGATTACAG	GCGTGAGCCA	CCGCACCCGG	CCCTAAACCC	120
TAGGTTTTGA	CTTCTGTAAG	AAGGAAAGAT	TTAAACAAAC	AAACAAACAT	TAAATTACAA	180
CCATAATAAA	CAAAAAAACA	CTAAACTAAA	TTACAACCAT	AATAAAATCT	CCCAAAGTCC	240
GTAGGCACTG	ACATATTACA	GCCTTGCCAA	ATCAGAATAG	ATTTCTCATG	TGTTGTCAAT	300
,		CTCAGATCTC				360
CAAGTCTTTT	TAAAGTTTTG	AAAAACATGT	GCTATTTGGA	ATTACGTCAT	CCTCGAATAT	420
TAAACCTGAG	CTCAAAAACC	TATTGTTTGA	TATTGGAAAT	AGTTAACTCC	AGTTTTCTTC	480
TATTAAGATA	AAATTCTTTC	ATCATGTCTG	TGCCCTCTAA	AATAATACTC	CTATTGCTTT	540
GTCTTCCCCT	TCTCCCCTCC	TAGTCCTTCT	TTAGTCATTC	TATTTAGAAT	CAAGTCGCTC	600
ATGAGTTTAA	GAATTAGAGC	AGCAAGAAAT	TGGGCTAGAG	ATGTACAAAA	GCTTTGGACA	660
ATAGTAGTTT	TGCTTGTCCT	CATTCTTATT	AGAAGTGCTG	TTAATTTACT	GATAAATTCT	720
AGGACGGAAG	ACAAATCTTT	GCAACTGGTA	CTCGAG			756

- (2) INFORMATION FOR SEQ ID NO:795:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 648 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (11) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GAATTCGGCC	AAAGAGGCCT	ACCAGGAAGC	TCTCCTGCTT	GTCATGAAGT	GAGAACAATG	60
AAAAGTCATA	GCAGATACTC	AGTTTAACTC	TGTGTAGAAC	CTATTAGTGT	TTGAGCTGTT	120
ATTCAGATTT	GAATTCAGAC	TGTGTGTTGT	TTGCTTATGG	ACACTGCCTG	TCGTTCTGTC	180
ACTGTTAAAT	TAATGAGTCT	ATAAGGTTTT	TCTTCCAGAG	GCCATAGGTG	ACATCACTAA	240
AATTGCAAGA	TAAATTGTAA	TCTTTGNTGN	TGCTGCACTC	CCCAACCTCT	CCCCCACCCC	300
CCGTGGTGTG	CTGCTTTCTA	GATGAGCGTG	TTTTGGAGCA	GGCCCATCTG	GGACACTCTA	360
TGCTTTCACC	AAGGAAGTGC	GATCTGAGCA	GCCACAATCC	AGCCAAAAGA	GGATCGTAGA	420
				ATTTAGCCCA		480
TTATCCAACT	GAGTCTCTGA	CCAGCAATTG	GTGCATAATT	ATTACAGCAA	AAGTTAAGAA	540
				TTAATACCTG	TTACTAGTGG	600
ACTTCCTGTG	AGGAAGTTAG	TTTTTTGTTT	TGATGAAATG	CTCTCGAG		648

- (2) INFORMATION FOR SEQ ID NO:796:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 610 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

GAATTCGGCC	AAAGAGGCCT	AAGAGGCTGG	CCCCAGTCCC	AAGGAACAAG	AGATGGTCAA	60
GTCGCTAGAG	ACATATCAGG	GGACATTAGG	ATTGGGGAAG	ACACTTGACT	GCTAGAATCA	120
			CACATGGGAG			180
			ACCTAGAGTC			240
			CCCCTCCTAC			300
			GGACTGGCGC			360
			CTGCTTACTC			420
			GTAATGTGGC			480
			TTGGTCCCGG			540
TATTTTCTGG	GCTGGGGTAG	GAGGAAGGTT	GTTGCAGCCA	TCTACTGCTG	CTGTACCCTA	600
GAAGCTCGAG						610

- (2) INFORMATION FOR SEQ ID NO:797:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

GAATTCGGCC	AAAGAGGCCT	AGCCACTATC	CTGGTTACTT	GTGGATTCAC	CAAGCAGTCC	60
AGCAAGTCAT	CCGTAGAAAT	GAATGTTTGA	GGAGTCGTAG	TAGTATTTGA	GGCAATCTGT	120
TCCTCAATTG	${\tt CATTTTCACT}$	GTTGCTCATT	ATTTGTTGTC	TCTTGGCACA	ATGCAATTTT	180
CCAAAGTGTT	CTCCATCCTT	GTCCACAAAG	TCTTTCCCAT	CACTTCCAAA	TATGCCTCCT	240

CTTTCTGAAG GCGGTTCTTC GGACCTCTGT GCTACAGGGA CTCGAG	286
(2) INFORMATION FOR SEQ ID NO:798:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 163 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:	
GAATTCGGCC AAAGAGGCCT AGTTTTTAT TGGTTTGGAG ACTAGAGCCA ATAGTATAAT GTTCTCAAAG GAAACAGACT TGAGTTGTTG GATTAGAGGA ACTAACCCAA CTTATATGAT TTTTTTTTTG TTTTTGTCGT GTAGTTATGG CACTAGTCTC GAG	60 120 163
(2) INFORMATION FOR SEQ ID NO:799:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 443 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:	
GAATTCGGCC TTCATGGCCT AGAGGGAATG CGGAGAGGGG TGGAGAAATT CCATCTTTGT TAGGGCAGCA GTCAAGGATG AGTGAGTTAG CCTCTTAAGG AAGAGGCTAA GCTGTTAGAA TAAAGAGGTT TACAACATCA GCGGCTTAAA TCAAATAGAA GTGTGTTTCT CTTCTCACATG ACAGAGTAGA TGTGGCCTGG CATCTAGAAA GCATATTTGT CTCTGCTCCA CTGTGTCTTC CAGGGACCCA TTCTTCTCTT GTCTTCATGC TCCATCACTT CCTAGGGTGT TGTCTACACC TGCATAGCCA TAGCTAATTT TCCATTCTCA GCACCAACCA GGGGAACAGG AGGAAAGGTA GCCTCCTTTT CATGATAGGT GTGAAGTTAT GCAGGACACT CTCAGGGTGA ATGGACCACA GTGTGGCTCC TCCTGGGCTC GAG	60 120 180 240 300 360 420 443
(2) INFORMATION FOR SEQ ID NO:800:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 305 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:	
GCATGTGCAG CGGCAAAGAG AACCCGGACA GTGATGCTGA CTTGGATGTG GATGGGGATG ACACTCTGGA GTATGGGAAG CCACAATACA CAGAGGCTGA TGTCATCCCC TGCACAGGCG AGGAGCCTGG TGAAGCCAAG GAGAGAAGAG CACTTCGGGG CGCAGTCCTA AATGGCGGCC CTCCCAGCAC GCGCATCACA CCTGAGTTCT CTAAATGGC CAGTGATGAG ATGCCATCCA CCAGCAATGG TGAAAGCAGC AAGCAGGAGG CCATGCAGAA GACCTGCAAG AACGGTCGAC TCGAG	60 120 180 240 300 305

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

GAATTCGGCC	AAAGAGGCCT	AAACACTCAA	ATTTTACATT	TTGAGCAGTA	TTTACGCCTG	60
AATTAATTCA	CAAGTTTCAA	GGTCACTAAC	TTTGGTTATA	TTATATTATT	ATTTTCCAAT	120
TTAGCCACCT	CTTTATTTGT	ATAATAGAGC	ATACAGCAGC	ACATAAAACG	CAAAACTCTA	180
GGACATAAAA	AGTGGCATTC	GGACGATGTT	GCTCTGAAAT	TTATGCATTA	ATTAAACCGG	240
TATATATGTA	TGCATTAATT	AAACCAATAT	TTATGAAGTT	CCTACTGTGT	TACAGACGTG	300
GATCCAGGCA	CTGAGGATGC	AGCAGGCCAT	CCAAATATAA	AGTTACTTCC	TTAGGAAGCT	360
TCCATTCTAA	TGGGAGAGTG	TTGTTAAAGA	GATATATAAT	AATATGTAAA	ATGAATCCAT	420
AATGGTGAGT	ATTATGAAGA	ATAAAATTGC	CAGGTTTTCT	CGAG		464

- (2) INFORMATION FOR SEQ ID NO:802:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 650 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

GAATTCGGCC .	AAAGAGGCCT	AATCTTCTGC	CTGTTCTGAA	AAAGCTTTGC	TTCTTGTGAT	60
TTGTATCACG	AGGGGGAAAG	GTCCTTACTG	TTTTTCCAGA	CCTACAGTTG	TGATAGAGGC	120
TCCTCCCAGC	CCCGCCCACA	GACCCCAACA	GTGCCCTCTC	TCACAAATGG	ATTCTGGGGC	180
TTGGTCTTTA	TTTTTGTTTT	TGTTGGGGGC	AGCATATGGA	ACCCAAAAAT	AGTATCATAG	240
CCTAAATTTG	GAGCTTTGTG	CCAGCCTTGT	CTGTAGGATG	ACCCGTGTGG	GTCTCACCTG	300
GTGACTGGGA	GTCCACAGGG	GTCAGTTAGT	AGCAGGGAGC	TGCAGGGCGC	CTGTCAGCAG	360
AGACCGTCTC	ATTCCCCAAA	CCCAGGAGCC	AGAGGAACTG	ACGCCCGGAT	AAATGCCCAA	420
GCCGCCCCGG	GTGGGATTAG	TCGTCTACCT	TCCCAGAAAT	ACACCCTCCC	ATCCTGTGAC	480
TTGGATACAG	TTTACTGATG	AAATTAGGGA	ACCTCCTGCG	CCTTACCAAG	AAGCTGTGGC	540
TGGAACTTAG	TCAATGAAAA	ATGATTTGTA	AACTCTTTGG	AGCTGGCTTT	GAAAGAATGT	600
TTAAAATGAT	AGCTGATACT	GCCAGACAAC	AGAACAGGCC	GGCCCTCGAG		650

- (2) INFORMATION FOR SEQ ID NO:803:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 101 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

GAATTCGGCC AAAGAGGCCT AAGAGAACAG GAGCATTACA GTAAAATTCC TAAGTAGCCA
ACTGATTTGC AGTGCCAGAA ATGAATACCG ATCCACTCGA G 101

(2) INFORMATION FOR SEQ ID NO:804:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 723 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

GAATTCGGCC	AAAGAGGCCT	AGCTCTCTGT	ACCCAAGGAA	AGTGCAGCTG	AGACTCAGAC	60
AAGATTACAA	TGAACCAACT	CAGCTTCCTG	CTGTTTCTCA	TAGCGACCAC	CAGAGGATGG	120
AGTACAGATG	AGGCTAATAC	TTACTTCAAG	GAATGGACCT	GTTCTTCGTC	TCCATCTCTG	180
CCCAGAAGCT	GCAAGGAAAT	CAAAGACGAA	TGTCCTAGTG	CATTTGATGG	CCTGTATTTT	240
CTCCGCACTG	AGAATGGTGT	TATCTACCAG	ACCTTCTGTG	ACATGACCTC	TGGGGGTGGC	300
GGCTGGACCC	TGGTGGCCAG	CGTGCATGAG	AATGACATGC	GTGGGAAGTG	CACGGTGGGC	360
GATCGCTGGT	CCAGTCAGCA	GGGCAGCAAA	GCAGACTACC	CAGAGGGGGA	CGGCAACTGG	420
GCCAACTACA	ACACCTTTGG	ATCTGCAGAG	GCGGCCACGA	GCGATGACTA	CAAGAACCCT	480
GGCTACTACG	ACATCCAGGC	CAAGGACCTG	GGCATCTGGC	ACGTGCCCAA	TAAGTCCCCC	540
ATGCAGCACT	GGAGAAACAG	CTCCCTGCTG	AGGTACCGCA	CGGACACTGG	CTTCCTCCAG	600
ACACTGGGAC	ATAATCTGTT	TGGCATCTAC	CAGAAATATC	CAGTGAAATA	TGGAGAAGGA	660
AAGTGTTGGA	CTGACAACGG	CCCGGTGATC	CCTGTGGTCT	ATGATTTTGG	CGACATCCTC	720
GAG						723

- (2) INFORMATION FOR SEQ ID NO:805:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 406 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

GAA	TCGGCC	TTCATGGCCT	ACGGCCAAAG	AGGAGGAGAT	GGCGCCAGTC	AGGGAGCGGC	60
CGT	GCCCAG	ACAGTGAGGA	AGCGCGAAGG	CGGAGCAACC	GAGGAATCCT	CCGGAGAAGA	120
ATC	AGAGCCG	TCGCTACCGC	CACTACCGCC	ACCACCATGG	AAGGAGCAAA	GCCGACATTG	180
CAG	CTCGTGT	ACCAGGCAGT	GCAGGCGCTT	ACCACGACCC	AGATCCCAGC	GGAAAGGAGC	, 240
GCGC	CCTCTTT	TTGGCTTGGG	GAGCTGCAGC	GTTCGGTTCA	TGCATGGGAG	ATCTCAGACC	300
AGT"	IGTTACA	GATCCGGCAG	GATGTGGAGT	CATGCTATTT	TGCTGCACAG	ACCATGAAAA	360
TGA	AGATTCA	GACCTCATTT	TATGAGCTCC	CCACAGTACT	CTCGAG		406

- (2) INFORMATION FOR SEQ ID NO:806:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 329 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

C	FAATTCGGCC	TTCATGGCCT	ACGCCCGGGT	TGGAAGTGTG	CAGTCAATGA	GCTCCCGCTC	60
C	TCCTGGATC	CGTCTGTAGG	TCTCCCCGGT	GTGCATGAGC	AGCTCACTCA	CTGGCTTCTT	120
•	PAGGTGTTCG	CTGAGGGCTT	CCTGCTGCTT	CTTCCGCAGG	GCTGTGTTAC	GCTGCCAGTT	180

(2) INFORMATION FOR SEQ ID NO:807:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 225 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:	
GAATTCGGCC TTCATGGCCT AAGGTACTTT AATCAGTCTA AATACTTGAA CATTTTTATT TCAGTGGTAA AAAATAGACT GAGGCAGAGT GAAGTTATAA ATTAGAATCT AAAAATTTAC CCTTCAACAT TAATATTTTT TAGTGCTCTA ATATAAAACA CAGAAAACCT ATCTCAAATA TAAAAGATGA ATATAAAATT ATTAATTAAA CAACTGGCGC TCGAG	60 120 180 225
(2) INFORMATION FOR SEQ ID NO:808:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 275 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:	
GAATTCGGCC TTCATGGCCT AACTTGCTCT TCTGTTTCTA GTTTTATAAA GTGAAAGCTG CAATCATTGA TTAGAGACAG TTCTACGCTA AAGTCATAAT GACATTTTAT GTAATTTCTT TTTTCTTTTT TTTGAGACAG AGTCTCGCTC TGTTGCTCAG GCTGGAGTGC AGTGGAGTGA TCTCAGCTCA CTGCAACCTC TGCCTCCCAG GTTCAAGCGA TTCTCCTGCC TCAGCCTCCC GAGTAGCTGG GATTACAGGC CCCCACCAAC TCGAG	120
(2) INFORMATION FOR SEQ ID NO:809:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 253 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:	
GCGATTGAAT TCTAGTTGCC TACCTACCAA ACTACCTACT GAACTTTTTA ATTTGAAGAT ATTCTTCCTG GACTACTTGT TTATAGTTTA TTAAATGAAC TGCTCTATTT CTAAAAACTT TATTTTTAAA GTCCTTTCCC GTTTAGAATG CGGCATACTC TTGCTTGTGG GGTATATAC TCTGATCGTG ATAACTACCT ACCGAAAACC TTTCATGGCT CCTTGCCAAC TACAAAATTG CGATATCCTC GAG	60 120 180 240 253
(2) INFORMATION FOR SEQ ID NO:810:	

(A) LENGTH: 283 base pairs

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:
GAATTCGGCC TTCATGGCCT AGATTGAATT CTAGACCTGC CGACGCGGGG AGAGACAAAA AAGAGAAAGT CTTTGAAAAG CACAAGGAGA AGAAGGATAA AGAGTCCACA GAAAAGTACA AGGACAGGAA GGACAGAGCC TCAGTGGACT CCACGCAAGA TAAGAAAAAT AAACAGAAGC TCCCCGAGAA GGCTGAAAAG AAGCACGCTG CCGAAGACAA GGCTAAAAGC AAACACAAAG
AGAAGTCGGA CAAAGAACAT TCCAAGGAGA GGAAGTCCTC GAG
(2) INFORMATION FOR SEQ ID NO:811:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 316 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:
GAATTCGGCC AAAGAGGCCT AGGCTTCCAC CCAGGAAATG ATCCAGAGCC TCTTTTATGT TATGTTTTTT GTTTGTTCCT TTCAAGACAA TCGATCAAGC CAGAGGCATT CCCCACCCTT 12 CAGCAAGACA CTTCCCAGTA AGCCCAGCTG GCCTTCAGAG AAAGCAAGGC TCACCTCCAC 18 CCTGCCGGCC CTGACTGCTT TGCAGAAAACC TCAAGTCCCA CCCAAACCCA AAGGCCTCCT 24 TGAGGATGAG GCTGATTATG TGGTCCCCGT GGAAGATAAT GATGAAAACT ATATTCATCC 30 CACAGAAAAG CTCGAG 31
(2) INFORMATION FOR SEQ ID NO:812:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 256 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:
GGGATGCATA GATTTAGTTC TGCCTCACAG GCAGGTAGCC TGAGCTCCTA GGGGGAACTG TTTTTGCTAA GTAGGGAATG AAAAGCATGT TTATTTAAGC ACAAAATTAA ATCTCTCCTA TTTTTTATATG ATTTCCCGTT GTTTTCTTC CTGTAGGGAA ATCTGCTGTG ATAGAGAACT GCGTAACAGG CCTTTTCTGT GAGCGCTCAC TCATACATTA TGCACGACGT GGCTAAGATC TTTGATGGCA CTCGAG
(2) INFORMATION FOR SEQ ID NO:813:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 317 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

GCAAGCGGCG CATGCAGGAG	GAGAAGCAGA	AGTCTGTCAA	CGTCAAGAAG	ACCATCCTGG	60
AGATGCGCTA CGGGGCTGA	T GTGGATGCCG	GCTCCATTGT	GCACGCCGCC	CAGAAGCTGG	120
GCGAGCCTCC CGTGCTGCC	C GTATCTCGCA	TGGCCTCCAT	CCCCTCCATG	ATCGGGGAGA	180
AGCTGCCCAC CGCCAAGGG	TTGGAGGCCG	GGCTGGACAC	ACCCAAGGTA	GCCACCAAAG	240
GCAACTATAT CGAGGTGCGG	ACAGGCGCCG	GCGGGGACGG	TCTGGCTCGG	CCCGAGGATG	300
ACCTCCCGGA CCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:814:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 370 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GAATTCGGCC TTCATGGCCT	ACGAACTCCT	GACCTCAAGT	GATCGGCCTG	CCTCAGCCTC	60
CTAAAGTGCT GGGATAGCCA	CTGTGCCCAG	CCTAGCCCTT	CTTCAAATGT	TTGGTAAAAT	120
TCAGCATTGA AGCCATCAGG	TCTTGGGCTT	TTTGCTGGGA	GATTTTTAT	TATGGCATCA	180
ATCTCATTAC TTGTTACTGG	CCTGTTTAGG	TTTTCAGTTT	TTTCATGGTT	CAATCTTGGT	240
AGGTTGTTTG TGTCTAGGAA	TGTATCTGTT	TCTTCTAGGT	TTTCCAGTTT	CTTGGCGTAT	300
AGTTACTCAT AGTAGCCACT	AATTATCCTT	TGGATTTCTG	CGGTATTGGT	TGTAGTGTCC	360
CCATCTCGAG					370

- (2) INFORMATION FOR SEQ ID NO:815:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 382 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCAAGCCTAT	CTTTTAGTCT	60
TCCTAGAAGC	ACCGTGTTCT	GTGGAACTCA	GCATCAGCAG	CTTTGCTGAG	GACTCCCCCA	120
TCTTCCTTTC	CTTCCCCGGA	AAGCACAGAC	CTAAGTGAGT	CTTCACTGGA	TCCCAGCTAA	180
CAGCTTCTGC	CCATTCCTAT	CTTTCCACAG	AGCCAGTGGC	AGCCCCAGCT	GCAGCAGCTA	240
CGTGACATGG	GCATCCAGGA	CGATGAGCTG	AGCCTGCGGG	CCCTGCAGGC	CACCGGTGGG	300
GACATCCAAG	CAGCCCTGGA	GCTCATCTTT	GCTGGAGGAG	CCCCATGAAC	TCCCTGCTTC	360
CCCTGAACCC	CCAGCACTCG	AG				382

- (2) INFORMATION FOR SEQ ID NO:816:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 274 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GCCACGGTGC	TCATTCAGAC	TACCCGTGTG	CCCAAGCAGG	TGGCAGTACC	CGCGACAGAC	60
ACCACTGACA	AGATGCAGAC	CAGCCTGGAT	GAAGTCATGA	AGACCACCAA	GATCATCATT	120
GGCTGCTTTG	TGGCAGTGAC	TCTGCTAGCT	GCCGCCATGT	TGATTGTCTT	CTATAAACTT	180
CGTAAGCGGC	ACCAGCAGCG	GAGTACAGTC	ACAGCCGCCC	${\tt GGACTGTTGA}$	GATAATCCAG	240
GTGGACGAAG	ACATCCCAGC	TGCAACATCT	CGAG			274

- (2) INFORMATION FOR SEQ ID NO:817:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 356 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

GAATTCGGCC	TTCATGGCCT	ACAAAAATAC	ACCTGTGGTC	CCAGCTGCTC	GGGAGGCTGA	60
NTTACGAGAG	TCCCTTGAAC	CTGGGAGGCG	GAGGTTGCAG	TGAGCTGAAA	TCATGCCACT	120
GCACTCCAGC	CTGGGCAACA	GAGCGAGACT	CTGTTNAAAA	TAAAAAAAA	AGCGAGAGAT	180
CGAGAGAGAG	TGCACGTGAG	AAGACTAGTA	GTTGCTATGG	ACTGGGGGAG	AAGGAACGGG	240
TTACAGGGTT	TCTTTTGGGG	ATAACGAAAA	TGTTCTAAAA	CTGGACTGTG	GTGATAACTG	300
CACAACTCTG	TGAATGTACT	AAAAACTACT	GAACTGGCCG	GGCGCGGCAG	CTCGAG	356

- (2) INFORMATION FOR SEQ ID NO:818:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 184 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GAATTCGGCC TTCATGGCCT	AGGCAGGGTG	TCAACTTATT	TAATTCTAAA	AATAGTATAT	60
TCATAGAGAT ACTATCATCO	TCATTTCATA	TATTCAAAAA	ATTCAAAGAA	GTTAAGTAAA	120
TTGCCAAAAG, TCACCCAGAT	AATAAGTAGA	AAAGATGGTA	ATGAAATCCA	GGTTGGCCTT	180
CGAG					184

- (2) INFORMATION FOR SEQ ID NO:819:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 349 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

GAATTCGGCC TTCATGGCCT ACAACAACAA CAACAACAAA ACATCATCCG GGGAAGCTTT TCAATATCCT GACGTTGGGT CTCTCCAGTG TAGATGGAAA TATGGAATTG GGAATAGACA TCGATATTTT TGGAGGTCCC CAGGGGTTAC CAATGTGCAG ACAGGTTTGG GAACCACTGC ATTAGGCATT TTACATTTAT TTAGGGCTTT CACTGGATTT GTCACCCCAT ACTTTCATAA TCCATTTTTT CTGATTTTT TTCTGGTTTT TGGTGAGGGT ATAGTTGGGA TGGGGTTTTT TTTTTTTGTCC TCCCACCGCT CGCCCCCATC CAGTGTGGAC GTACTCGAG	60 120 180 240 300 349
(2) INFORMATION FOR SEQ ID NO:820:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 167 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:	
GAATTCGGCC TTCATGGCCT ACTCTTTCCT TGAAGAATTT GTTGAAGACT TCAGAAGTGA TGCTGGCTGC TTTCTTCATT AGGTTGAGCT CCCCATCCTC CTTTACAGCG ATGGTATATG CCACAACTGC ACTGATATCT ATTTTGTCAA AGCCTTCAGG TCTCGAG  (2) INFORMATION FOR SEQ ID NO:821:	60 120 167
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 733 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:	
GAATTCGGCC AAAGAGGCCT AGCGAAATAA AACAAGGGAG TCAGCAAAAC CAGAAATTTC AGCAATGTCA GCTCATGACA AGGCTGCATT ATCAGAAGAG GAACTGGAGA GGAAGTCGAA	60 120
ATCTATCATT GATGAATTTC TACACATTAA TGATTTTAAG GAAGCCATGC AGTGTGTGGA AGAGCTGAAT GCCCAGGGCC TACTACATGT TTTTGTGAGA GTGGGAGTGG AGTCCACCCT	180
GGAAAGGAGC CAGATCACCA GGGATCACAT GGGCCAACTA CTCTATCAGC TGGTACAGTC	240 300
AGAAAAACTC AGCAAACAGG ACTTTTTCAA AGGTTTTTCA GAAACTTTGG AATTGGCAGA	360
TGACATGGCC ATTGATATTC CCCATATTTG GTTGTACCTT GCTGAACTGG TGACCCCCAT	420
GTTAAAAGAA GGTGGAATCT CCATGAGAGA ACTTACCATA GAATTTAGCA AACCTTTACT	480
TCCTGTTGGA AGAGCTGGGG TCTTGCTATC TGAAATATTG CACCTACTAT GCAAACAAAT	540

(2) INFORMATION FOR SEQ ID NO:822:

TAAGCGACTC GAG

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 512 base pairs (B) TYPE: nucleic acid

GAGCCATAAG AAAGTGGGAG CCTTATGGAG GGAGGCTGAC CTCAGCTGGA AGGACTTTTT

ACCAGAAGGA GAAGATGTAC ATAATTTTCT TTTGGAGCAG AAGTTGGACT TCATAGAGTC

TGACAGTCCC TGTTCCTCTG AAGCACTTTC AAAGAAAGAA CTGTCTGCCG AAGAGCTGTA

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

600

660

720

733

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

TGCCAGATAG	TTCTGCAGAA	GAAATCACTG	TTTGTCCTGA	GACACAGGTA	AGTTCCTCTG	60
AAACTTTTGA	CCTTGAAAGA	GAAGTCTCTC	CAGGTAGCAG	AGATATCTTG	GATGGAGTCA	120
GAATAATAAT	GGCAGATAAG	GAGGTTGGTA	ACAAGGAAGA	TGCTGAGAAG	GAAGTAGCTA	180
TTTCTACCTT	CTCATCCAGT	AACCAGGTAT	CCTGCCCGCT	ATGTGACCAA	TGCTTTCCAC	240
CCACAAAGAT	TGAACGACAT	GCCATGTACT	GCAATGGTCT	GATGGAGGAA	GATACAGTAT	300
TGACTCGGAG	ACAAAAAGAG	GCCAAGACCA	AGAGTGACAG	TGGGACAGCT	GCCCAGACTT	360
CTCTAGACAT	TGACAAGAAT	GAGAAGTGTT	ACCTCTGTAA	ATCCCTGGTC	CCATTTAGAG	420
AGTATCAGTG	TCATGTGGAC	TCCTGTCTCC	AGCTTGCAAA	GGCTGACCAA	GGAGATGGAC	480
CTGAAGGGAG	TGGAAGAGCA	CGTTCGCTCG	AG			512

## (2) INFORMATION FOR SEQ ID NO:823:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 423 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

GAATTCGGGC	CTTCATGGCC	TACTCTCATC	TGTATCTGTT	TCCTCTAACT	TTACTGAAAA	60
GATAGAATTC	ATTAAGCATG	AATTCTACCA	TCTTCTCCCT	ACTACAGCTC	TGTCAAAAAG	120
ATGTTGCTCT	CTGAGCCCAA	CTCTCCCTCA	GTCCCCAGGA	TTCTGTCCCT	GTCCACCTTT	180
AATCTTTTCC	TTTCCTGATT	TTATGTTATA	AGTTATTTAG	ATTTCGATGA	GAGATAATCG	240
TACCTAGAGT	ATGGGAGAAC	TATTTAAGGT	TTACAGGTTG	GGTGGAACCC	TTGTATATAC	300
TAGATGGTAC	TGTGAGGGCT	TGCCACACTG	TCAGCCTTCA	TCTGAACAGA	GCAGAAAGTG	360
TTTCTGCATG	TTCACCAAGC	CCTGCTGGAC	TGTATCACTT	TTCTCTGTGG	GCCAAAACTC	420
GAG						423

- (2) INFORMATION FOR SEQ ID NO:824:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 353 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

GAATTCGGCC	TTCATGGCCT	AGCGGCCTCA	GATGAATGCG	GCTGTTAAGA	CCTGCAATAA	60
TCCAGAATGG	CTACTCTGAT	CTATGTTGAT	AAGGAAAATG	GAGAACCAGG	CACCCGTGTG	120
GTTGCTAAGG	ATGGGCTGAA	GCTGGGGTCT	GGACCTTCAA	TCAAAGCCTT	AGATGGGAGA	180
TCTCAAGTTT	CAACACCACG	TTTTGGCAAA	ACGTTCGATG	CCCCACCAGC	CTTACCTAAA	240
GCTACTAGAA	AGGCTTTGGG	AACTGTCAAC	AGAGCTACAG	AAAAGTCTGT	AAAGACCAAG	300
GCACCCCTCA	מסמממממממ	CCCAACCTTT	TCTCCCAAAA	ACATCATCTC	CAC	353

- (2) INFORMATION FOR SEQ ID NO:825:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 506 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

GAATTCGGCC AAAGA	AGGCCT AGGAGTAAGG	ATGCAGAAAT	GATTGCAGCA	TATTTCATTC	60
TCTACGCAAG GATGT	TTCCTC GGAAATGGAG	GCGACATTGC	TGCCTGCTTT	TTTGAGGGAA	120
TTGATGATGT TCACT	rggaag gaaaatggga	CATTAGTTCA	AGTAGCAACT	ATATCAGGAA	180
ACATGTTCAA CCAAA	ATGGCA AAGTGGGTGA	AACAGGACAA	TGAAACAGGA	ATTTATTATG	240
AGACATGGAA TGTAA	AAAGCC AGCCCAGAAA	AGGGGGCAGA	GACATGGTTT	GATTCCTACG	300
ACTGTTCCAA ATTTG	GTGTTA AGGACCTTTA	ACAAGTTGGC	TGAATTTGGA	GCAGAGTTCA	360
AGAACATAGA AACCA	AACTAT ACAAGAATAT	TTCTTTACAG	TGGAGAACCT	ACTTATCTGG	420
GAAATGAAAC ATCTG	STTTTT GGGCCAACAG	GAAACAAGAC	TCTTGGTTTA	GCCATAAAAA	480
GATTTTATTA CCCCT	TTCAAC CTCGAG				506

- (2) INFORMATION FOR SEQ ID NO:826:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 337 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

GATGGAGCAG	TTCCAGAAGG	AGAAGGAGGA	ACTGGACAGG	GGCTGCCGCG	AGTGCAAGCG	60
CAAGGTGGCC	GAGTGCCAGA	GGAAACTGAA	GGAGCTGGAG	GTGGCCGAGG	GCGGCAAGGC	120
AGAGCTGGAG	${\tt CGCCTGCAGG}$	CCGAGGCACA	GCAGCTGCGC	AAGGAGGAGC	GGAGCTGGGA	180
GCAGAAGCTG	GAGGAGATGC	GCAAGAAGGA	GAAGAGCATG	CCCTGGAACG	TGGACACGCT	240
CAGCAAAGAC	GGCTTCAGCA	AGAGCATGGT	AAATACCAAG	CCCGAGAAGA	CGGAGGAGGA	300
CTCAGAGGAG	GTGAGGGAGC	AGAAACACAA	GCTCGAG			337

- (2) INFORMATION FOR SEQ ID NO:827:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 216 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

GAATTCGGCC	AAAGAGGCCT	ACAGGTACAG	AATCATATGA	ATGTTTCTTT	CTTTCTTTCT	60
TTTCTTTCCT	TCTTTCCTTC	TTTCTTTCTT	TCTTTTTTG	AGACAGAGTC	TTGTTCTGTT	120
GCCAGACTGG	AGTGCAGTGA	CTCAATCTCA	GCTCACTGCA	ACCTCCACCT	CCCAGGTTCA	180
AGCAATTGTC	CTCCCTCAGC	GAGGACCTGC	CTCGAG			216

- (2) INFORMATION FOR SEQ ID NO:828:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 386 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

TTTTCTTCTT ACTATGACCA ACTACGGAGT CTAACTTTCC CGATGCACAT	AAAGAGGCCT TTTTGGAGTC AGAGCCAGAT TCCTTTTCAT ATCATCAATG TCAGCAACTC TGCAACTCAT	AAAGTACATT GATGATTACC CAGTATACTT TACTGTGATA TACCTTCAGT	GCCAATATGA AAACAGGATT TAGGCTGTGT ATCGCAAACT	AACTTATCAG CCCATTTCGT CAGTGAATGC CAAGACTATC	TGGGATGAAG CAAAATGTAG TTCTGTCCAA CCAAATATTC	60 120 180 240 300 360 386
CATTCATCAA	TGCAACTCAT	CTCGAG				386

- (2) INFORMATION FOR SEQ ID NO:829:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 293 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GAATTCGGCC	AAAGAGGCCT	AGCTGAATCC	TAGATTTCAG	CTTCTCACTC	AGAATTTAAG	60
CTGTTTTCAG	TACCAGAAAT	ATTTAAGACT	GTTAGTTTAA	CTTCTAAGAA	TAGCAGATAA	120
AGCGTATAGG	TGTTTTGAGA	TAACCGTATT	CATAGGAAAA	ACAAACATAA	AACTTTCATA	180
ATTTTGGGAA	GAGTTACACA	CAAAAATATC	ATCATTGAAT	AATTAGTACA	ACAAAAATGC	240
ATTTGTTTGT	CCTAAAGGTT	GAAATGAACA	GAATCATGAT	GGGAATACTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:830:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 146 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

GAATTCGGCC	AAAGAGGCCT	AATTGAATTC	TAGACCTGCC	TATGTCCTAT	TCCCTGTGTC	60
CTGCAAGACC	CCCTTTGGTT	TGGTTTTCTT	TTCTTTTCTT	TTTTTTTTT	TTGAGACTGC	120
GTCTTGCTCT	GTCTCCCAGG	CTCGAG				146

- (2) INFORMATION FOR SEQ ID NO:831:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 158 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

GCGATTGAAT TCTAGACCTG CCTCTCATCC ACTATTGTCT TTCCCCAATT TTTTTCTAGC
CTTATCTTCC AGAATTCCTC TCAGACATAG GTGGCCCTGG TTGCTTGATC CTGTCTCTAA 120

158

GTTGGTCTTT CATGTTTTCT CTCCTCAGAT TGCTCGAG

ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTTA AAAAGAGATA ATTAAATTTC TCCTATATTT TATTTCATTT ATTTTTTCAG TCATGCTCCT TCTGTATCTC CTATATTTTA TTATATTACT TACATGGCTT TATTTTTACA ATAACTCTTT TTTTCCCTTC 240	(2) INFORMATION FOR SEQ ID NO:832:	
GAATTCGGCC TTCATGGCCT AGCTGATTTA AATCTAAAAA CTGGATAAGA AGCTGTGGCT TGTAATTAAA AATGACCTT TATTCACTAG ACCTACAGTT TGCTTTTTTC ATATGTTAAG AAAAGTTTAA TATCCTGCT. CTCTATTCA GTCTTAGGGG CACCACTAC AGTTAAGCCT AAAGATTTC GTGGGTAAAA CCATTTGAT TACCATCTG CTCTGCTGCC AGTTATGCTA ACCAAACTCT CTTTGTTTCT GGATGCTAAA TCTGTCCACCT TGTGCCTAA CTACATCCTA ACTCCCGTCA ACTCGAG  (1) SEQUENCE CHARACTERISTICS: (A) LEMGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDENNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: CDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:  GAATTCGGCC TTCATGGCCT AGCCCCGGA GCCCACCACA GTCCCCAGGA TGTGATAAAA ACAATTTTTA TACTTCTTAT CTCTTTCTAG TAGTCTACAT CCCATTCCCA GTCTTCCAA TCATAAAAAT TTGTGGTGGG TAGAACAGT TTCTTCACAT TGTTTTAACTAT TTTGTGTTTT TTTGCTTTATT CTTTAAGCAT TGTTTAAATAT TGTTGTGGGT ATGAACAGT TCTTACAAAAAT TGTGTGGGGT AGCAACAGT TCTTCCAAG TCTTTACCTA TCTTGTTTCT TGTCATTATT CTCTAAGACAT TAATACAGAA ACCAGAACCA AAATTTAATAT TGTGTGGGGT ATGAACAGT TCTTCAGAAC TGTTTTAAAG TTTTACTAT TCTTGTTTCT TGTCATTATT CTCTAGAACAT TCATACAGAA ACCAGAACCA AAATTTAATAT TGTGTGGGGT ATGAACAGT TCTTCAGAAC  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 396 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:  GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTTTATTA ACACTGAGAA ACACCTAACT ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTTA AAAAGAACATA ATAAAATTT TATTTTATT TATTTCTTT ATTTTTTATA TAAGAGACATA TAAAATTTAA ATTAAATTT CTCCTATATTT TATTTCTTTA TAAGAGACTT TAATTTTTAA ATTATTCCTT TCCTTATACT TAATTTTTAA TAATACTCTTT TTTTCCCTTC CTCTATATTTA TTAATTTACT TACATGGCTT TATTTTTAAC ATTAATTACCT TCTTGTATCTCC CTCTATATTTA TTATTTCATT TATTTTTAAC ATTATTTCAA TATAACTCTTT TTTTCCCTTC CTCTATATTTA TTATTTCATT TATTTTTAACA ATTAATTA	(A) LENGTH: 317 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
GAATTCGGCC TTCATGGCCT AGCTGATTTA AATCTAAAAA CTGGATAAGA AGCTGTGGCT TGTAATTAAA AATAGACCTT TATTCACTAG ACCTACAGTT TGCTTTTTTC ATATGTAAG AAAAGTTTCT GTGGTGTAAA CCATTTTGAT TACCATCTG GTCTCAGGGG CACCACTAC AGTTAACCCT AAAAGATTCT GTGGTGAAA CCATTTTGAT TACCATCTG CTCTGCTGCC AGTTATGGTA ACCACACACTC CTTTGTTTCT GGATGCTAAA TCTGTCCACT TGTGCCTTAA CTACATCCTA ACTCCCCGCA ACTCGAG  (2) INFORMATION FOR SEQ ID NO:833:  (i) SEQUENCE CHARACTERISTICS:	(ii) MOLECULE TYPE: cDNA	
TGTARTTARA ARTAGACCTT TATTCACTAG ACCTACAGTT TOCTTTTTC ATATGTTAG ARAAGTTTAA TATCCTGCT. CTCTATTCA GTTCTAGGGG CACCACTATC AGTTAACCCT ARGAGTTTCT GTGGGTGAAA CCATTTGAT TACCATCTTG CTTGTGTCCA GTTATGGTA ACCACACTCT CTTTGTTTCT GGATGCTAAA TCTGTCCACT TGTGCCTTAA CTACATCCTA ACTCCCGTCA ACTCGAG  (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: CDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:  GAATTCGGCC TTCATGGCCT AGCCCCCGGA GCCCACCACA GTCCCCAGAG TGTGATAAAA CACATTTTTA TACTTCTTAT CTCTTTCTAG TAGTCTACAT CCCATTCCCA GTCTTCCAA TCATAAAAAT TTGTAGTTA TTTAGTCAC ACTTGAACCT TGATACAGAA ATCAGAACCA AATTTTAATT TGTTGTGGGT ATGAGACAGT TTCTGTCATG TTTTAATTT TTCCTTAAAG CTTTTACCTA TCTTGTTTCT TGTCATTATT CTTAAGCCAT TGATACAGAA ATCAGAACCA AATTTAATAT TGTTGTGGGT ATGAGACCAGT TTCTGCATG TTTTAATTT TTCCTTAAAG (C) INFORMATION FOR SEQ ID NO:834:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 396 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:  GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTCTATT ACACTGAGAA ACACCTAACT ACCTTATATG AATTAAAATTT CCCTAAGTTA TAAGACCACTT GAATTTTTA AAAAGAGATA ATTAAAATTC TCCTATATTT TATTTCATT ATTTTTTCAG TCATGTTTTA AAAAAGAGATA ATTAAATTC TCCTATATTT TATTTCATT ATTTTTTCAG ATAATTTTA TAAAAAGAGATA ATTAAATTTTA TTAATTTACT TACATGGCTT TATTTTTTCAG ATAAACTCTTT TTTTCCCTTC 240	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:  GAATTCGGCC TTCATGGCCT AGCCCCCGGA GCCCACCACA GTCCCCAGAG TGTGATAAAA 60 ACAATTTTA TACTTCTTAT CTCTTCTAG TAGTCTACAT CCCATTCCCA GTCTTTCCAA 120 TCATAAAAAT TTGTAGTTTA TTTAGTTCAC ACTTGAACGT CCTATGAAAC TGTTTTAAAC 180 ACTTTAATAT TGTTGTGTGT ATGAGAACGT TTCATACAGAA ATCAGAACCA 240 ATTTAATAT TGTTGTGGGT ATGAGACGT TTCTTGTAGT TTTTAATTT TTCCTTAAAG 300 TTTTACTATG TACTTCATAT ATACCGGGCA CTTCTCGAG 339  (2) INFORMATION FOR SEQ ID NO:834:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 396 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:  GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTCTTATT ACACTGAGAA ACACCTAACT 60 ATCCTAATAG AATTAAAATT CCCTAAGTTA TAAGACACTT GAATTTTTATA AAAAGAGATA 1ATAAAATTTC TCCTATATT TATTTTTATA ATTATTTCACT TCATGTTTTT TTTTCCCTTC 180 CTATATTTTA TTATTTATT ATTATTTCAC TCATGTCTT TTTTCCCTTC 240	TGTAATTAAA AATAGACCTT TATTCACTAG ACCTACAGTT TGCTTTTTTC ATATGTTAAG AAAAGTTTAA TATCCTGCT: CTCTATTTCA GTTCTAGGGG CACCACTATC AGTTAACCCT AAAGATTTCT GTGGGTGAAA CCATTTTGAT TACCATCTTG CTCTGCTGCC AGTTATGGTA ACCAAACTCT CTTTGTTTCT GGATGCTAAA TCTGTCCACT TGTGCCTTAA CTACATCCTA	120 180 240 300
(A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:  GAATTCGGCC TCATGGCCT AGCCCCCGGA GCCCACCACA GTCCCCAGAG TGTGATAAAA 60 ACAATTTTTA TACTTCTTAT CTCTTTCTAG TAGTCTACAT CCCATTCCCA GTCTTTCCAA 120 TCATAAAAAT TTGTAGTTTA TTTAGTTCAC ACTTGAACGT CCTATGAAAC TGTTTTAAAC 180 CTTTTACCTA TCTTGTTCT TGTCATTATT CTTAAGCGT TGTAACAGAA ATCAGAACCA 240 AATTTAATAT TGTTGTGGGT ATGAGACAGT TTCTGTCATG TGTAACAGAA ATCAGAACCA 339  (2) INFORMATION FOR SEQ ID NO:834:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 396 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:  GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTCTTATT ACACTGAGAA ACACCTAACT 60 ATCCTAATAG AATTAAATTT CCCTAAGTTA TATTTTTCAT GAATTTTTTA AAAAGAGAATA 180 ATTAAAATTC TCCTATATTT TATTTTTATT ATTTTTTCAG TCATGGCCCT TCTGTATCTC 180 CTATATTTTA TTATATTACT TACATGGCTT TATTTTTACA ATAACTCTTT TTTTCCCTTC 240	(2) INFORMATION FOR SEQ ID NO:833:	
GAATTCGGCC TTCATGGCCT AGCCCCCGGA GCCCACCACA GTCCCCAGAG TGTGATAAAA 60 ACAATTTTA TACTTCTTAT CTCTTCTAG TAGTCTACAT CCCATTCCCA GTCTTTCCAA 120 TCATAAAAAT TTGTAGTTTA TTTAGTTCAC ACTTGAACGT CCTATGAACA TGTTTTAAAC 180 CTTTTACCTA TCTTGTTTCT TGTCATTATT CTTAAGCCAT TGATACAGAA ATCAGAACCA 240 AATTTAATAT TGTTGGGGT ATGAGACAGT TTCTGTCAT TTTTAATTT TTCCTTAAAG 300 TTTTACTATG TACTTCATAT ATACCGGGCA CTTCTCGAG 339  (2) INFORMATION FOR SEQ ID NO:834;  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 396 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:  GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTCTTATT ACACTGAGAA ACACCTAACT 60 ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTA AAAAGAGATA 120 ATTAAATTTC TCCTATATTT TATTTCATTT ATTTTTTACA TCATGGCTCT TCTGTATCTC 180 CTATATATTTA TTATATTACT TACATGGCTT TATTTTTTACA ATAACTCTTT TTTTCCCTTC 240	<ul><li>(A) LENGTH: 339 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
GAATTCGGCC TTCATGGCCT AGCCCCCGGA GCCCACCACA GTCCCCAGAG TGTGATAAAA 60 ACAATTTTTA TACTTCTTAT CTCTTTCTAG TAGTCTACAT CCCATTCCCA GTCTTTCCAA 120 TCATAAAAAT TTGTAGTTTA TTTAGTTCAC ACTTGAACGT CCCATGAAAC TGTTTTAAAC 180 CTTTTACCTA TCTTGTTCT TGTCATTATT CTTAAGCCAT TGATACAGAA ATCAGAACCA 240 AATTTAATAT TGTTGTGGGT ATGAGACAGT TTCTGTCATG TTTTAATTTT TTCCTTAAAG 300 TTTTACTATG TACTTCATAT ATACCGGGCA CTTCTCGAG 339  (2) INFORMATION FOR SEQ ID NO:834:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 396 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:  GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTCTTATT ACACTGAGAA ACACCTAACT 60 ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTTA AAAAGAGATA 120 ATTAAATTTC TCCTATATTT TATTTCATTT ATTTTTTCAG TCATGCTCCT TCTGTATCTC 180 CTATATTTTA TTATATTACT TACATGGCTT TATTTTTACA ATAACTCTTT TTTTCCCTTC 240	(ii) MOLECULE TYPE: cDNA	
ACAATTTTA TACTTCTTAT CTCTTTCTAG TAGTCTACAT CCCATTCCCA GTCTTTCCAA TCATAAAAAT TTGTAGTTTA TTTAGTTCAC ACTTGAACGT CCTATGAAAC TGTTTTAAAC 180 CTTTTACCTA TCTTGTTTCT TGTCATTATT CTTAAGCCAT TGATACAGAA ATCAGAACCA 240 AATTTAATAT TGTTGTGGGT ATGAGACAGT TTCTGTCATG TTTTAATTTT TTCCTTAAAG 300 TTTTACTATG TACTTCATAT ATACCGGGCA CTTCTCGAG 339  (2) INFORMATION FOR SEQ ID NO:834:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 396 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:  GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTCTTATT ACACTGAGAA ACACCTAACT 60 ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTA AAAAGAGATA 120 ATTAAATTTC TCCTATATTT TATTTCATTT ATTTTTTCAG TCATGCTCCT TCTGTATCTC 180 CTATATTTTA TTATATTACT TACATGGCTT TATTTTTACA ATAACTCTTT TTTTCCCTTC 240	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 396 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:  GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTCTTATT ACACTGAGAA ACACCTAACT 60 ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTA AAAAGAGATA 120 ATTAAATTTC TCCTATATTT TATTTCATTT ATTTTTTCAG TCATGCTCCT TCTGTATCTC 180 CTATATTTTA TTATATTACT TACATGGCTT TATTTTTACA ATAACTCTTT TTTTCCCTTC 240	ACAATTTTTA TACTTCTTAT CTCTTTCTAG TAGTCTACAT CCCATTCCCA GTCTTTCCAA TCATAAAAAT TTGTAGTTTA TTTAGTTCAC ACTTGAACGT CCTATGAAAC TGTTTTAAAC CTTTTACCTA TCTTGTTTCT TGTCATTATT CTTAAGCCAT TGATACAGAA ATCAGAACCA AATTTAATAT TGTTGTGGGT ATGAGACAGT TTCTGTCATG TTTTAATTT TTCCTTAAAG	120 180 240 300
(A) LENGTH: 396 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:  GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTCTTATT ACACTGAGAA ACACCTAACT ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTTA AAAAGAGATA ATTAAATTTC TCCTATATTT TATTTCATTT ATTTTTTCAG TCATGCTCCT TCTGTATCTC 180 CTATATTTTA TTATATTACT TACATGGCTT TATTTTTACA ATAACTCTTT TTTTCCCTTC 240	(2) INFORMATION FOR SEQ ID NO:834:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:  GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTCTTATT ACACTGAGAA ACACCTAACT ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTTA AAAAGAGATA ATTAAATTTC TCCTATATTT TATTTCATTT ATTTTTCAG TCATGCTCCT TCTGTATCTC 180 CTATATTTTA TTATATTACT TACATGGCTT TATTTTTACA ATAACTCTTT TTTTCCCTTC 240	<ul><li>(A) LENGTH: 396 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
GAATTCGGCC TCATGGCCTA TGACTTTTAA GTTTCTTATT ACACTGAGAA ACACCTAACT ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTTA AAAAGAGATA ATTAAATTTC TCCTATATTT TATTTCATTT ATTTTTCAG TCATGCTCCT TCTGTATCTC CTATATTTTA TTATATTACT TACATGGCTT TATTTTTACA ATAACTCTTT TTTTCCCTTC 240	(ii) MOLECULE TYPE: cDNA	
ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTTA AAAAGAGATA ATTAAATTTC TCCTATATTT TATTTCATTT ATTTTTCAG TCATGCTCCT TCTGTATCTC CTATATTTTA TTATATTACT TACATGGCTT TATTTTTACA ATAACTCTTT TTTTCCCTTC 240	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:	
AGCTCAAGCA ATCTTCACGC CTCAGCCTCC CAAAATTATA GGACTACAGG CATGAGCCAC 360	ATCCTAATAG AATTAAATTT CCCTAAGTTA TAAGACACTT GAATTTTTTA AAAAGAGATA ATTAAATTTC TCCTATATTT TATTTCATTT ATTTTTTCAG TCATGCTCCT TCTGTATCTC CTATATTTTA TTATATTACT TACATGGCTT TATTTTTACA ATAACTCTTT TTTTCCCTTC TTTTATTTAT TTGTTTATTT TTGGAAACAG AGTTTCCTTA TGCTGCCCAC GCTGGTCCTG AGCTCAAGCA ATCTTCACGC CTCAGCCTCC CAAAATTATA GGACTACAGG CATGAGCCAC	60 120 180 240 300 360 396

- (2) INFORMATION FOR SEQ ID NO:835:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 294 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

GAATTCGGCC	TTCATGGCCT	ACTITITACTO	ATGCATAATT	TTGTAAAATC	CTACATTGGT	60
CATTTGGAAA	ATATTGATTC	ACTGAGTAAT	AÇAACTCTTC	CAAATGTTGA	ATGTTTCATT	120
CTACAATATC	AGAAACTCAA	TTTGTTAATG	TTACTACTAG	TCTCATCAGA	AATGTCTTTA	180
AGTATTTGTT	AACTGGCAAA	CTCATAGTGA	CGACTACAGG	CTTTCCAGAA	TTTTCATTTT	240
CATTTGAAGT	CTGAATTTTA	TCAACTATAA	ATACTGTCAG	TTGTTTCCCT	CGAG	294

- (2) INFORMATION FOR SEQ ID NO:836:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

GAATTCGGCC TT	CATGGCCT ACTCTGA	TAC TAACTGTAG	T CTACATTTAT	ACATTGTGTC	60
TGAATGCTGG TT	TTGTGGCT TCACTAG	CTC CCTTTTTCT	C TCTCCTTTTT	TATCCTGTCT	120
TTTGCTGCTG CT	TTCCACCT TCTGTCC	AGC TCCATCTTC	A GACAGCTCCC	TGTATAACGC	180
TCCACTTCCT GA	GTATTCCA GTTGCCA	GCC TCCTTCAGC	A CCTCCTCCAT	CATACGCTAA	240
AGTCATCTCA GC	TCCAGTGT CAGATGC	CAC TCCTGATTA	T GCTGTAGTGA	CTGCTTTGCC	300
ACCTACTTCC AC.	ACCCCCTA CACCACC	ACT GCGACACCC	A GCGACACTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:837:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 355 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

GAATTCGGCC	TTCATGGCCT	ACCGGACCTT	GAAAATGGAA	TGTTCAGAAA	CACATGTGCA	60
AGGGAGCTGT	GCCAAGCTCA	TGTTGCGAAC	AGGCCTCCTG	ATGAAGCTTC	TCAGCGAGCA	120
GCAGGAAGCA	AAGGCATTGA	ATGTAGAATG	GGATACGGAC	CAACAAAAA	CAAATTATAT	180
TAATGAGAAC	ATGGAACAGA	ATGAACAGAA	AGAGCAGAAG	TCAAGTGAGC	TCATGAAAGA	240
AGTTCCAGGA	GATGACTATA	AGAACAAACT	CATCTTCGCA	ATATCTGTGA	CTGTAATACT	300
AATAATTTTG	ATTATAATTT	TTTGTCTTAT	AGAGGTGAAT	TCACATATGC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:838:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

${\tt GAATTCGGCC}$	TTCATGGCCT	AAAAATCTA	GTTGAGAAAA	AGAAAGAAAC	CAAGAAGGCT	60
AATCACAAGG	GTTCTGAAAA	TAAAACTGAT	TTAGATAATT	CTATAGGAAT	TAAAAAATG	120
AAAACCTCAT	GTAAATTTAA	GATAGATTCA	AACATAAGTC	CGAAGAAGGA	TAGCAAAGAA	180
TTTACACAAA	AAAATAAGAA	AGAGAAAAA	AACATTGTTC	AACATACTAC	AGACTCTTCT	240
CTCGAAGAAA	AACAAAGGAC	ATTAGACTCA	GGCACCTCTG	AAATTGTGAA	ATCTCCCAGA	300
ATCGAGTGTT	CTAAGACAAG	AAGAGAAATG	CAATCAGTGG	TTCAACTCAT	AATGACAAGA	360
GACAGTGATG	GTTATGAAAA	CTCAACAGAT	GGTGAAATGT	GTGACAAAGA	TGCTCTGGAG	420
GAAGATTCAG	${\bf AAAGCGTTAG}$	TGAAATAGGA	${\tt AGTGATGAGG}$	AATCTGAAAA	TGAAATTACA	480
AGTGTTGGTA	${\tt GAGCTTCAGG}$	TGATGACGAT	GGAAGTGAAG	ATGATGAAGA	GAAGCTCGAG	540

- (2) INFORMATION FOR SEQ ID NO:839:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 539 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

GAATTCGGCC	TTCATGGCCT	AGCATTTCAT	CTCTAAATTG	GGGAGAATAG	AAGCATCTAC	60
TTCATGTAGT	AGCCAGGATT	AGAAGAGGGA	GGAATAACTG	GGCCCTGGAT	AGAATGTGAT	120
GAATGTATAT	TCTTAATGAG	AAGTGGAAAT	AATTTGTGGT	TGAGAGCTGT	GCCTCAGATC	180
AGAGTGACAG	GATACATGGC	TAGGCTATAT	TTTCCAGCAG	ATTAAGAGCT	GCAGCCCAAG	240
ACTCTGAAAT	ATGAAGAAAA	AAGGAGAAGA	TGACAGCATA	TCTTTTTAAA	GAAATATTTT	300
CCAGCCAAAT	GGTGCAGCAG	AGGACTTCCA	GGAATTTGTT	CTTGTTCTGT	ATCAAAGGTG	360
AAGAGTTCGT	AGCCTTCAAG	GAAACAAGAA	ACCATGGGAT	GGAGTGAAGG	AAGGTGGCCT	420
GGAACCAGCT	GCTGAGCCTC	TCTGAGCCCC	AGTTTCCTCG	TCTCTAAAAT	GGGGCTGATC	480
TCCTCTCCCT	CAGACTGTTG	TTGCAGGAAT	TAAAACAGGT	GTTGAGTGGG	CTGCTCGAG	539

- (2) INFORMATION FOR SEQ ID NO:840:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 297 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

TTCCACAGCT	CTGATATTCA	GTAACCCATG	TGGAGAACAA	AAGGATTTTG	CTCCATGAAG	60
TCTAATTGCC	TGCTGAATAA	ATAAATAAAT	AGATGAAGCA	CTGCATGCAT	TAAATGAAAG	120
TAAATATTGA	CCCTGCCACC	ATATGTTTGC	TGGGGTGCTG	GCTGAAGTGT	GCTGGCAGGT	180
CCAATCAGTC	AGAGTCTGCC	AGCCCAGCAA	GCAGGAGAGA	CAGGAATATC	AAAAAGGCGC	240
TCCTGCTTGT	GCCTTAATCT	TTGTCCAACC	CCCAATTCCT	CCACCACAGG	CCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:841:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 366 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

GAATTCGGCC	TTCATGGCCT	ACCITATTAG	TGATTGGCGA	TTCAGGCCAT	GTCATAGGGC	60
CTTTCAGACA	AAAGGTTCTT	ATCCCAGTCA	GCTGGCCAAA	ACATTAACTT	TGGATTTCTT	120
ACCCTGCTAC	AGCATCTTCT	AGAAAGGCAG	CAAGATAATA	TTGTGGCAGT	GCACAGATAA	180
CATCAGGGTA	GACTTGACTG	GAGAAAACCA	AATTCTGCGC	TTGCTCCTGT	GTGCCCCCAT	240
CCAGCTGTGC	ATGCACACAC	AGGACACCTT	TCTAGTATGA	AGAACTTGCA	TCATGTCTGC	300
CCTCTATTGA	GCACCCCCTT	CTAGAAATAC	TTCCAAGTAT	TAGCATGTGA	ACTGTTGACT	360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:842:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 190 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GCGATTGAAT	TCTAGACCTG	CCTCGAGCTG	ACTTATGAAT	TCTTTCTGTG	TGATCGTAAA	60
AGTGCAGAGT	TTATTGCAAA	GAGAATCTTC	ATCTGAATCC	TCAGCCTGGG	AATCTTCCTC	120
TTCCACCGCC	AACTCCTCCA	CCCAGTCTGA	GTCTACTTCA	ATGGCCCGCT	CTTCCCCATC	180
CGCACTCGAG						190

- (2) INFORMATION FOR SEQ ID NO:843:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 627 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

GAATTCGGGC	TTCATGGCCT	AAGCTCCGCG	AGCCCCCTAC	AACTCGTTTC	CTTCCGTTCA	60
CCTTCGCAGG	GCGGCGACTG	GCGGCGCGAT	GGACCTGACC	GGGCTCCTGC	TGGACGAAGA	120
AGGCACCTTC	TCCCTCGCCG	GCTTCCAGGA	CTTCACGTTC	CTCCCAGGAC	ACCAGAAGCT	180
GAGTGCCCGG	ATCCGAAGGA	GGCTCTACTA	TGGCTGGGAT	TGGGAAGCCG	ACTGTAGCCT	240
GGAGGAGCTC	TCCAGCCCGG	TGGCAGACAT	TGCTGTCGAA	CTGCTCCAGA	AGGCAGCCCC	300
CAGCCCTATT	CGCCGACTCC	AGAAGAAATA	CGTAGCTCAT	GTGTCCCGGG	AGGCATGCAT	360
CTCCCCATGT	GCTATGATGC	TGGCTCTGGT	GTACATTGAA	CGGCTCCGGC	ACCGAAACCC	420
AGACTACTTG	CAGCATGTGT	CATCCTCTGA	CTTGTTCCTG	ATCTCCATGA	TGGTGGCCAG	480
TAAGTACCTC	TATGATGAAG	GGGAGGAGGA	GGAGGTCTTC	AACGACGAAT	GGGGAGCTGC	540
TGGGGGTGTG	GCCGTGCCCA	CTCTCAATGC	CTTGGAGAGG	GGCTTCCTGA	GTGCCATGGA	600

627

TTGGCATCTC TACACTGAAC GCTCGAG

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:	
GAATTCGGCC TTCATGGCCT ACCTGAGCTG CCGAAGCCGC CGTCCTGCTC TCCCGCGTGG	60
GCTTCTCTAA TTCCATTGTT TTTTTTAGAT TCTCTCGGGC CTAGCCGTCC TTGGAACCCG ATATTCGGGC TGGGCGGTTC CGCGGCCTGG GCCTAGGGGC TTAACAGTAG CAACAGAAGC	120
GGCGGCGGCG GCAGCAGCAG CAGCAGCAAT CTCTTCCCGA ACACGAGCAC CACAGGCGCC	180 240
CGAAGGCCGG AACAGGCGTT TAGAGAAAAT GGCAGACGAT ATTGATATTG AAGCTCTAGC TCGAG	300 305
(2) INFORMATION FOR SEQ ID NO:845:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 409 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:	
GAATTCGGCC TTCATGGCCT ACCAGAAAAA ACTTACATTG AAGAGAGGAT TCCTTGTTTT	60
GACTATGTGT GTTTCTGCCG TCTTAGGCAG CCAACGTATT GGTTTACATG GATCTGGAGG ATTATGCACA CTAGTGTTGA GTTTCATTGC AGGGACAAAA TGGTCCCAAG AAAAGATGAA	120
AGTCCAAAAG ATTATTACGA CTGTATGGGA TATTTTTCAA CCACTTCTTT TTGGTTTAGT	180 240
TGGAGCAGAA GTATCTGTTT CATCGCTTGA ATCAAATATT GTTGGCATAT CTGTTGCCAC	300
TCTAAGTTTG GCATTATGTG TTCGAATTTT AACCACATAT CTATTGATGT GCTTTGCTGG TTTTAGTTTT AAGGAGAAAA TATTTATTGC TTTAGCATGC ATGCTCGAG	360 409
(2) INFORMATION FOR SEQ ID NO:846:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 370 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:	
GAATTCGGCC TTCATGGCCT AGGCACGGTA CATACGATTA TTATAAACAT CAGCTGCGGT	60
TCTGGGAGTG AGCTTGTGTC GTGTTAGTGC CATCTCCCTG ACAAATCTGA CCTGTACCCA CATCTCAGGC TGGGAAGGAG TAGCTGGGCC TCCCTTTAAT GCAGCGGCAC TGGTTTGGGT	120 180
CACAAGAGCT GGTTTGATCA ACCCCTGACT CCCCCTGGCG GGAGGTGCTC GTCACATCTG	240
GGAGCCTGAG CAGAGGTGCC GGGGGCTTGG AAGCTGGAGA AATGATGGAT CTTTCTCCAG	300
GAGAAACAAT TCTTATCTTC ACATCNGCCC CGTGCTCCAA ATGAAGAGCG CGTTTGCATA	360
372	
· .	

GCTGCTCGAG	. 370
(2) INFORMATION FOR SEQ ID NO:847:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 504 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:	
GAATTCGGCC TTCATGGCCT ACGCGGGCC GAGCGGAGGC GGAGTCGGCG GGCTGGAGGC AAAGCTGGAA AGGACAGTGG GAAGGCCAAG GCTAAGGCAG ACAGAGAGCT GGGCTACAGT TTCCTGTGGG CCGCATCCAC AGACACTTGA CACAAGCCAT GGAAGGGTGG GTGCCACTGC TGCCGTGTAC AGTGCTGCAC CCTCACTGCA GAGGTGCTGG AGCTGCAGG TAATGCTTCT AAGGATCTCA TATCACTCCG CGTCACTTGC AGCTTGCAAT CCGTGGTGAT GAAGAGTTGG CAAGGCTACC ATAGCTGGGG GTGGTGTAT CCCTCACATC CACAAATCTC GAAGGGACAG CAGAAAACTG CTTAGAGGGA TGCTTTAACC AACCTCTTCC TTGTACTGTA ACTGGGACCT CGAG	TATCTCGCTC 120 AGACTCGCAC 180 TTCTGGAGTA 240 AAGTAAAGCG 300 ATTCTCTTAT 360 TGATTGGAAA 420
(2) INFORMATION FOR SEQ ID NO:848:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 436 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:	
GAATTCGGCC TTCATGGCCT AAACAAGCAG AGGGACTCCC CAGATAGCTT TTAGCTTTAT AACAAGTGTA GTTTTAGGCT CTGTCTTGGC ATACTTGAGA TGCTTCAAAA CAGGCATTTG AACTCGCTGT TTAATCAAAAT TCTTCTTTAA GTTTCTCATA GAGAGCATAT ACACTTAACC CTTGAACAAT GTAGGGGTTG TCAACCCCCT GTGAAGTAAA AATTTGCTAA TAACTTTTGA CTCCCCCAGA AAATAGCCTA CTATTGATTG GAAGTGTTAC CAACAGCATA CACAGTTAAC TATGTAATAT GTGTTATCCA CTATATTCTT ACAATAAAGT TAGCAAAAGA ATTAGGAATC CTCGAG	GCACAATGGC 120 TCTAAAGTGA 180 GGGTGGGGAG 240 ACTTAACTAT 300 ATATATTTTG 360
(2) INFORMATION FOR SEQ ID NO:849:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 502 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:	

60 120

GAATTCGGCC TTCATGGCCT ACATGAGCCC AGGAGTTGAA GGCTATAGCC TGGGTGACAC AACAAGGCCC CATCTCTAAA AAATATATAA ATAAATAAAG TTAAGGATGC TGCGTGGTTT

TCGGCCTCCC TTTTTGAAGA AAAATATTAT ACATGTATAC CTATTTTTGT	AAAGAGATTG AGGTAATAAA AGAGTTTTTG GCCAGGCTCT GGCTTACACC AGAGTGCTGG GATTACAGGC ATGAGCCACC GCGCCCAGCC GGAAGTAGGT GTCAGCTGAA AACAACTGTT GCCGTATTCG GAATTTAAAA TTTTAATTTG AACTGAGAAA TTATTGTATA TATTTATGGT ATCACAGCGTG ATGTTATGAT AATGCAGAAAT GATTAAATCA AGCTATTTAA CATAGCTGTC ACCTCAAATA GGTCAGAAAT TTGAAATTTA TTATCTCAGG AATTTTGAAA TGTACAATAC ACTGTTCTCG AG	180 240 300 360 420 480 502
(2) INFORM	ATION FOR SEQ ID NO:850:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 291 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:850:	
CAGAAGATAT GAATTTGACA CTGAGACTTG CTTCAAGTTC	TTCATGGCCT AGATAAAAAG AAACAAAAAA GAGAAGATAT GATAAGAGAA ACCATAAATA TTTGGCACAG AGACGTGAGG AAGAAAAAGC TCAGGAGAAA GAATATTAGA GGAAGACAAG GCAAAGAAGT TGGCTGAGAA GGACAAGGAG AAAAGGAGGC AAGGAGACAG CTTGTGGATG AGGTCATGTG TACAAGAAAA AAGAAAAAGTT GCAACGAGAA GCTAAAGAAC AGGAACTCGA G	60 120 180 240 291
(1)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 311 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:851:	
GTTGGGTGGA GTGTTGTATA GTTCTGTATT	TCTGTTGGTT GGAGTGTTCT ACTATTGTTG GGTGGAGTGT TCTATCTTCT GTGTTCTGCT GTTGTTGGGT GGCGTGTTGT ATATTCTGTT GTTGGGTGGC TTCTGTTGTT GGGTGGCGTG TTCTATCTTC TGTTGTTGGG TGGATGATT CTGTTGGGTG GCATGTTCTA TCTTCTGTTT TTGGGTGGAG CGTTCTATCT GGCGCATTCT ATATTCTGTT GTTGGGTGGC GTGTTCTGTA TTCTGTTGTG G	60 120 180 240 300 311
(2) INFORMA	ATION FOR SEQ ID NO:852:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 532 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

GAATTCGGCC CTTCATGGCC TAGTCTCATC TCAGAGTACT CAGAGAAACT ATTTTTTAAT 60 CTCTAGATAT CAATCAATGA ATATTTATTA TTAAATACCT GCTATGTGCC AGATGGTGTT 120

AATTATAAGT	TTGTTCTCTT	TTTGTCGTGC	TACTTAGGCT	TTTATCATTT	TGTCCTATCA	180
TTAGGGAAGT	GGCTCCNNNN	CTTACAGCTA	ATTTTTTTT	CAATTTACTA	ATGACTTTTT	240
GTGGAGGTGG	GGATCTCTTC	TGTTCAACAT	TTTCTATGAT	TCATCTCAAT	CCTCCAGTGA	300
TTATTAAAAA	ACAGTTGCAG	TAAGTTCAGT	CATAGGGGCA	CTGGAATGAG	TCCTTAAAAC	360
TTTATGCTGC	TGCTTTTGCA	ATGATGGATT	GCCTGAGAAT	TAAGGAAAGA	TAACTACTCT	420
CTTGGTCACT	GTATTTCCAA	TCAACCATAT	CCTCCCAGAA	TATGATTTCT	TCCCTCAGGC	480
ATTTTAGAAA	AGAGACAAGA	GACAGATTTT	TTTTTTCAGG	CAATGACTCG	ΔC	532

- (2) INFORMATION FOR SEQ ID NO:853:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 415 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

GAATTCGGCC	TTCATGGCCT	ACTTTTTGAT	AAGCAACTAG	TGGTCTCATT	ATCAGAGGTC	60
CCTGAGGGGC	CCTACAGGCC	CCCCCAGGTT	CTGCCCCCAA	GATTCTAAGA	GAGACCTTGT	120
GCTAGGGCTC	TAGTCTTGAT	${\tt GTTCTTTGCA}$	TTGTTTGGAT	ATGAAGCCCA	GGATATGTGG	180
GCACAATAAG	GTAAATCATG	AGATGTGAAG	GAGAATGAAG	ATCAGGCCAG	AGGTCACCAT	240
TCATTGAAGA	GCCAGAGAAA	AAGAAAATTA	GTGCACAGAT	TTGTGTAGAT	TTACAGAGAA	300
CTTCTATTTG	CTGCAAGAAC	TTCATCAGGC	GCTGCACCAT	GCCTGATTTG	GAAAGGAGCT	360
TCTTTGGGGC	CTGATAGAAC	TGAATTAATA	TGAAGAAATT	GAAGTGGCTC	TCGAG	415

- (2) INFORMATION FOR SEQ ID NO:854:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 324 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

GAATTCGGCC	TTCATGGCCT	AGTAAAATTA	GCTGAAAAAT	AATTTTCCAA	TGCAAATACT	60
AATGAGGGTT	ATATGACCGT	TGTCCAAAGC	ATTTGCAGTG	CTGCATGACA	TTTGTCCTAA	120
AACCTGACTC	TTAAAACATT	CCTTGTGAAA	ATAGAAATAT	TCCCATGCCT	AGATTCCAAA	180
TAATAAAAGA	CACTGAGAGT	GTTTTCAAAA	TTAATGGACT	GATTTAAATT	TCACTGGAAA	240
GCAGCTTTTT	AAAACTAAAT	TGTCTGGATG	TGGCCTCCCT	GTGATCACTT	CCAACTGCTT	300
ACTGCCAACT	TCTGGCGGCT	CGAG		•		324

- (2) INFORMATION FOR SEQ ID NO:855:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 616 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

 $||f_{ij}||_{L^{\infty}(\mathbb{R}^{n})} \leq \frac{2}{\pi} \sum_{i=1}^{n} |f_{ij}||_{L^{\infty}(\mathbb{R}^{n})} \leq \frac{2}{\pi} \frac{2}{\pi}$ 

CNNTTCCCCC	mmat mac a a a					
	TTCATGGCCT					60
	TCACAATCAT					120
GGCGCTGCCA	TGCTGAAGGT	GACCAGCAAC	ACAGCCCCCA	GGATGGTCAG	TTGTTCCAGC	180
TGCAACTGGA	GCTCGTGGAA	GCGAGACTGG	TCCATTAAAA	CTGTTTCGGG	GAACGGCCTC	240
TGGAGGTGGT	CCCACTTCAG	AAGCTTCAGG	TAAGCGTAAT	TCTGGACAGC	AACAGGGCTC	300
AGCCTGGGCA	TGTCCCCAGA	GCCAGCAGCC	ATTCCCCCCA	CTGGCAGGGC	GTGTTTATAC	360
TTCTGAGTCA	TAAGGTCCTC	TGAGGCTTCT	TCCAGCCACT	GGGTGACAAA	GTCCAGGGAA	420
TTTGGTTGCC	TCTCCAAAAT	CTCTTGAAAC	TTCTTCCTTT	CGTATTCAAC	TGACTGCTGC	480
ATGAGATGAG	GCCTGATGCT	ACTGATAGCA	AAGTTGGCCA	TGTCCACTTT	CATTAGGTCC	540
AACACAGAAA	AAATTTCTCT	GAAAAGGGGC	ACTATTTCCT	TAATGTCCTT	TAGTTTCTTA	600
ACTTCCTCAT						616
						0.10

- (2) INFORMATION FOR SEQ ID NO:856:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 497 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

GCTCTGGGTG AAAAGATCTC					60
GAAGTTGCCT TGCTTTGATA	CTGCAAATTC	AGTATTTGTA	CACTGGAATG	ATAAAAAGAT	120
GTTCCACTTT CTTTTCAGCC	AGAAAGCTTC	CTCGTTGTGT	GTGTGCGTGT	GTGTCCCATC	180
CTATTGCCTG TTCTTTCTAA					240
GAACATTATG GGGCCCACCA					300
TCAAGGAAGA AATCAGAACA					360
GTTTGGAAAC TGACCAGCAA					420
TTCCAGGACC AGAGATTAGG	TAACTAGCTA	CAGGCCAGAG	GAATGCTTCC	CTCTCTAGAT	480
CAACAAGCAC CCTCGAG					497

- (2) INFORMATION FOR SEQ ID NO:857:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 262 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

CTTCATCCC MACAMOC	amaa mmmammmmm	a mmmaaaaaa			
GTTCATGGCC TAGATGC	CIGG TITGITIT	G TTTTCGTTT	TTTGAGACAG	TCTTGCTCTG	60
TGACCCGGGC TGGAGTG	GCAG TGGTGCGAT	C TCGCTCATTG	CAACCTCTGC	CTCCCAAGTT	120
CCAGCAAGTC TCCTGCC	CTCA GCCCCCCAC	C GAGTAGCTGG	GACTACACGC	AAGTGCCACC	180
ACGCCCAGCT ACTTTTT	IGTA TTTTTAGTA	G AGATGGGGTT	TCACCATGTT	GGCCAGGCTG	240
GACTCGAATT CCTGACC	CTCG AG				262

- (2) INFORMATION FOR SEQ ID NO:858:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 441 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

GAAACTATAA	TCATCAGTAC	TGTAATGAGC	AATTATGAGG	CCTACAAGCC	TTCCACAGGA	60
GCTATGGGAG	ATCGACTAAC	GGCAATGAAA	GCAGCTTTCC	AGTCACAGTA	CAAGAGTCAC	120
TTTGTTGCAG	CCAGTTTAAG	TAATCAGAAG	GCTGGAAGTT	CTGCTGCTGG	GGCAAGTGGG	180
TGGACTAGTG	CAGGGAGCTT	GAATTCTGTT	CCAACTAACT	CAGCACAACA	GGGCCATAAC	240
AGTCCTGACA	GCCCCGTCAC	CAGTGCCGCC	AAGGGCATCC	CAGGCTTTGG	CAATACTGGC	300
AACATCAGTG	GTGCCCCTGT	GACCTACCCG	TCTGCCGGAG	CCCAAGGAGT	CAACAACACA	360
GCTTCAGGGA	ATAACAGCCG	AGAAGGGACT	GGGGGCAGCA	ACGGGAAAAG	AGAGAGATAT	420
ACTGAGAACC	GGGAACTCGA	G .				441

- (2) INFORMATION FOR SEQ ID NO:859:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 384 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

GAATTCGGCC	TTCATGGCCT	ACTGGTCGCC	AATGTGCTGC	AGGTCATGGC	TCCGGAATCA	60
AATTGGGCTC	AAACGGGGCA	AGCTCCAACA	CAGTGGAGCC	TGGCGCTACT	CCCACCTCCA	120
CCTTGCGGAT	CTCAGAGCTG	CAGGATGGCT	CTGCCCACCG	CACCCTGAGC	TGGCCCCGCT	180
TGGGGCTGGC	ATTGGGGGAC	${\tt AGTGTGTTCT}$	GGGCGTCTCT	GCTCCTCTCT	GCTGGTGCCT	240
GTGCCTCTGC	TGGCCGCCCA	CTCATAGATG	TCAGAGCCAC	AGGACGGCCC	CGCAGAATCC	300
CTGCGCCGAC	CCTGCCGGGG	GCTGGCTTTG	GTGCACATGC	AACTCGTCAT	CGTGGTCCCC	360
ATGGGCACCT	CTGCTCTTCT	CGAG				384

- (2) INFORMATION FOR SEQ ID NO:860:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 421 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

GAATTCGGCC	TTCATGCCTA	CGTTTCCCGA	GAAACCAAGC	CACAAAAAGT	ACAGGGCCGC	60
CCTGAAGAAG	GAGAAACGAA	AGAAACGTCG	GCAGGAACTT	GCTCGACTGA	GAGACTCAGG	120
ACTCTCACAG	AAGGAGGAAG	AGGAGGACAC	TTTTATTGAA	GAACAACAAC	TAGAAGAAGA	180
GAAGCTATTG	GAAAGAGAGA	GGCAAAGATT	ACATGAGGAG	TGGTTGCTAA	GAGAGCAGAA	240
GGCACAAGAA	GAATTCAGAA	TAAAGAAGGA	AAAGGAAGAG	GCGGCTAAAA	AAACGGCAAG	300
AAGAACAAGA	GAGAAAGTTA	AAGGAACAAT	GGGAAGAACA	GCAGAGGAAA	GAGAGAGAAG	360
AGGAGGAGCA	GAAACGACAG	GAGAAGAAAG	AAAAAGAGGA	AGCTTTGCAG	AAGGGCTCGA	420
G						421

- (2) INFORMATION FOR SEQ ID NO:861:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 271 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

GGATTTCTTT	GGAATGGGCA	AAGAAGTGGG	GAATCTGCTA	CTGGAAAACT	CACAGCTTCT	60
GGAAACCAAA	AACGCCTTGA	ATGTGGTGAA	GAATGACCTG	ATTGCCAAGG	TCGACCAGCT	120
${\tt GTCCGGGGAG}$	CAGGAGGTGC	TGAGGGGCGA	GTTGGAGGCT	GCTAAGCAGG	CCAAAGTCAA	180
GCTGGAAAAC	CGTATCAAGG	AGCTGGAAGA	GGAACTGAAA	AGAGTGAAGT	CCGAGGCCAT	240
CATCGCCCGC	CGTGAACCCA	AAGTTCTCGA	G			271

- (2) INFORMATION FOR SEQ ID NO:862:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 288 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

GCGGCTCTTT	GGGAGGTGGT	CAGGGGAAAA	GATGGTCAGT	GCTTTTTCTG	GACAAATCCA	60
GGGGCCAATT	GAGGTGGGGA	GTCTATGAGA	AGGGCCCTGT	CAGCTGAGGC	GAGGGAAAGG	120
GCAGAGGACC	TAGAATAAAA	GGATATGGCC	TCTCTGTGCA	CTAGCAGGAT	GGGTAGGAAA	180
${\tt GGGAGATATG}$	AAAAGACGAA	ATGGGGACCG	GGTGCGGTGG	CTCACGCCTG	CAATCCCAGC	240
ACTCTGGGAG	GCCAAGGCAG	GCAGATCACC	CGAAGTCAGG	AGCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:863:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 326 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

GA GGAGATGGAT	TTGATTCTCG	TGGCAAACGT	GAATTTGATA	60
GA TCTTCTTTTT	CACATTACAG	TGGCCTGAAG	CACGAGGACA	120
T CACAACTGGG	GAACTGTCAA	AGACGAATTA	ACAGAGTCCC	180
AA ATATCTTATA	ATTACAGTGA	CTTGGATCAA	TCAAATGTGA	240
T GAAGAACATC	ATCCAGTGGC	AGACACTGAA	AATAAGGAGA	300
IT CTCGAG				326
֡	GA TCTTCTTTT CT CACAACTGGG AA ATATCTTATA	GA TCTTCTTTTT CACATTACAG CT CACAACTGGG GAACTGTCAA AA ATATCTTATA ATTACAGTGA GT GAAGAACATC ATCCAGTGGC	GA TCTTCTTTTT CACATTACAG TGGCCTGAAG CT CACAACTGGG GAACTGTCAA AGACGAATTA AA ATATCTTATA ATTACAGTGA CTTGGATCAA GT GAAGAACATC ATCCAGTGGC AGACACTGAA	GAGGAGATGGAT TTGATTCTCG TGGCAAACGT GAATTTGATA GA TCTTCTTTTT CACATTACAG TGGCCTGAAG CACGAGGACA CT CACAACTGGG GAACTGTCAA AGACGAATTA ACAGAGTCCC AA ATATCTTATA ATTACAGTGA CTTGGATCAA TCAAATGTGA GT GAAGAACATC ATCCAGTGGC AGACACTGAA AATAAGGAGA IT CTCGAG

- (2) INFORMATION FOR SEQ ID NO:864:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 546 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

GGAATGGGGA	GAGGGATCTA	CCAAGGTNAC	AGCAGTTTTT	TGAGCAGCTG	GCACGTGCCT	60
CTGCTGCCAA	CATGATGAGG	TACAGAACCC	AGCACAGGGA	ATGCTCAGCC	TGTGACTGTG	120
AGCTGGATGT	GAGAGTCTCC	TGAGGACCCT	CGGTATACTC	AGAGCATTTC	CTCTCAGGGT	180
GCAGGAAGAG	GAAAGCAGAG	GAAGTGGACT	TGAAGGACCA	AAGGTGGGAT	CCTAGCTGGG	240
CCAATCACTG	AGAAGCCATG	TGGTCTTGGG	CAAGTCATTC	CCTTCTCTGA	GCCTCAGTTT	300
CCCCATCTGT	AAAATGGAGG	TAATGATACT	ATGCCTACCT	CATCATCATG	CTGTGAAGAT	360
			ATTACCCATT			420
			ACTCTGAAAC			480
			TGCCATGCCC			540
CTCGAG						546

- (2) INFORMATION FOR SEQ ID NO:865:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 808 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

GAATTCGGCC	AAAGAGGCCT	AAGGATTCAT	AGTATAAATC	TTTAATTTAT	CACAGTCTGT	60
ATTAAGTAAT	ACTAAACCAC	TTCGCATATA	AATACATCAC	AACAGTATAC	TTCCGTTTAT	120
GCTATCTTGG	TCTTTGTACT	TTTGTTTTTG	TACATTTTAC	TTTGGCATAA	ATGTCAAAGT	180
			TTTGCCTCTC			240
			CTATACACGT			300
			${\tt TTTTTTTTT}$			360
			CTATTTCGGC			420
			CCCGAGTAGC			480
			${\tt GTAGAGATGG}$			540
			GCCCACCTCG			600
TACAGGCGTG	AGCCACCGCA	CCTGGCCTAT	TCTGTCCCTT	TTTAAAGCAG	TTCTCTTTTA	660
AAAAATTGTG	GTAAGATATA	AATCACATAA	AATTTGCAGT	TATAACCATT	TTAAAGTATA	720
TAATTCCATG	GCATTAATTA	CAGTCACAGT	CTTTTACAAC	TATTATTACT	ATGTATTCCT	780
AAAGTTTTTT	TACCCTCCCC	CCCTCGAG				808

- (2) INFORMATION FOR SEQ ID NO:866:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 361 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

GAATTCGGCC	TTCATGGCCT	AAAAGAAAAT	GGCTTCAGTA	AGTTAGGATG	AAAAATGAAA	60
			TTTAAAAAAA			120
ACCTCCTCTC	CCCACCCCAA	ACTAAAAAA	GAAAAAAAGG	TTTTCTAATG	AAAATCTTTA	180
AAAATACTGT	${\tt CAGTATTTTA}$	AAATTTTCAA	CAGTATTATA	AAAACATTGC	ATCTCCCCAC	240
CTCTAATATG	CATATATATT	TTTCCTGCTA	AAATTGGTTT	CTACAATTGA	GTAAATGGCA	300
AATACATGAA	GCAATGTCCC	TAAATTTTAT	AAAGAAATTA	TATTTAATGC	ACATTCTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:867:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 880 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

GAATTCGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAGCCA	AGAATTCGGC	ACGAGGAAAA	60
${\tt CAGTCTTTTA}$	ACCTTTCAAA	ATGCCACAAT	GTGCATTTTA	GATTGCCCTT	AGTTTCCCAA	120
CTCTCAGTAT	ATAGAGACTC	AATTAGAAAA	GAAATGGTGC	TAGTAGCTTC	AACCCACTGG	180
TATGTATTTG	AGGAACTGTT	CCTGGTAGAA	GGCAGTACCG	TGTCCCTTGG	TATTGCTACT	240
GTGCCTGCTA	TGTTACTTCT	TTATGTATAT	${\tt GATATGGAAG}$	TAACTCCTTT	TATACATGTG	300
GAGAAGTTTC	ACAGCTTTTT	TTCATAGTCA	TTGCATTAAA	ATGTCTGCTG	AGGCTGGGTG	360
TGGTGGCTTA	CGCCGGTAAT	CCCAGCACTT	TGGGAGGCCA	AGGTGGGTGG	ATCACCTGAG	420
GTTGGGAGTT	CAAGACCAGC	CTGACCAATA	TGGTGAAACT	CCGTCTCTAC	TAAAAATACA	480
AAAATTAGCT	GGGTATGGTG	GCGCACACCT	GTAATTCCAG	CTCCCGCCGG	GCGACTCGAC	540
CAAAGAGGCC	GGAATTTGGC	CCTCGAAGCC	${\tt AAGAATTCGG}$	${\tt CACGAGGGGT}$	ATTTTTATTT	600
TTANTTNTTC	TGTTTCTCTC	TNGAGTGTAT	AGTGTAGAGG	GGGTTTCTGT	CTTGAGTGTA	660
GGCCTGGAGA	TTTCCCTTAT	ATGGTACAAA	CCAGCAATGA	ATTAAGAGGT	CTCTTTTCTC	720
CAAGATCTAG	TGTTTTGTAC	TAGGAGAACT	CTAAAAAGTA	TCTATTTCAC	TGTAGTGCCA	780
AAGTACAAAT	TTATTTGGAT	TTATTTTTTG	CCATCTTATT	${\tt TTTTAATATA}$	TTTCTTTTTC	840
TATGTTGTGC	TTCTTTCCCA	CCTCATCTCT	CCTCCTCGAG			880

- (2) INFORMATION FOR SEQ ID NO:868:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 366 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

GAATTCGGCC	TTCATGGCCT	AGTCATGGCT	TTAGAATCTG	GAGAAGAGTC	TGACTCACTT	60
CTTTCCTGAG	${\tt GGGATGCACT}$	GGGTTTCACA	TCAAGTTCTT	GAGAGGATCC	CGAACGACTT	120
CTCTGCCCCA	$\tt GGGGAGTCCG$	AGCCACAGTT	TTCTGATCAA	CTGATGATTC	TGACCCGCTT	180
CTTTCTCTCT	${\tt GGGGGGTAAG}$	ACACTTGTTG	TTGAGCTCTG	GGGATGATGG	AGAACGACTC	240
CTCGGCCTAG	${\tt GAGTCTGAGG}$	CAAAGCTTTC	GGTTCTGGGG	AAGAATCACA	TTCGCTTCTC	300
CCTCTAGATG	${\tt GCGTTCTAGG}$	TATATCTTTC	ATTCCAGGAG	AGGAĆCCAGA	CAGGCTGTGC	360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:869:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 529 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

GAATTCGGCC	TTCATGCCTA	GAGGATCTTC	TCCTGACCCA	GCATCGCTCA	TCACAATGAA	60
GAACCAAGAC	AAAAAGAACG	GGGCTGCCAA	ACAATCCAAT	CCAAAAAGCA	GCCCAGGACA	120
ACCGGAAGCA	GGACCCGAGG	GAGCCCAGGA	GCGGCCCAGC	CAGGCGGCTC	CTGCAGTAGA	180
AGCAGAAGGT	CCCGGCAGCA	GCCAGGCTCC	TCGGAAGCCG	GAGGGGGCTC	AAGCCAGAAC	240
GGCTCAGTCT	GGGGCCCTTC	GTGATGTCTC	TGAGGAGCTG	AGCCGCCAAC	TGGAAGACAT	300
ACTGAGCACA	TACTGTGTGG	ACAATAACCA	GGGGGGCCCC	GGCGAGGATG	GGGCACAGGG	360
TGAGCCGGCT	GAACCCGAAG	ATGCAGAGAA	GTCCCGGACC	TATGTGGCAA	GGAATGGGGA	420
GCCTGAACCA	ACTCCAGTAG	TCAATGGAGA	GAAGGAACCC	TCCAAGGGGG	ATCCAAACAC	480
AGAAGAGATC	CGGCAGAGTG	ACGAGGTCGG	AGACCGAGAA	GCCCTCGAG		529

- (2) INFORMATION FOR SEQ ID NO:870:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 372 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

GAATTCGGCC	TTCATGGCCT	AATTTGAGCT	TCAAGTCTCC	ATGTGTATAA	TGTGGGGTTG	60
ATGCTGTGGT	GCTCCAAGGT	GTTGGGGGGT	TTTAGGCAGA	GTTCTTATGC	TTAATATAGG	120
				TCTTCATCTG		180
				AATTCTATCT		240
TTTAGTGTCC	TGTCTGTTTC	TAAATCTACT	GGGCAGTTGG	AGACATTGTC	TTTTGTTCCC	300
TCATCTATCT	TCTGTATCCA	CAGTTGATAA	TTGTCTATGT	TTTTAGTGTG	TTTTAAGGAA	360
ACTAGTCTCG						372

- (2) INFORMATION FOR SEQ ID NO:871:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 574 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

GAATTCGGCC	TTCATGGCCT	AGGTGGTGGG	TGCCTGTAGT	CCCAGCTACT	TGGGAGGCTG	60
AGGCAGAAGA	ATTGCTTGAA	CCCGGCAGGC	AGAGGTTGCA	GTGAGCTGAG	ATCGTGCCAC	120
		AAGAGTGAGA				180
ATGTACACAA	ATATGGACAG	CACTGGCAAG	AAGTGTGGCA	AAAACACATG	TGGTTCTCTT	240
GTTTTGGGCT	CAGACATGTG	GCTGTGCCAT	TACAGACCCC	CGGGATTTAG	AATCCTCCTT	300
		TCGTGAGCAC				360
		CCTTGACGAC				420
		TAGGATCGCC				480
		AGCCCCCCAG				540
		CCATTAGCCT				574

- (2) INFORMATION FOR SEQ ID NO:872:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 528 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

GAATTCGGCG TTCATGGCCT	ACCAGACTAC	TACGGACTCA	TCTAACAAAA	CAGCACCGAC	60
TCCAGCATCC AGTGTCACCA	TCATGGCTAC	AGATACAGCC	CAGCAGAGCA	CAGTCCCCAC	120
TTCCAAGGCC AACGAAATCT	TGGCCTCGGT	CAAGGCGACC	ACCCTTGGTG	TATCCAGTGA	180
CTCACCGGGG ACTACAACCC	TGGCTCAGCA	AGTCGCAGGC	CCAGTCAACA	CTACCGTGGC	240
TAGAGGAGGC GGCTCAGGCA	ACCCTACTAC	CACCATCGAG	AGCCCCAAGA	GCACAAAAAG	300
TGCACACACC ACTACAGTTG	CAACCTCCAC	AGCCACAGCT	AAACCTAACA	CCACAAGCAG	360
CCAGAATGGA GCAGAAGATA	CAACAAATTC	TGGGGGGAAA	AGCAGCCACA	GTGTGACCAC	420
AGACCTCACA TCCACTAAGG	CAGAACATCT	GACGACCCCT	CACCCTACAA	GTCCACTTAG	480
CCCCCGACAA CCCACTTCGA	CGCATCCTGT	GGCCACCCCC	AACTCGAG		528

- (2) INFORMATION FOR SEQ ID NO:873:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 611 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

GAATTCGGCC	TTCATGGCCT	AAGCTGCACA	AAACGTAGAA	AGAAGACATA	GCGCCTGCCA	60
GGGGAATAGG	AAATGAGGGC	ACTTACACAT	TAATGTGAAT	TAGTAATTGT	GGTATAGAAA	120
TGTTTTATAG	TGAAAGATTC	AAATTTGCTT	TTCAAGAAAA	ATGCCAAAAG	CTATTTAAAT	180
AATTCGAGGT	TACATCGTAG	GTTTTGATTT	TTCTCAATTT	AAGATACAGA	AATACAGCAA	240
GCCTTAATAT	AAAGTTTCCT	AAAGTTTCTT	CAAGTATTTT	TTAAGGTGGA	GAAATGCAGG	300
AATTGTATAA	CCAGAATTGT	TTCTGCCTTT	AGCTTTTCAG	AACTTGAGAT	GTGGCAGCAC	360
TGGACTGGGT	TTTTTTTAAAT	GTTAGGACTA	GGAATGTTTG	CTCTTGTTAA	TTATGAATTA	420
ATTGATTATT	AAGTTTAGAA	TGCATTTTTA	CAAGTATCTA	ACTATCAAAT	TGTGTTTAGT	480
AACTTGAGTG	TATGCACAAG	TTTGATCAAC	AGCAAAATAG	AGTTCTGAAT	TTCTTTTAAA	540
GTGATGATAT	ATTATTTTGT	GAAACTTTGT	GTTTGAAAAT	GTTTATTTCT	GTTTATGGTG	600
TAATACTCGA	G					611

- (2) INFORMATION FOR SEQ ID NO:874:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 303 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

GAATTCGGCC	TTCATGGCCT	ACGAGCGGTG	AAGGAGGAGA	CCAAGGAGGA	TGCTGAGGAG	60
AAGCAATAAA	TCGTCTTATT	TTATTTTCTT	TTCCTCTCTT	TCCTTTCCTT	TTTTTAAAAA	120
ATTTTACCCT	GCCCCTCTTT	TTCGGTTTGT	TTTTATTCTT	TCATTTTTAC	AAGGGACGTT	180
ATATAAAGAA	CTGAACTCAA	CATTCAGGTT	GTTTTTTTT	TTGTTTCTAA	GTTTTTGCCC	240
TATTGAAGAT	GACTTCAGAA	AATCCATTCC	CCAGTCATGA	AAATGTACTG	TGCTATTCTC	300
GAG						303

(2) INFORMATION FOR SEQ ID NO:875:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 348 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

GAATTCGGCC	TCATGGCCTA	ACGGCAGCGG	CAGCCTCTGA	AAAGAATCGG	GGCCCAAGAA	60
AAGGCGGTCG	TGTTATCGCT	CCCAGGAAGG	CGCGCGTCGT	GCAGCAGCAA	AAGCTCAAGA	120
AGAACCTAGA	AGTCGGAATC	CGGAAGAAGA	TCGAACATGA	CGTGGTGATG	AAAGCCAGCA	180
GCAGCCTGCC	CAAGAAGCTG	GCACTGCTGA	AGGCCCCAGC	CAAGAAGAAA	GGGGCAGCTG	240
CCGCCACCTC	CTCCAAGACA	CCTTCCTGAG	GACGCTGGCC	CCAGTGCAGG	CCAACATCCC	300
ACCCCCTACC	TCCATATGGG	ACCTTGCAAG	TCATCCCACT	TCCTCGAG		348

- (2) INFORMATION FOR SEQ ID NO:876:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 586 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

GAATTCGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAGCCA	AGAATTCGGC	ACGAGGAGAC	60
TATTTTCCAT	TTCACACAAG	AAATCTTTGA	TTATTCAGTA	AAAAGAGGAA	ATATAAGAAA	120
AAAAATCAGA	CTAGTCTGGC	CAACATGGTC	TAAAAATACA	AAATTAGCCA	GGCATGGTGG	180
CGGGCGCCTG	TAATCCCAGC	TACTTGGGAG	GCCCAAGCAG	GAGAATCGCT	TGGACTCGGG	240
AGGCGGAGGT	TGCAGTGAGC	CGAGATCATG	CCACTGCACT	CCAGCCTGGC	AGACAGAGCA	300
AGACTCCCTC	TCCAAAAAAG	TTAAAAAAAA	AAAAGAAAAA	AAAGGCCGGG	TGCAGTGGTT	360
${\tt CGGCCTCCCA}$	AAGTGCGGGG	ATTACAGGCG	TGAGCCACCA	TGCCCGGCCA	CTTTCTGTAT	420
${\tt TTTTTAATAA}$	ATAAGAAATA	CACATTTAGT	AGTAGTTACA	AAGATCTGTA	GGCCGTAGCA	480
AATATTCAGT	AACTGGAAGA	TGCCAATGAA	CATTGTTGGG	TAGTATTTAA	ATAACAAAAT	540
GTTCAAATAT	TTGACAAGAT	TAACAACACT	ACACGGCCTT	CTCGAG		586

- (2) INFORMATION FOR SEQ ID NO:877:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 445 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

GAATTCGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAGCCA	AGAATTCGGC	ACGAGGGTAA	60
	TTATGTATTT					120
	GGTAGAATTC					180
TTCTTCAGAC	TGGAATATTA	TTCTCTAGTG	TAGAAGAAAA	CATTTTCTGC	TTACAAAACA	240
AATAGTAAAT	ACTCTAAAAT	AGGGGTTGGC	AAACTTTTCT	TAAATAAAAG	GCCAGATGGT	300
AACTATTTTA	GGTTTTGTGG	GCCATGTGTT	GATAACTATT	TTAGGTTTTG	TGGGCTACGT	360
ATGGGGTCAC	TCTCCCATTC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTTTC	420

TGTGTGTG AGCGGCGCTC TCGAG

445

(2) INFORMATION FOR SEQ ID NO:878:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 586 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:	,
GAATTCGGCC AAAGAGCCGG AATTTGGCCC TCGAAGCCAA GAATTCGGCA CGAGGGGGTC TCCATTCCCC GAGAAGCCAG GGGCAGGGTG GGATGGGAA GACCAGGAGC AGAGTCGAGC CTCACAGAAG CCAGCGGGG TCTCTGCTCA GCACCCCAGC CGGGGCTCTG GACCAGGGT AACAGCCCCA GTTCATCCCA ACCCCTCTCA GAGCCTCAAG AGGGGTAGCT CGGCTGCCGG AAGAGAGGGG TGCCCTATCC CTGGCAACCC CTCCACGTAG CGTACCCCAG CACCTGCCAC CGCCTTTGCC ATTTCTTTGA GCTTGAAGTT AACTCTCTTA GAGTCTAACT TTGGTTCATT TCTGCACAGG TACAATAGAT GACTTTATTT GTTTAAAATG TTTAATATAT ATACATACAT ATATATATAT TTGTCTGTAA GAATTATGTT TTAAACAGCT GCTGTAGGT ACCTTTTTT AAGTAAATCT TACAGTGGAG TATATTTTTT AAAGCACAAA ATTGGTGCCA AGACTGGGTG AGAAATGTAC ATTACCCCCT TATTATTTTG CGTCGGATTC CTCGAG  (2) INFORMATION FOR SEQ ID NO:879:  (1) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 414 base pairs	180 240 300 360 420
(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:	
GAATTCGGCC AAAGAGCCGG AATTTGGCCC TCGAAGCCAA GAATTCGGCA CGAGGGGAAA ATCTTGTCCT AAAAATATAT GAGTTTGGGG GTAAGGGGTG GGATAGCCAA GCAAAATCAG TAATTATTTT AAAATGAACA TATGAATTTT TATTAACTTT TAGTTAAATA CAGATTTTAC AACGAGGTCA GGATTAAAAA CAACCTGTCC TGTTTTGTCA GTTCCCAGCT TCTTCGTTTA GAATAAATTA GACCAAAAGA AGAAACGTGC TTGTCTCTGT ATACCCGCAG AATGAAGTTA CTGTTGTTAA AACCGGATTT TTTCATTTTA CTAGGTTCCG CTCTCTCCCT CGAG	120 180 240
(2) INFORMATION FOR SEQ ID NO:880:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 402 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:	
GAATTCGGCC AAAGAGGCCG GAATTTGGCC TCGAAGCCAA GAATTCGGCA CGAGGGTAAT TTTAAAAATT TATGTATTTT CTAGCATTTG CCTCAAGGAT TGAAATTTTT TTTTTTACTT	60 120

GTGTTTACAG GTAGAATTCT TTATTTAAAA AGTCAGTTGA ATATCAAAAC TATTTGATAT TCTTCAGACT GGAATATTAT TCTCTAGTGT AGAAGAAAC ATTTTCTGCT TACAAAACAA ATAGTAAATA CTCTAAAATA GGGGTTGGCA AACTTTTCTT AAATAAAAGG CCAGATGGTA ACTATTTTAG GTTTTGTGGG CCATGTGTTG ATAACTATTT TAGGTTTTGT GGGCTACGTA TGGTGTCATT CTCCTATTCT CTCTCTATCA CCTACCCTCG AG	180 240 300 360 402
(2) INFORMATION FOR SEQ ID NO:881:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 352 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:	
GAATTCGGCC AAAGAGGCCG GAATTTGGCC CTCGAAGCCA AGAATTCGGC ACGAGGGGCC GTTTTTTTTT TTTTTTTTT TTTTTTCNNG NNAGGCTTTC CCTAGGTGAT TTTTAATTGC TATTATAAAT AAATATCCAT TTTTCCCATA AAATATTGCT ATATGTTAGT ATATTAATCT TGTACTGTTA CCTTTTCAA CTCTATTGGT TCTGATAGCT TGTCAGTTGT CTACCTTTCA TCTTCTAGGT AAATATTCT TACAAATAAT GAGATTTGCT CCTACTTTCC AATTTATCTC ATTACTTTTA CTNNTCTTAC TGCACTGGCT AGGACACCAC TACCTTCTCG AG	60 120 180 240 300 352
(2) INFORMATION FOR SEQ ID NO:882:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 351 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:	
TTTTTTTTT TTTTAACTT AAAAATAGTT GTATTTATAT TCCACAATTT GTTCAAATAC TGGTTTTCTT ATAAACTTC TACAGGATGT TTTTAAACAA ATTCTTCACA TTGTGTTTTG ACTATGTACT TGCGGAATTT CAGGGAAATA GTTCTGTGTA TTTTTAATAG CTTAATTTGT ACTAAAGGGA TGGTAGGTGG TCACATGCAG TCCATGTGGG ATTCTAACAT GACATTTAGT GAGTTTTCTG ATGTGACCA TCCCTTTGAT GCTGAAGGTA ATGCATCTGT TGAAAGAAGT GACTGTAGAT TTGGATTACT GCTCTCGCA TCCCCTCTT TTCTGCTCGA G	60 120 180 240 300 351
(2) INFORMATION FOR SEQ ID NO:883:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 548 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:	
GAATTCGGCC TTCATGGCAA GAAGGAGNCT TAGCATCAAA CTTTGGAAAG GGAAGCCAGA GAAAAAGGTA GAATGGACAA GTGACACTGT GGACAATGAA CACATGGGCC GCCGTTCATC CAAATGCTGC TGTATTTATG AGAAAACTCG GGCCTTTGGC GAGAGCTCCA CGGAAAGTGA	60 120 180

TGAGGAGGAA	GAAGAGGGCT	GTGGCATACA	CACTGTGTAC	GTGGCCACCG	CAAAGGACGG	240
GTTNTGCAAC	CCTAGGACCG	ACCCCCACCA	CCCTTCCCCA	GCTCCTGACC	NTTCCCAGCC	300
CCCTCCAGGG	CCAATGCAGC	ACTAAATCCC	TCTCTCCTCC	AGCATTCCTG	TGTCTGTCTG	360
GCCCTAAATG	TATCCATGTG	GCTACTTCTC	CAGCCCCCTC	CTTCCCTNTC	TTCTGCCTGA	420
TAGAGGGAAG	AGGAAGAGGA	GGACGAACAG	AGATCCTGAA	ATTCTGACTT	GCTGCTATTC	480
CAGAACCCAG	CCTCCTGGGT	TTCCCCAGTC	CTCATTTTTC	CTCCCAATAC	CCACCCTTCT	540
CTCTCGAG						548

- (2) INFORMATION FOR SEQ ID NO:884:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 446 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

GAATTCGGCC	TTCATGGCCT	AAAAAATACA	AAAAATTAGC	CGGGCGTGTT	GGCGGGCGCC	60
TGTAGTCCCA	GCTACTTGGG	AGGCTGAGGC	AGGAGAATGG	CATGAACCTG	GGAGGCGGAG	120
CTTGCAGTGA	GCCGAGATCG	CGCCACTGCA	CTCCAACCTG	GGAGACACAG	CGAGACTCCG	180
TCTCCNAAAA	ААААААААА	AAAAAAACAC	ACTTGTCTTA	CAAAGACTAA	CAAAAGATAC	240
AAAATAAAAT	AACTTTACAG	CATCATTAGA	AAGCGAACAA	AATCCTAAGA	TAGATACATT	300
TATCTTTCTT	GTTTTAGAAC	TTTTTCTGTG	TAATGGAATG	GAAATGCTTA	ATCTTGTTTC	360
AATGTTTTCA	GTGTTTGTGC	TTTGTCAAAT	TGAGGTTGGA	TGTTAAAGCC	CTTACTACTG	420
TATTATACAA	AGCAGCGAAC	CTCGAG				446

- (2) INFORMATION FOR SEQ ID NO:885:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

GAATTCGGCC	TTCATGGCCT	AGCCGGCGCC	GCCGNGTCTT	CCCGGTCTCC	TTTCCCGGCC	60
GCACAGGGTT	TTATAGGATC	ACATTGAÇAA	AAGTACCATG	GAGTTTTATG	AGTCAGCATA	120
TTTTATTGTT	CTTATTCCTT	CAATAGTTAT	TACAGTAATT	TTCCTCTTCT	TCTGGCTTTT	180
CATGAAAGAA	ACATTATATG	ATGAAGTTCT	TGCAAAACAG	AAAAGAGAAC	AAAAGCTTAT	240
TCCTACCAAA	ACAGATAAAA	AGAAAGCAGA	AAAGAAAAAG	AATAAAAAGA	AAGAAATCCA	300
GAATGGAAAC	CTCCATGAAT	CCGACTCTGA	GAGTGTACCT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:886:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 388 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

		AAAAATCTAA				60
TCAACATTGA	GACAATGTAG	AGATATATTA	TGGTATAAAA	TGAAGCATTT	GCACGAACTT	120
		AAGAAGTTGC				180
		TTCCAGAAGG				240
		${\tt TTTTTTTTT}$				300
TTCAGGCTGG	AGTGCAGTGT	TGCAATCATA	GCTCACTGCA	GCCTTGACCT	CCTGGCCTCA	360
AGTGATACCC	CTGTCTCAGC	CTCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:887:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 364 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

GCCCCAGTCT AAGGCATTTA	AAATTAAACA	GCTCTTCAAC	GCCCCAAGTT	ATTTCATCAG	60
GCTAAGAACT TCTCCGAGAA	ACGCACAAGA	AGGCAGGCAA	ACAGGTGGGT	AGGTGAGAGG	120
TCACGGGGCT CCATCTGCAA	GCTCCATCTA	CAAGGCATCA	ATCTGCGTTG	TGGCATCAAC	180
GTTAAAATGT TCTACAGCTT	AGGGATCTTC	TTGAAGCAAG	GTTCCAAGCA	CAAAACTAGT	240
ATGACCGGAG GCTCAATTTA	GAAGATGCAG	CATCTGAAAA	CCTTTACCCC	AGGAAAGGAG	300
GGGTGCCTGC TGGCATTCAT	GGGCTCTGGA	ACAAGCATTT	ATTCAAAGCT	GATGGCCCCT	360
CGAG					364

- (2) INFORMATION FOR SEQ ID NO:888:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 416 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

GCACCCCCAA	ATGCCAGCCT	CTCCTTTCTT	CCCATCCACC	AGTATACTGC	GGGGCCATTT	60
CTGGTCTTTG	TCCAACAGGA	AACCCATTTC	TGGTGGGATA	TGCCTTCCAG	TGCCACAGGG	120
CCACTCACCC	CATGCATCTC	TGTCCTGCCC	GTCAGTGCTG	GGACGGACAG	CAAGGGCAAG	180
CCCAGTGTCT	GGCGGATAGG	TGGGTGGGAA	CAGAGAGGGG	AGAATGCCGT	CCTAAGCTTC	240
TGCTTGGGGA	TCCCCCACAC	GACCTGGGTA	CTGCCTGGGA	AACCTGTCCT	AAGTAAAACT	300
		CGGCCTGCGA				360
CGCCTTTGTÇ	CTCATTTTGA	GCTGCAAGCT	GGGTCAGCGG	CTCTGAAGCC	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:889:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 349 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

GTAGGCCATG	AAGGCCGAAT	GGAAAAAGTC	AGTTAAAGAG	GACTCAGTCC	CCACAGGTGC	60
					AAGTAGAATC	120
AGCCTTACAA	ACAGTGGACC	TCAACGAAGG	AGATGCTGCA	CCTGAACCCA	CAGAAGCGAA	180
					GACAAATGAC	240
			GCCAGAGCCT		GAGCACCACA	300
GAAGGGTAAA	GAGGGCTCCT	CGAAGGACAA	GAAGTCAGCA	GCTCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:890:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 719 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

GAATTCGGCC	TTCATGGCCT	AGACCTGCCT	CGAGGATGCT	CTGGGTTTGC	TGTAGTCGTC	60
TGTTACTGGT	CNTGTTAGGA	GGAGGGCCAG	GGGGACCCCC	ACCTGGGGCA	GTCCCTTCTG	120
		GCTGGAGCAG				180
		GCGAGACACC				240
		GCGCCGACTA				300
		CGATCTCTTG				360
		TGAGCCACTG				420
		TCACTGTGGG				480
TAACTTCTTT	TGTTATTTAG	GAAGGTTTAT	ATTAATATTT	TAATTCTACA	TTGGATAATT	540
CCTATATCAA	AACTATTGTT	GACAATCAGT	TACAGATGGA	ACTTCGTCTA	CTCTTTCTCC	600
	CCTGCTCTTT			GTTGACTAGT		660
AAACAAATTG	GGGCCGGCCA	GGCATGATGG	CTCATGCCTG	TAATCCCAGA	CAACTCGAG	719

- (2) INFORMATION FOR SEQ ID NO:891:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 453 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GAATTCGGCC						60
GCTCCAGCCT	CAGTTCAGCT	TTCCACACTG	CTTGCAGAAA	TTCCTTCATT	TATCTTGAGT	120
TTCTCCTCTC	ACTCCCATGG	TAGCTTTTCC	ATTCCCACTG	CCTCTTCTCA	CATTTCAGTA	180
GATGAGAATA	GAAGCCATAG	GAAGCAAACT	TCCTCAACCT	CCAGCCAACC	GCCGAGCGAT	240
GGGCATCTCT	CGGGACAACT	GGCACAAGCG	CCGCAAAACC	GGGGGCAAGA	GAAAGCCCTA	300
CCACAAGAAG	CGGAAGTATG	AGTTGGGGCG	CCCAGCTGCC	AACACCAAGA	TTGGCCCCCG	360
CCGCATCCAC .	ACAGTCCGTG	TGCGGGGAGG	TAACAAGAAA	TACCGTGCCC	TGAGGTTGGA	420
CGTGGGGAAT '						453

- (2) INFORMATION FOR SEQ ID NO:892:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 350 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

CNATTCCCCC	TTCATCCCCT	ACCAGCCTCT	GGGCTGAGGC	AAACACCTCT	CACCCCCCC	60
GWW11 CGGCC	TICMIGGCCI	ACCAGCE ICI	GGGCIGMGGC	AMAGACCICI	GAGGCCCCGI	o u
CCACCCAGGA	CCCCTCCACC	CAGGCCTCCA	CTGCGTCCTC	CCCAGCCCCA	GAGGAGAATG	120
CTCCGTCTGA	AGGCCAGCGT	${\tt GTGTGGGGTC}$	AGGGACAGAG	CCCCAGGCCA	GAGAACTCTC	180
TGGAGCGGGA	GGAGATGGGT	CCCGTGCCAG	CGCACACGGA	TGCCTTCCAG	GACTGGGGGC	240
CTGGCAGCAT	GGCCCACGTC	TCTGTGGTCC	CTGTCTCCTC	AGAAGGGACC	CCCAGCAGGG	300
AGCCAGTGGC	TTCAGGCAGC	TGGACCCCTA	AGGCTGAGGA	ACCCCTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:893:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 467 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

AACAGGAGAT	GGACAAGCTG	AAGGAGCAAT	ATGATGCTGA	GTTGCAGGCC	CTGAGGGAGA	60
GTGTGGAAGA	AGCAACCAAG	AATGTCGAGG	TCTTGGCGAG	CAGGAGCAAC	ACTTCAGAGC	120
AAGACCAGGC	GGGGACTGAA	ATGCGCGTGA	AGCTTCTGCA	GGAGGAGAAT	GAGAAGCTGC	180
AGGGAAGAAG	CGAAGAGCTG	GAGCGGAGAG	TTGCTCAGCT	${\tt TCAAAGGCAG}$	ATCGAGGACC	240
TGAAAGGCGA	TGAAGCCAAG	GCGAAGGAAA	CGCTGAAGAA	GTACGAGGGA	GAAATACGAC	300
AGTTAGAGGA	GGCCCTTGTG	CACGCCAGAA	AGGAAGAAAA	AGAAGCTGTG	TCAGCCAGAA	360
GGGCCCTGGA	GAATGAACTG	GAGGCTGCTC	AGGGAAATCT	GAGTCAGACT	ACCCAGGAGC	420
AGAAGCAGTT	GTCTGAGAAG	CTCAAAGAGG	AGAGTGAGGC	GCTCGAG		467

- (2) INFORMATION FOR SEQ ID NO:894:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 315 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

GAATTCGGGC	TTCATGGCCT	ACTCAGCTTT	CCTGGTCTCC	CATCTGAACT	GCTTCTTTGT	60
GCACCTCTTG	TTCTTTCTCT	TGGCTCCCAG	TCTTGATTCC	TGTGATCACT	CTTGCATCAC	120
TAATTGCACA	AGTGATTTCA	GGTGCAATTC	TGATTAGCCT	GCGTCCACAC	AGTGATCGAT	180
GATCCTATGT	GCCTAGAAAG	GACACTGTGT	GCTGCTCATG	ACCTGCAACA	GGAAAAAAGC	240
CATTTCTTGT	TAGCAGTGTA	AGAACCTTAG	AGCAAAGGAG	TTGACCTTCT	GATTGAATAT	300
AAGCACAACC	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:895:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 302 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GGGCTTAGTT	AGGAGCTATG	GCTAAACATC	ATCCTGATTT	GATCTTTTGC	CGCAAGCAGG	60
CTGGTGTTGC	CATCGGAAGA	CTGTGTGAAA	AATGTGATGG	CAAGTGTGTG	ATTTGTGACT	120
CCTATGTGCG	TCCCTGCACT	CTGGTGCGCA	TATGTGATGA	GTGTAACTAT	GGATCTTACC	180
AGGGGCGCTG	TGTGATCTGT	GGAGGACCTG	GGGTCTCTGA	TGCCTATTAT	TGTAAGGAGT	240
GCACCATCCA	GGAGAAGGAC	AGAGATGGCT	GCCCAAAGAT	TGTCAATCTG	GAGGAACTCG	300
AG						302

- (2) INFORMATION FOR SEQ ID NO:896:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 473 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

GAATTCGGCC	TTCATGGNCT	ANTCTCATTT	NAAATATATC	CTTACTGAAA	CATCTGGAAT	60
AACGTCTGAC	CAAATATCTG	GGTACAGTGA	TCCAGCCAAG	TTGAGACATG	AAATTAATCA	120
CCATGGCCTA	CATTTTTATC	TGTTTGGCTG	CAATTCTGTC	AAAGGCTTCT	GCTCTTCATA	180
ACATTTCACT	CACTAGCTCC	ATGAAGCCAT	ATGATACAAA	CCTTGCCTGT	GTAGCCTTCA	240
${\tt CTTTTTTCCA}$	AAAGAAGTCT	ATTAAATGCC	AATCAAGTAT	CTTCTCCTCC	AAGCTCAGTA	300
GCTCGGGCCT	TCAACAGCTG	TTCCCCATTC	CGATCCATCT	CCCTGAGCTA	CCCTGGCATT	360
CTTATCAGGA	CACTGGAGGA	ATCTATGTAT	GTGCCTCTAA	AGATTCAGCA	CCCAAACATG	420
ATAGAAATCA	CTGTGTTCAC	ACTGTATCTC	TATATCTGCC	CATCCCGCTC	GAG	473

- (2) INFORMATION FOR SEQ ID NO:897:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 594 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

GCTCGAGTGA	AGTGGTATCT	CATTGTGGTT	TGGGTTTTAA	TTTTATAATA	TTTTAATTTT	60
TAAAATCAAA	AGAATATACT	GGGGCTGGGG	TGGTGGCTCA	AGCCTGTAAT	CCCAGCACCC	120
TGGGGGGCCA	AAGGGGGTGG	ACCACCTGAG	TTTATGAGTT	CAAGACCAGC	CTGGCCAACA	180
CGGTGAAACC	CCATCTCCAC	TAAACATACA	AAACTCAGCC	GGGTATGGTG	GCAGGCACCC	240
GTAATCCCAG	CCTCTCAGGA	GGCTGAAACA	${\tt GGAGAATCAC}$	CTGATCCGGG	AGGTGGAGGC	300
TGCCATGAGT	CAGAATCACG	TCACTGCACT	CCAGCCTGAG	AGGAGACCCG	TACAAAAAA	360
AAAAAAAAA	ATATATATAT	ATACACACAC	ACACACACAC	ACAAGGATTT	TAGATTTGAA	420
AATGATGTTT	TTTACTCATT	TCAAAATGTA	CTGTAACCTT	TCTTTGGTTC	TTACTGTTTT	480
CATTTAACTT	TCTCTGTTTT	CAAGAAAAAT	TGTCTTTATT	GACATTTGTA	AAAAAGAATG	540
TGTTTTGCCC	AGTTATTAAG	TATTTTATTT	TTATGCAATT	TCAGAACACT	CGAG	594

- (2) INFORMATION FOR SEQ ID NO:898:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 302 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

GAATTCGGCC	TTCATGGCCT	ACTGTACATT	TTTTTTAAAG	TTTGTTGAAA	AGAATATTGT	60
CTTATTCTAT .						120
GAAAGCAGCA	CTTAGGGCTG	CCTGTTCTAT	ACCCTACAGT	CAGACAGGAA	AAGAACTGAA	180
AATGGCACCC	TTCTGACATT	CTGAGGCAGC	TGGACTGGCA	GCCAAGTAAA	GGAGAGTGAT	240
GAGGTGGTGT	GGGGAGGGTG	GGGAGGCAGC	GCGAGGGTGC	TCTCCACAGG	GTAGGTCTCG	300
AG						302

- (2) INFORMATION FOR SEQ ID NO:899:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 475 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

GCGGCCTTCA	TGGCCTAGTG	CTTGTCAGTT	TGGAAAGTCA	CAGGGAGTTT	ACCATTCTAT	60
AATTAGAGTA	GGAGGAAAAT	GAGAACCCAC	TGGTAGAAGA	AGAAGCAACA	GTCTTCTAGG	120
GTCTGGCATT	TGATGAGATA	GGTATTCAGT	TACTGTGCAT	TTCCATTGTT	TTTCCATGGC	180
AGAACATACG	GCAGAGATTT	GGGAACTCGC	ATGCCTGAAG	CCAGGTTATT	CTTATGTTCT	240
GTAACTATGT	TGCTCGCAGG	GCTGTTGTTG	TCAGAGTAGT	GAGTTGTGCC	CCAGACAAAT	300
GGGGTGCTGG	TCTGCTCCCA	CAAATCTTTA	TCCCAGTCTT	CATCGCAAGG	AGGGCACTGC	360
CAAGTGCTCT	CAGCCAGAGT	CTCTTGTCTA	AGGCTCCTGG	TTTGGTTGAC	AACATCTTGC	420
TCAATACAAC	TTCTGTCATC	ACAGCTTGAG	ATATGATGAC	TAATTTCAGC	TCGAG	475

- (2) INFORMATION FOR SEQ ID NO:900:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 507 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

GAATTCGGCC	TTCATGGCCT	ACAGCTGCCT	TTTTCTTTAA	AGGGGTTCTT	GTCTTCTGGA	60
			CGTTCTTCAA			120
			TTCACTTCTT			180
			TCGATGTGAA			240
			AGCCGCTGGA			300
GTCCCGAAAC	AACTGAAGGC	CTGGCCCGCC	GCCCACCCGC	GCAGGATGTG	ACTGCAGCCC	360
TGCTGCGGTC	CCCAGCTCCC	CGAGGGCTTG	GCTTTCTCCG	GGACGCTTGT	CACGCCAGCG	420
TGCCCCAGCT	TCCTAGGACC	TGAGAACTCT	GCCTTTTCTC	AAGTCCCTGC	AACCCAGGAG	480
GCCTGCCCGG	GTGCTAGTAG	GCCATGA				507

(2) INFORMATION FOR SEQ ID NO:901:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 495 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA .
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

GAATTCGGCC	TTCATGGCCT	AGTTTGGATT	TTCATATTAG	GGATACTCAA	CTGGTATTAT	60
TATTCTGGCC	CCTGCAAATT	TTTCAGTAGG	TCCCCTAGTA	TGTCATGCCA	GGGACTATGN	120
GAGTTCCTGG	GAATAGCACT	GTAANACATT	CTTGAGTGGG	TCCTTGACTC	CATTGAGTTT	180
ATAATCTCGT	AGGAGGAAGG	CTATGAAGAA	TTCTAATAAA	GCAAAGCAAG	CAATCACAAC	240
AAACCTTCCT	CTTTAACTTA	TCAAAAATGG	AAACTTTGAA	GAGCTGCTCT	TTAATAAATC	300
ATTGGAAAGC	ACCAGGACCC	AGGTGTTTTG	ACTCAGCCTC	ATTTCAGACT	GAGATCTGAG	360
GCCATGATAA	CTCATGTGCC	TATATATGCT	GATAATCACC	ATTACCTATA	CCATTCTTTA	420
CATTCTCTCA	TCTACACAAT	CATCTTCAAC	TCTCTCTCAT	CCACTTCAGC	GATTGAATTC	480
TTTACCGGCC	TCGAG					495

- (2) INFORMATION FOR SEQ ID NO:902:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 266 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

GAATTCGGCC	AAAGAGGCCT	AGAATTCCAG	ACCTAGCTCA	ACCCATGCCT	CCTTTCCTTC	60
CTTCCCTCCT	TCCTTTCTTT	CTTTTTCCTT	TTCTCCTTCC	CTCCCTTCTC	CCTTTCTTCC	120
TTCTCTCCCT	CTTTCTCTTT	CTCCCTTCTT	CCTGCTCTTC	CTTCCTTCCT	CCCTCCCTCC	180
$\tt CCTCCCTTCT$	TTCCTTTCCT	CCCTCCCTTC	CATTCTTTCC	TCCCCCACCC	CCCGTTTCTT	240
CTCTTTGGAG	AGATGTACAG	CTCGAG				266

- (2) INFORMATION FOR SEQ ID NO:903:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 410 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

GAATTCGGCC	AAAGAGGCCT	AAATGAGAGC	TGAGTGAAGT	GGATGCCCCT	TATAAAAACA	60
TCAGATCTCG	TGAGAACTTA	CTATCACTAG	AATAGCATGG	GGGAACCACC	CCATGATTCA	120
GTTACCTGCC	CCCAGGTCTC	TGCCACCACA	CATGGGGATT	ATGGGAACTA	CAACTCAAGA	180
TGAGATTTGG	GTGGGGACAC	AGGCAAATTA	TATCAGCTGT	TGTGCTCATT	AGTTTGTATA	240
TCATCCTTGG	CTCCTTTAGC	ACTATAAGGG	CAGGATTGAG	TCCTTGCAAC	AGAAACCATT	300
CAGCCTGCAA	AGCTGAACCT	ATTTACTTTC	TGACCCTTTA	TGGAAAAGTT	TACTGATCTC	360
TGGACTAGAC	AGTTTTTTAA	AAATGACATC	TTATGACCGG	GATTCTCGAG		410

(2) INFORMATION FOR SEQ ID NO:904:

(A) LENGTH: 326 base pairs

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:904: GAATTCGGCC AAAGAGGCCT AGCCGAGACT CTGTCTCAAA AAAAAGAAAA AAAGCTGCTT 60 TGGGTCTTAT GAGGGAGGG ACTGGGAATC TAGGTGTTTC AAGCGCCCCA GGCGATTCTT 120 AAGGTCACAC AAGCTTGGGA GACACTTCAT TAAGCAAAAT CTTTTGGCCG TTTTGTTCTG 180 GTTGAGCCTC AGTGTCTATT CATTGAGTGG TCACCAAGAG TTTGGGGTGG ACTGATCATC 240 AGCATTTACA GGTTTGGAAA TTGAATTTAG TTTTACTACT CAGAGCTTAT TAGACTTGAG 300 CAGATTTAAA CGGAAGGACA CTCGAG 326 (2) INFORMATION FOR SEQ ID NO: 905: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 410 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEO ID NO: 905: GAATTCGGCC AAAGAGGCCT AGGAACTGTT TTGACCCTGA AGGCTATTTA ATCCACTGTC CCCTACAAGG CCTCACAAGT GCTGGGGGAA AAAAAACAGC AATGAGGATG ATCCTGAGTT 120 AATGTGTATG CTCCGCAAGA GAGCTTGCCT ATACCTTGAT TATTTCATAA AATCACATGT 180 TAATACATTG CTTTCAGAAT GAAATACTGA CTTGATCTGA TAGGAGAAAA TGGTAATATT TCATAGTTGT TTTCCAAAGA CAAATTTAAA TGTTGTCTGT TATCTCCTTA CTTAGTTTAA 300 GAATTTAGTT TTGAACCCCA TTGACTTTGT CATTTGCAAT TTTAAAAATA TTTGGGACTG 360 GGCATGGTCG CTCACGCCTG TAATCCCAGC ACTTTGGGAG GCATCTCGAG 410 (2) INFORMATION FOR SEQ ID NO:906: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 498 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:906: GAATTCGGCC AAAGAGGCCT ACGCTTCCCG GGTTCAAGCG ATTCTCCTGC CTCAGCCTTT TGAGTGGCTG GGACTACAGG TGGATGCCTC CATGCCTGGC TAATTTTTTG TATTTTAGTG 120 GAGACAGGGT TTCACCGTGT TGCCCGGGCT GGTCTTGAAC TCGTGAGCTC GGGCAATCCA 180 CACTCCTTGG CCTCCCAAAG TGCTAGGATT ACAGGTGTGA GCCACTGCAC CCGGTCGAGG 240 TACAGTTTTG AAGTTCATGC AAATCTCATC ATTTGCTCTT CTGCAACAAA ACATTTTCTT 300 TCAACTTATT TTGCCTGTGT GAAGCTCAGT GCTTTAACTC ATATATGGAG TTATCTTCTT CCCTCAGACT GGAGACGTTG GTGAAATTGG GGCTAGACTG AAGATGTCTA AGGTGGCTTG 420 ATTGACAAAG GTCTCTCCTC ATCCCCAAAA TAAATAACAT TTTTTCATTT ATAATAGTAA 480 TACACCAGTC GACTCGAG 498

- (2) INFORMATION FOR SEQ ID NO: 907:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

GAATTCGGCC	AAAGAGGCCT	AAACTGGTGC	TGGTTTCACA	TCACGACAGC	AACGGGATTC	60
TTTTGCTTTG	AAAATGTTGC	AGTCCACCTG	TCCAACTTGA	TCTTCCGGAC	ATTTGACTTG	120
${\tt TTTCTGGTTA}$	TCCACCATCT	CTTTGCCTTT	CTTGGGTTTC	TTGGCTGCTT	GGTCAATCTC	180
CAAGCTGGCC	ACTATCTAGC	TATGACCACG	TTGCTCCTGG	AGATGAGCAC	GCCCTTTACC	240
TGCGTTTCCT	GGATGCTCTT	AAAGGCGGGC	TGGTCCGAGT	CICTGTTTTG	GAAGCTCAAC	300
CAGTGGCTGA	TGATTCACAT	GTTTCACTGC	CGCATGGTTC	TAACCTACCA	CATGTGGTGG	360
GTGTGTTTCT	GGCACTGGGA	CGGCCTGGTC	AGCAGCCTGT	ATCTGCCTCA	TTTGACACTG	420
TTCCTTGTCG	GACTGGCTCT	GCTTACGCTA	ATCATTAATC	CATATTGGAC	CCAGACTCGA	480
G						481

- (2) INFORMATION FOR SEQ ID NO:908:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 764 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

GAATTCGGCC	AAAGAGGCCT	AGAAACAATG	GTTTTCAGAC	ACTGAAAGTT	CATAGTACAG	60
GACTGTGATC	TCTGCGAGAA	GGGGGAATAA	TGAGGTGAGT	CCAGTGATTG	CTCAGGCGAA	120
TGGCCTGGAG	GCAGTTTCTA	GGCAGCAAAG	CAGGGAGAGG	GAAGCCAGAG	ACCAGTGGTC	180
CTGCTGTGTT	GAGGAGATGG	AGATCAGTGT	CACCGGAGGC	CAAGGTGAGT	AAGTGAGAGG	240
AGAGGAGGCA	GCAGCACACA	GACAGAGAGT	GCTGTAGATC	TGCAGTGGGT	CCCCTGGAGT	300
CCTTGGTTGA	GTGAAGGTGT	TAGAAGAAAC	TACTTAAGCC	AAGAAATGAG	TAACTGGAAA	360
TTAGTAGAGC	AAATAATTTA	CAGATCATCT	ATGGGGCTGG	GAAAAGTTTG	TGTTTCCACT	420
AGCCAGAGTA	GAAATAACTC	ATAATGCATG	GGTCATCAGG	TGGAGTCCTC	CAACAGGTGT	480
TGCCTTAGTA	CTGAGGTCAA	ATTGTCCCTA	GACCAAAGGC	TTCTTTGGAC	TTCCCCTAAC	540
AAAGCTTAAA	GACAAGCCTT	GGAAGGATCA	AACTAATTTC	AAGAAACTTA	ACTGTGAATC	600
AGAATAAAAC	CCAATACCAT	TTATAGGAAT	ATAACAAAAT	CCATCAACAN	ACNACATAAC	660
ACTCATAATT	ACCAACATTC	AGTAAAAAAT	TACTGGAAAC	AGAGAAATAT	AAATTATGGC	720
CCATAATTAG	GAAAAAAGGG	TAATCATTAG	AGGTAGAACT	CGAG		764

- (2) INFORMATION FOR SEQ ID NO:909:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 157 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

GAATTCGGCC	AAAGAGGCCT	ACTAAGGACT	TGTTTCGGAA	GGAGCTGACT	GGCCAATCAC	60
AATTGCGAAG	ATGAAGGCTC	TGTGGGCCGT	GCTGTTGGTC	ACATTGCTGA	CAGGATGCCT	120
AGCCGAGGGA	GAGCCGGAGG	TGACAGATCA	GCTCGAG			157

- (2) INFORMATION FOR SEQ ID NO:910:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 487 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

GAATTCGCGG CCGCGTCGAC AGAATAGACC TGGTTTGTGA ATTATGGCCT GGATTTCACT	60
TATACTCTCT CTCCTGGCTC TCAGCTCAGG GGCCATTTCC CAGGCTGTTG TGACTCAGGA	120
ATCTGCACTC ACCACATCAC CTGGTGAAAC AGTCACACTC ACTTGTCGCT CAAGTACTGG	180
GGCTGTTACA ACTAGTAACT ATGCCAACTG GGTCCAAGAA AAACCAGATC ATTTATTCAC	240
TGGTCTAATA GGTGGTACCA ACAACCGAGC TCCAGGTGTT CCTGCCAGAT TCTCAGGCTC	300
CCTGATTGGA GACAAGGCTG CCCTCACCAT CACAGGGGCA CAGACTGAGG ATGAGGCAAT	360
ATATTTCTGT GCTCTATGGT ACAGCAACCA TTGGGTGTTC GGTGGAGGAA CCAAACTGAC	420
TGTCCTAGGC CAGCCCAAGT CTTCGCCATC AGTCACCCTG TTTCCACCTT CCTCTGAAGA	480
GCTCGAG	487

- (2) INFORMATION FOR SEQ ID NO:911:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 478 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

GAATTCGCGG	CCGCGTCGAC	AGTTACTGAG	CACACAGGAC	CTCACAATGG	GATGGAGCTA	60
TATCATCCTC	TTTTTGGTAG	CAACAGCTAC	AGGTGTCCAC	TCCCAGGTCC	AACTGCAGCA	120
GCCTGGGGCT	GAGCTGGTAA	AGCCTGGGGC	TTCAGTGAAG	TTGTCCTGCA	AGGCTTCTGG	180
CTACACTTTC	ACCAGCTACT	GGATGCACTG	GGTGAAGCAG	AGGCCTGGAC	AAGGCCTTGA	240
GTGGATTGGA	ATGATTCATC	CTAATAGTGG	TAGTACTAAC	TACAATGAGA	AGTTCAAGAG	300
CAAGGCCACA	CTGACTGTAG	ACAAATCCTC	CAGCACAGCC	TACATGCAAC	TCAGCAGCCT	360
GACATCTGAG	GACTCTGCGG	TCTATTACTG	TGCAAGGGAC	AGCTCAGGCT	ACGACTATGC	420
TATGGACTAC	TGGGGTCAAG	GAACCTCAGT	CACCGTCTCC	TCAGCCAAAA	CGCTCGAG	478

- (2) INFORMATION FOR SEQ ID NO:912:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 433 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

CGCCCTGACC AGGCACCTAT ATTTGATGGT TCCTGAGTTT AGTAAAACAC	CCGCGTCGAC CCAGGATGCC GCGCAGCAGA GCTCTGATTC TGGGGGTCCT ACCATGCTCA GCCTCTGTGG AGGTGAAGAC GACATTGAGG CCGACCACGT GGTATAAGTG TATATCAGTC TCCTGGAGAC ATTGGCCAGT ACACATTTGA GATGAGTTGT TCTATGTGGA CTTGGATAAG AAGGAGACTG TCTGGATGCT GGCCAATTGG CAAGCTTTGA CCCCCAAGGT GGACTGCAAA ACATAGCTGT AACTTGGGAG TCTTGACTAA GAGGTCAAAT TCCACCCCAG CTACCAATGA GCGACTGTGT TCCCCAAGTC CCCTGTGCTG CTGGGTCAGC CCAACACCCT GAG	60 120 180 240 300 360 420 433
(2) INFORMA	ATION FOR SEQ ID NO:913:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 139 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:913:	
	CCGCGTCGAC GCAAGATGGA TTCACAGGCC CAGGTTCTTA TATTGCTGCT TCTGGTACCT GTGGGGACAT TGTGATGTCA CAGTCTCCAT CCTCCCTGGC GGAGAGAAG	60 120 139
(2) INFORMA	ATION FOR SEQ ID NO:914:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 166 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:914:	
TCCTTCTTGC	CCGCGTCGAC ATCATGGCTA CCCTGCGTGT CCCACTCCTG GTGGCTCTCG TGTGGCAATT CAGACCTCTG ATGCAGGTCC CTATGGTGCC AATGTGGAAG CTGCCAGGAC TACATCCGTC ACCCTCTGCC ATCACG	60 120 166
(2) INFORMA	ATION FOR SEQ ID NO:915:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 590 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii.)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:915:	
CTATGTTCCC GGGGGACCTT CACTGCTGCT GTGGCAATGG	CCGCGTCGAC TTCTTGGGCA GCACAGAAGA CAGAGCCGAT TTTGACCAAG TGTGATGGAG ACCTTCGAAA TCAATGATCC AGTGCCCAAG AAGAGAAATG CTGCATGGCA GTCATGGCCA TCCACCTGAT CCTGCTCACG GCAGGTACTG GATTCAAGTT CTCAATCTGC AGGAGCAGCT CCAGATGCTA GAGATGTGCT ATCACTAGCT ATCGAGGACA AGCCCTTCTT CTCGCTGCAG TGGGCACCCA GGTACCTAGA GCACAGGGGC TGCAAGCCTT GCAGGCCCAG CTCAGCTGGG	60 120 180 240 300 360

TCCATACCAG CCAGGAGCAA CTCCGTCAGC AGTTCAACAA CCTCACTCAA AATCCAGAGT TGTTCCAGAT TAAAGGTGAA CGAGGCTCCTC CAGGTCCAAA AGGGGCCCCG GGTGCTCCTG GAATCCCCGG GCTGCCTGGG CCAGCTGCTG AGAAGGGAGA AAAGGGGGCT GCAGGTCGTG ATGGAACCCC AGGTGTCCAA GGACCCCAGG GCCCACCAGG AAAACTCGAG	420 480 540 590
(2) INFORMATION FOR SEQ ID NO:916:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 592 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:	
GAATTCGCGG CCGCGTCGAC GGAAGAGCAA TGAAAACATA TGCTCCTACA TTATTCATGT TTCTATGGCT GCAGCTGGAT GGGATGAGCC AAGGTGAGCA GGTGGAGCAG CTTCCTTCCA TCCTGAGAGT CCAGGAGGA TCCNGTGCCA GCATCAACTG CACTTATGAG AACAGTGCCT CCAACTACTT CCCTTGGTAT AAGCAAGAAC CTGGAGAGAA TCCTAAGCTC ATCATTGACA TTCGTTCAAA TATGGAAAGA AAGCAGACCC AAGGACTCAT CGTTTTACTG GATAAGAAAG CCAAACGTTC TCCCTGCACA TCACAGACAC CCAGCCTGGA GACTCAGCCA TGTACTTCTG TGCTGCAAGT GAGAGCACCA ATACAGGCAA ATTAACCTTT GGGGATGGGA CCGTGCTCAC AGTGAAGCCA AACATCCAGA ACCCAGAACC TGCTGTTACC CAGTTAAAAG ATCCTCGGTC TCAGGACAGC ACCCTCTGCC TGTTCACCGA CTTTGACTCC CAAATCAATG TGCCGAAAAC CATGGAATCT GGAACGTTCA TCACTGACAA AACTGTGCTG GACAATCTCG AG  (2) INFORMATION FOR SEQ ID NO:917:	60 120 180 240 300 360 420 480 540
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 166 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:	
GAATTCGCGG CCGCGTCGAC GAATGAGGTG CTCTCTTCAG TTCCTGGGGG TGCTTATGTT CTGGATCTCT GGAGTCAGTG GGGATATTGT GATAACCCAG GATGAACTCT CCAATCCTGT CACTTCTGGA GAATCAGTTT CCATCTCCTG CAGGTCTAGT AAGAGC	60 120 166
(2) INFORMATION FOR SEQ ID NO:918:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 200 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:	
GAATTCGCGG CCGCGTCGAC GTCTGAGAGG AACCCTTCTC TGAGGATGGA CACTTCTCAC ACTACAAAGT CCTGTTTGCT GATTCTTCTT GTGGCCCTAC TGTGTGCAGA AAGAGCTCAG GGACTGGAGT GTTACCAGTG CTATGGAGTC CCATTTGAGA CTTCTTGCCC ATCAATTACC	60 120 180

200

TGCCCCTACC CTATAGTGAG

(2) INFORMATION FOR SEQ ID NO:919:

<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 231 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:	
GAATTCGCGG CCGCGTCGAC CCAACCTTCC GGAAGCCTCC CCATCAGCAC CATGAACCCA AGTGCTGCCG TCATTTTCTG CCTCATCCTG CTGGGTCTGA GTGGGACTCA AGGGATCCCT CTCGCAAGGA CGGTCCGCTG CAACTGCATC CATATCGATG ACGGGCCAGT GAGAATGAGG GCCATAGGGA AGCTTGAAAT CATCCCTGCG AGCCTATCCT GCCCACGTGT T	60 120 180 231
(2) INFORMATION FOR SEQ ID NO: 920:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 115 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:	
GAATTCGCGG CCGCGTCGAC GTTTTGTTAT TGTTACGAAG TAAATGATTC GTATGCTGTA CATAGCTGTT ATAGAAGTGG CGATTAGTGT AATTAGTAGG GCTCAGGCTC TCGAG	60 115
(2) INFORMATION FOR SEQ ID NO:921:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 213 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:	
GTTGAATTCT AGAAATCAAA ATTAATTTGA CAAAGGAAAA GCAGATGCCG GAAACTTCTT CCCAGTCTGT CATACAATTC ACCACTGGCC AGGTGCTGAG AGAAGCATTA GGGAACAGTG TGGGTTGTGT CAGAGTTGGA CGGCTCCATC CCTTTGGCTT CATTATCTTC CTCCTCATGG AGATTCTAAA GCAACCCGTC GACGCGGCCG CGA	60 120 180 213
(2) INFORMATION FOR SEQ ID NO:922:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 504 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
308	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

CCATTCAAAT GTTGCTTTCA ACCCACTGGT ACGCTCTCAG GTGGCCCAGG TTCTTTAGAT	AAGAGGCCTA TCCACATGCT TCGGCTCCAT ACCAGGTGCG GGACATGTCT TGGACCAGAC ACACGGGCAC	GCATTCAGGG AATGACCGTG GTGCCTGTTC GCTTATTGCC CGGCTCCAAG AACGCCCTCA	CTGGTCCACG TGGCTGTCCA CAGTCACCAC AACAAAAGAC TCCAGTAACC CCCCCACCCG	GCCTGGCTTT CAGCCCCGAC TGTTCGCCAA AGAGCTACGA TCCTGGATCT GCTCCCACTA	CTGGTTTGAC AGAGCCCCTG GGCAGGGGAC CATCAGTATT GAAAAACCCC CACATCTCCC	60 120 180 240 300 360 420
TTCTTTAGAT TCGGAAAACA		AACGCCCTCA GGGCAGCACC	CCCCCACCCG	GCTCCCACTA	CACATCTCCC	

- (2) INFORMATION FOR SEQ ID NO:923:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 119 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

GAATTCGGCC AAAGAGGCCT ACATTCATCA AGTCATCCAA CTTCTATAGT CAAAGCAGGA 60 TCATGTGGCG AAGCATATGC TCCACAAGGG TGGATAGCTT TTTTCATGGA ATTCTCGAG 119

- (2) INFORMATION FOR SEQ ID NO:924:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 706 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

	AAAGAGGCCT					60
GTTGGAGGAC	ATAATTCATG	GATCATAGCT	CCAGAAGTGA	AAAGGGAGGA	AATGTAGACA	120
	TTAGCCATTG					180
GAAGATAGCT	GGGGGAGTAT	AGACAAGTTG	TAAGAATGAA	GGAAGGAAGG	CAAGAGCAGA	240
CTTGTCGGAT	GAATTTTATT	TTCTCTATGA	AGTTTGAGAA	TTAAACTTTA	TGCTGAGAAG	300
GAGGGCAGGA	GAGACTGTAT	ATGGAATGTA	AGGTTTGGGA	TAACCAATGT	AAGTTTTGGG	360
AATGAGAAAG	CCACCTAGGG	ATGAGGAAAA	AATATTTAAA	ATTTTGTATC	CACTGAAAAT	420
	TGTAAAATGA					480
TGGATTTATT	TTGTTATTTT	TCTCTATATT	TGTAGTATTT	TACAGTAAGC	ATGTATTACC	540
TTTATAGTGA	AAAAGTGTCA	TTTTTTTACA	TTGGTCAATT	TTTTGTTATT	AAATTTCATG	600
CTTGTTTTTA	ATTGTTTCTT	GTGTGTATGA	TTGCAATATC	AGGTATTTGA	TGTGGTGATG	660
TGTGTGATTC	AGAAGTCAGA	AGACTTAAGT	TCCGACACCC	CTCGAG		706

- (2) INFORMATION FOR SEQ ID NO:925:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 651 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

GAATTCGGCC	AAAGAGGCCT	AGGATTCAAA	TTATTCTGAC	AGACCTGTGT	GGCAGTTCAG	60
GCTGATAGCT	GGAGTTTCTT	GTCTTTTTCT	ACATGGCCTT	TCATCTTCCA	AGAGTTAGAC	120
TATGATTCTT	CACATCATGA	TGGCTTAGGG	TCCCAAAAAG	AAAAGAGTAG	AACTTGCAAT	180
ACCTCTTAAG	CCCTATGCCC	AAGAACTCAT	ACAGTGATAC	TTCTGCCACC	TTGTGTTAGT	240
CAAAGCAAGT	CACAAGGCCA	GCCAGATTCA	AAAGAATGGA	AAAATAGACT	CAATTTCCTG	300
GTGAGAAGTA	GCAAGGTCAC	ATTGCAAAGG	AGTCTGGACA	TGGGAAGGAG	TTACTCATTT	360
GTGGCCTTTA	TAATAATCTT	CCACAAATGC	CTGTAATTTG	GGCACTGTGC	TTAGTACTGG	420
TGATAGAAGA	TAAGTAGCTT	ATTTCAGTAT	CTTAATTTTG	TTTTATATAT	TTGATAATTT	480
TATGATGCAG	GTTCACTGTG	CACTGGTATC	AATCCCAGGG	GAGGACTGTA	AACACCTTGC	540
CAATACTGTG	TACCAGTA: C	AATCCACTGG	CATGAGTCTG	GTGAGACAGA	ACACACAATA	600
AGTTTAGGGA	AGCAACTTTA	TTACTCACAG	ACAGGCAGCA	AGGGACTCGA	G	651

- (2) INFORMATION FOR SEQ ID NO:926:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 700 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

GAATTCGGCC	AAAGAGGCCT	AAAAAGATGA	AAGGACCAAT	CAAAGATTTA	ATTAAAGCTA	60
AAGGGAAAGA	TTTAGAGACA	GAGAATGAAG	AAAGAAATTC	TAAGTTGGTG	GTGGACAAAC	120
CAGAACAGAC	AGTGAAGACC	TTTCCACTGC	CAGCTGTTGG	TTTGGAAAGA	GCAGCTACTA	180
CAAAGGCAGA	TAAAGACATC	AAGAATCCAA	TCCAACCATC	CTTCAAAATG	ATAAAAATT	240
CTAAACCAAT	GACTACTTTC	CAAGAAGAAA	CCAAGGCTCA	GTTTTACGCA	TCAGAGAAAA	300
CCCTCCTAAA	AGAGAACTTG	CCAAAGATTT	GCCTAAATCA	GGAGAAAGTC	GATGTAATCC	360
TTCAGAAGCT	GGAGCGTCTT	TACTGGTTGG	CTCAATAGAA	CCTTCTTTGT	CAAATCAAGA	420
TAGAAAATAT	TCCTCAATTC	TACCTAATGA	TGTACAAACT	ACCTCTGGTG	ATCTCAAATT	480
GGACAAAATT	GATCCCCAAA	GACAGGAAAT	TCTAGTAAAA	TTACTAGATG	TGCCTACTGG	540
TGATTGTCAT	ATTTCTCCAA	AGAATGTCAG	TGATGGGGTT	AAAAGGGTAA	GAACATTATT	600
AAGCAATGAG	AGAGATTCCA	AAGGCAGGGA	TCACCTCTCA	GGAGTCCCTA	CTGATGTTAC	660
AGTTACTGAG	ACTCCAGAAA	AGAACACAGA	ATCCCTCGAG			700

- (2) INFORMATION FOR SEQ ID NO:927:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 378 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

GAATTCGGCC AAAGAGGCCT	AGGGGTGGTG	GAGGCGTGGA	CCCAACGGTG	ACCGTCGGGA	60
TGGAGCAAGG GCAAGGAGAG	GCTCTGGCCC	AGACACAGCT	TGGAAAAGCT	CATCTCCCTC	120
TGGGGTTTAA AAACTCAAAG	CAAACGGAGC	AAGCCTGGCG	GCCCTGGGGA	TGGGGGCAGGG	180

CCTCTACCTC ACTGTGATCT TCGACCTGGC GACACAGGAC AGCCACACAG AAGCACGCCA ACACACTTAA AGCTTTGCTC CAACTAAATC ATTTAGTTTC CCTTGAAGAA ATAACTGAAA AAAAAAACAA CTGCTGACAT CTATGTCTGT AGCTCGATTT TACAGTCTGC TCTTTGTGAG AAAGGAAAAT CACTCGAG	240 300 360 378
(2) INFORMATION FOR SEQ ID NO:928:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 426 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:	
GAATTCGGCC AAAGAGGCCT AATATTCAC ATTTCTCTTT TCTAAAAGTG TAAATTTTC ACTTTAAAAAT GAAGCAAGAA TTAAATAAAT AGAACAAATA CCATATATCA TCACAGAGTC AATATATTAT GGTCCTGTC TGACCAAGTG TTGCATTCTA TTTTGTGTTAC CAGAACTGCA GGGCTTTCTA TGGCTACATG GTCAGTGCAT GCTCAGACAG CTGTTAAAAAT CAAAACCTTC ACTGTGCTGG GTCACCTGGT AACTACTGTC TATCTCACAA GTGCATTCTG CTGACATTCA AGGGTTAAAAC TGGTTTCTAG TAAATACTGT GCTTTAAAGT AGTACATACT GTGAGCTGTG TTATTAGAAA CCTGCTTGTC CTTGTGTCTG AAAATAAGGA GGAACACTCT CGCACCAAAT CTCGAG	60 120 180 240 300 360 420 426
(2) INFORMATION FOR SEQ ID NO:929:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:	
GAATTCGGCC AAAGAGGCCT AGGTAAATGT TAGTGGAAAA TTTTATGAGT ATATGCTGAA AGGAGAGATT AGTTCACATG AACTCAATAA TGTTCAAGAT AATGAAATGC TTAGAAAAGGT TACTTTTGAT CCAGAAGTAT TTTTCAACAT ATTACTTCCT CCTATCATAT TTTATGCAGG TTATAGCCTG AAAAGGAGAC ATTTTTTCG AAATCTTGGG TCTATCCTAG CATACGCTTT TCTTGGAACA GCAATTCTT GTTTCGTTAT TGGGTCAATA ATGTATGGCT GTGTAACGCT GATGAAGGTA ACGGGACAAC TCGAG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:930:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 406 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:	
GAATTCGGCC AAAGAGGCCT ATGGACACCC TGTGCCCCAA GCCGATGGCC CCACCCAGCA GCATCAGCAC AGNTGCCCCC CTTCTCCGCA GAGCAGGCTC TCCTTTACGG GACTCTCCTC	60 120

TTCCCTCCCA CCTGATGCGC ATCAGCAGCC ACGGGCCTGG CCCTTGAATC TTGTCTAACT GCACTCGCTG CCTGGTGGCC TCATCCCACC CCAAGACCAC TGCACTGATG GCTCCAACCC CAACTTCTCC CTGCACTCAG CTTATGAATA CGACGGCCCT CATTGCATCC ATGCAGAGAC CTCAGAGGCA GCTCAGCTCA	180 240 300 360 406
(2) INFORMATION FOR SEQ ID NO:931:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 246 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:	
GAATTCGGCC TCATGGCCTA CCAGACTGTA AACATTCCAG GTCCTGAAAA AGTGTTGGAC CAGTCTCCTA CTGTTATGTT CTCCAGTTTT AAAAATGTAA AATCAGTTGA AACACTCGAT CAGAAGGCAG ATGAAGTCCT TGACTGCAGA AGTAACCAAA ACAGACCAGA TGAATGCAAA AGTGAAGGTC AGTCAGCCAA GGAGATGCTA AGTAGTGACC AGAGAGAGAC TGTCACCGGA CTCGAG	60 120 180 240 246
(2) INFORMATION FOR SEQ ID NO:932:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 278 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	,
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:	
GAATTCGGCC TTCATGGCCT ACTCCATTGT CACGCCAATT TCCCCTAGTC CAAGTTTTT CTTTGCTGAT TCCTTTGTCC ATGTGTCTT TGAGCCTCTC TCATCTTGTC TTTCCTCCTT TCCTAGGAGC AGCTCCTGAA GCAGCAGCAG CAGCACCAGT GGCAGCAGCA TCAACAGGGC TCTGCCCCTC CTACCCCAGT GCCCCCATCA CCACCACAGC CTGTGACCCT GGGGGCTGTG CCAGCTCCAC AGGCTCCACC CCCGCCCCAC AACTCGAG	60 120 180 240 278
(2) INFORMATION FOR SEQ ID NO:933:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 421 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:	
GAATTCGGCC TTCATGGCCT ACGAGTGCGA CCAGCCAGAT GAGCGCCCGG TCCTGGTGAA GAGCATTCAC TACCTCTACT TCTCCATGAT CCTGTCACG GTCACCCTCA TCACTGTCTC CACCGTGAGC TGGTTCACAG AGCCACCCTC CAAGGAGATG GTCAGCCACC TGACCTGGTT TACTCGTCAC GACCCCGTGG TCCAGAAGGA ACAAGCACCA CCAGCAGCTC CCTTGTCTCT TACCCTCTCT CAGAACGGA TGCCAGAGGC CAGCAGCAGC AGCAGCGTC AGTTCGAGAT	60 120 180 240 300

GGTTCAAGAA AACACGTCTA AAACCCACAG CTGTGACATG ACCCCAAAGC AGTCCAAAGT GGTGAAGGCC ATCCTGTGGC TCTGTGGAAT ACAGGAGAAG GGCAAGGAAG AGCTCCCGGC C	360 420 421
(2) INFORMATION FOR SEQ ID NO:934:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 449 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:	
GAATTCGGCC AAAGAGGCCT AAAATAGCAA AGATGGAACA TGGACCTAAA GCAGTGACTA TTGCAAATTC TCCATCAAAG CCTTCAGAAA AGGATTCTGT AGTTTCCCTT GAGTCCCAGA AGACACCTGC TGACCCAAAA CTGAAAACTC TAAGTCAAAC CAAAAAAAAC AAAGGATCTG ATAGCTCACT CTCTGGTAAC AGTGATGGCG GAGAAGAAT TTGTGAAGAG GAGAGGAAT ATTTTGATGA TAGCACAGAA GAAAGGTTTT ACAAGCAGTC TTCCATGTCT GAAGATAGTG ATAGCGGTGA CGACTTCTTC ATTGGGAAAG TCAGACGGAC ACGAAAGAAG GAAAGTAGTT GTCATTCTTC AGTTAAGGAA CAAAAACCAC TAGAAAAAAGT GTTTCTTAAA GAAGATACAG GTGAAACTCA TGGGGATACA ACTCTCGAG  (2) INFORMATION FOR SEO ID NO:935:	60 120 180 240 300 360 420 449
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 421 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:	
GAATTCGGCC AAAGAGGCCT AAAAATAGTG ATTTTTTGAC TATCTATAGA TATTAGTTGG CATTCTACTG TAAGGAAAAC TTTCTTTTCT CCTGTACTTA TCATCGTCC CCCAGGAATC AGTCATTTTT CCAAGGAGAC CTAGTTCCTT TTTGTGAGGA GTTGTTTTGA GTTCATTTTT TATTTATTCT GAAGTTTTGA GTTCATTTTA CTATAATCTG CCTAGGTGTG ATTTTCTTTT TATTTATTCT GCTTAGGATT TGCAGAGATT TTTTTGAACC TGTGGCTTGA TGTCCATCAC TTTTGGAAAT TTCTCAGCCA GCATAGTATC TGCAGACTGT GTGTCTGTC CATTTCTCT CTTTTTCTCCT TGTAGGACTT CATTCACAAG GATGTTAGAA CTTTTTACCA TGGCTCTCGA G	60 120 180 240 300 360 420 421
(2) INFORMATION FOR SEQ ID NO:936:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 648 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

60

ATAGAAATGT	CATAATTTCT	CCTTTATTCT	TGAATGATAG	TTTTGTGGGA	TATAGACTTG	120
CTGGATATAG	AATTACTGGA	TATAGAATTG	CCAGATATAA	AATTCTTGGT	TCAAAGTTTT	180
TTTTCTTTGA	GGACTTTGAA	TGTCATCCCA	CTGTCTTCTG	GCCTCCATAG	TTTCTCATAA	240
TAAATCAGCT	GTTAATCTTC	ATTAAGTTTC	CTCTGTACAC	GAAGAGTCAC	TTGTCTCTTG	300
CTGCTTTCAA	ATTTTTCTCA	TTTGCTTTGG	GTTTTCACAC	TTTAATTATA	TGCCTTTCTA	360
TGTGGATCTC	TTTGAGTTTA	TCCTGCTTGG	AGTTCATTGA	GCTTTTTGCA	TCTGTATATT	420
AATTTCTTTC	ATCAGATTTG	GAGATGTTTT	TGGCATTTAT	TTCCTCAAAG	TTCTTTCTGC	480
TTCTTTCTCT	CCTTCTCCTT	CTGGGTCACC	ACAATGCATA	TGTTGGTCTA	CTTGATGATG	540
TCTCACAGGT	TCCTTAGACT	CTGTTTACTT	TTCTTCATAT	TTTTTTTTTT	CTGTTTCTTA	600
AATTTGGATA	ATTTTGGTTG	TCTTATATTC	AAGTTTGCTG	ATCTCGAG		648

- (2) INFORMATION FOR SEQ ID NO:937:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 160 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

GAATTCGGCC AAAGAGGCCT	AGAGGATGGG	AAGCTTGGGG	AGAGAAGATA	CTGAAATGCT	60
AGAAACTGAG CCAGTAGAGG	ATGGGAAGCT	TGGGGAGAGA	GGACATGAGG	AAGGATTTCT	120
GAACAACAGT GGGGAGTTCC	TCTTTAACAA	GCAGCTCGAG			160

- (2) INFORMATION FOR SEQ ID NO:938:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 399 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

GAATTCGGCC AAAGAGGCCT	AGAAAAACTC	AGGAAAGAAA	TTGCAGACTT	CGAACAACAG	60
AAAGCAAAAG AATTAGCTCG	AATAGAAGAG	TTTAAAAAGG	AGGAGATGAG	GAAGCTACAA	120
AAGGAACGTA AAGTTTTTGA	AAAGTATACT	ACAGCTGCAA	GAACTTTTCC	AGATAAAAAG	180
GAACGTGAAG AAATACAGAC	TTTAAAACAG	CAAATAGCAG	ATTTACGGGA	AGATTTGAAA	240
AGAAAGGAGA CCAAATGGTC	AAGTACACAC	AGCCGTCTCA	GAAGCCAGAT	ACAAATGTTA	300
GTCAGAGAGA ACACAGACCT	CCGGGAAGAA	ATAAAAGTGA	TGGAAAGATT	CCGACTGGAT	360
GCCTGGAAGA GAGCAGAAGC	CATAGAGAGC	AGCCTCGAG			399

- (2) INFORMATION FOR SEQ ID NO:939:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 519 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

GA.	ATTCGGGC	AAAGAGGCTA	GAAGCATCGA	AAGCGTTGGA	GAGGTGTTAC	CGGTAACGGC	60
GG	CGAGAAGG	GTGTTCCCGA	ACTAGAGTGG	GGCATACATA	ATCTTGCTGC	TATGCTTCGA	120
AG	CTGTAGTC	TGAATCAACC	TAAGTTTTAA	ACAGAAGGTG	AACCTCTGAG	ATAGAAAATC	180
AA	GTATATTT	TAAAAGAAGG	GATGTGGGAT	CAAGGAGGAC	AGCCTTGGCA	GCAGTGGCCC	240
TT	GAACCAGC	AACAATGGAT	GCAGTCATTC	CAGCACCAAC	AGGATCCAAG	CCAGATTGAT	300
TG	GCTGCAT	TGGCCCAAGC	TTGGATTGCC	CAAAGAGAAG	CTTCAGGACA	GCAAAGCATG	360
GT	AGAACAAC	CACCAGGAAT	GATGCCAAAT	GGACAAGATA	TGTCTACAAT	GGAATCTGGT	420
CC	AAACAATC	ATGGGAATTT	CCAAGGGGAT	TCAAACTTCA	ACAGAATGTG	GCAACCAGAA	480
TG	GGGAATGC	ATCAGCAACC	CCCACACCCC	CCCCTCGAG			519

- (2) INFORMATION FOR SEQ ID NO:940:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 268 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

GAATTCGGCC	AAAGAGGCCT	AAGAAATTAT	ACCATTTTAT	GGAATGTCAA	GCTACATCAC	60
CCGAGAAGAC	CAGTACAGCA	AGCCTCCGCA	CAAAAAACTG	AAAGACCGCC	AGATCGATCG	120
CCAGAACCGC	CTCAACAGCC	CTCCTTCTTC	TATCTACAAA	AGCAGCTGCA	CAACAGTATA	180
CAATGGCTAT	GGGAAGGGCC	ATAGTGGTGG	AAGTGGCGGA	GGCGGCAGCG	GTAGTGGTCC	240
CGGAATTAAG	AAAACAGAAG	CGCTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:941:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 535 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

GAATTCGGCC	AAAGAGGCCT	AAGCCTCGCC	TTACACTTAA	GTGCACCCGA	TCCTGCCTCT	60
GGCATCTCAC	AAACGTCACT	CCCTGGAACA	AATTTGTGAA	GGCCTCCAGA	CCACAGTGTC	120
CTCATCTGTA	AAATGGGGGT	AGTAGTAATC	CTTGCCTCAT	AAAGTTCTTG	GCAAGGATTA	180
GATGAGCGAG	CATGTGAGTT	TGGCCTCCGT	TTAAACACTC	CATAAAGTTT	CCTTTTAGGA	240
TAACAGCAGG	CCGTTTTAGA	ACCTTCCAGA	GGTTACTTAT	TCAGATATCC	TTAGGTGACG	300
ATTGGGAAGC	TGCCGTTTCT	TGAGAGCCTC	CTGGGTGACA	GATGGAGAGT	GGCCCTGGCG	360
TGACCCTTGA	CCCTATCCTT	GAGGCTTTCC	TGCCCGTCTC	CTGCCTCGAA	TGTGCTCCGC	420
AGCACATGGA	TCAGGATGGG	GAAGGGGCTG	TGTCACTGGA	TACCTTCGGC	CCCTGCCCAC	480
GTCTAGGGCC	TGTGAAAACG	AGGAGGGACA	GCAAAGAAAT	GGGGAAAGGC	TCGAG	535

- (2) INFORMATION FOR SEQ ID NO:942:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

GAATTCGGCC	AAAGAGGCCT	AAAATTGTTA	ATTCTAGTCA	CCCTGCAGTG	CTATAGAACA	60
CTGGAACTTA	TTCCTCCTAT	ATCACCGTAT	TTTTGTATCT	ATTAACAAAC	CTCTCCATAT	120
CCTCCCTCCC	TCCTACCCTT	CCCAACCTTT	GGTAATCACT	ATTCTCCTCT	CTACTTCTAT	180
${\tt GAGATCAATG}$	TCTTTATTTA	CTCGAAGTAC	TCTTAAAAGT	TTAGGACTTA	AGTATTTGAA	240
GAAATTCACT	TGCTTTTTGT	TTTTATTCTA	CTCAATACTT	TTTAATATAA	AGATTTACAG	300
TCCCCCCTTA	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:943:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 363 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

GAATTCGGCC	AAAGAGGCCT	ACAAACTCAA	GATGCCCGAG	TGGATTGGAG	GCGAGAGCGA	60
GCTCAGGAAG	TTTCTAAAAC	ATCATTTGCG	AGGAAAGAAC	TGTGAACTCC	TGCTGGTGGT	120
ACCAGAAGAG	GTAGAGGCTC	ATCAGAGTTG	GAGGACCGAT	GTGTAACAGT	TCTGCCCAAC	180
CTCCCTCTCG	CCTCAGCCCC	TTCAGTCCTC	TGTGACGTGC	TGTGGCCTCT	ACAGTGGGTC	240
TGCCCTTGCC	ACTTCCCCAA	ACATCTCATC	AAGTTTTTCC	CCTTCAGATC	TGACAGTGCA	300
ATAGGACAGA	CGTGTGGACT	GTTATAAGAA	CTACTCAGTG	TTTTGTTCCT	GGGCAAACTC	360
GAG						363

- (2) INFORMATION FOR SEQ ID NO:944:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 324 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

GAATTCGGCC	AAAGAGGCCT	ACTCTGACAG	TGTTTCTGAC	CTTTAGCATT	TCTTTTTGAT	60
TCTTTCTTAG	AATTCTCATC	TTCTGCTTAT	ATACCTGTCT	ATTCTTGCAT	GCTGTCTACG	120
TTTCCCATGA	GAGTCCTTAG	CACATTAATC	ATGGTTGTTT	TACATTCACA	GTCTGGTAAT	180
TCCAGCATCC	CTGCCACATC	TGAATCTAGT	TCTGATGCTT	GCCCTGTCTC	TTCAAACTCT	240
$\tt GTTTTTTTGC$	CTTATAATCT	TTTGTTGAAA	GCCGAACATG	ATTCCTGTAC	TGGCTCTTCT	300
GGAGGCTTCT	GCCCTGTTCT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:945:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 712 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

60	TTTCTCACGT	TGGATTCCAC	TCATTTCTCT	ACAGATGACT	AAAGAGGCCT	GAATTCGGCC
120	TTTGTACTTC	AGTTCCACTG	GATAAGTTTC	GAGGTGTTGG	GAGAGGAAGG	${\tt GTCAGAATGG}$
180	TTAGATTTGT	TTGTTTCAGC	GTTTCATCAT	TGGCAAATAG	AACACCCATG	TCGTCTGGCT
240	AGCAAGAAAG	GAGGAGGCTC	GAACGATTCT	GCTGTCTTGA	TTCCTGGAGT	TGACAGCGGT
300	GGGCAGTGCT	AGTAAGGAGT	TGGAGAAGGA	GTGTCTGTCA	TTGATTGGGT	AGTGTTTCAG
360	CATTTCCTGT	CTGGGGTTGA	ATCTCAATAC	TCTGTCCATT	CCGGGGCACT	AGCAAAATTC
420	CTGCTTAGCT	GAACTGAGTG	CTGACCACTC	TACCCTGCCT	GAGTCCTGAC	CTCAGATCAG
480	ACAAAGGCCA	TCTTGATAAC	ACACCCTGCT	TTGTGAACAG	CACCGCCTGT	GTATCGTAGA
540	ATAGAGGTCA	TGCCCAGAGC	CGGTCATTTC	GAATGGCCTT	CTGCTGTGTG	GCAGGGTCCA
600	CTCCTAAAAG	TAAAATGTTC	TTGAAAGTGT	CTCCTTTTGA	TAACATAACT	TTTTCACTAA
660	ATGCCTTCAA	CCTAAGCAAA	TGCCCCATAT	TCTTCAGATT	TTAGGCTCGT	CACTTATTTT
712	AG	ACTGTACTCG	GCTTGTCCAT	ACCGTAGGGA	ATATTGCTTG	TATGAAGTGG

- (2) INFORMATION FOR SEQ ID NO:946:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 305 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

GAATTCGGCC	TTCATGGCCT	AGTCTTGAAG	GATAAGACTT	GCCCAAGTGG	ATAAGGGGCG	60
AAAGGCATCC	CAAGAGGAGA	CAGTAACGTG	TGTATAAATG	AACGAAGGCG	TGAAATAGGA	120
TGGAGTGTTT	TGAGGAACCA	CAAGTAGCCT	TCTCTGAGTA	AGAGCATAGG	TTTGTGAGGA	180
GGACCTAGTG	TTGTTTGAAA	AAAGAGAGTG	ATCAATGGAA	GATGAGATAT	CAAGACAGGA	240
GAACCAAGGA	AGAAAAAGCA	GAGGACAGCT	GGAATGAATC	AAACCGAAGA	ACCAGGATCC	300
TCGAG						305

- (2) INFORMATION FOR SEQ ID NO:947:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 321 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

TTAAGTAAAT	TATATTGTAA	TAAAAAGGTA	GATAAACCAT	60
CGCCAACAAA	AGTGTGACAG	ACACACTAAA	AGCCCTCCAA	120
TCATTCTCAA	AGCTGACTCC	TTTTTTTTCT	TTTTCCTTTT	180
AATTTCAAAC	AGCTCCTTGA	CACTGCTTTT	CATGTTCAAA	240
TGGTAAAGGA	CCTCTTCCCC	TTCCTCCCCT	ACACATACAG	300
G				321
	CGCCAACAAA TCATTCTCAA AATTTCAAAC TGGTAAAGGA	CGCCAACAAA AGTGTGACAG TCATTCTCAA AGCTGACTCC AATTTCAAAC AGCTCCTTGA TGGTAAAGGA CCTCTTCCCC	CGCCAACAAA AGTGTGACAG ACACACTAAA TCATTCTCAA AGCTGACTCC TTTTTTTTCT AATTTCAAAC AGCTCCTTGA CACTGCTTTT TGGTAAAGGA CCTCTTCCCC TTCCTCCCCT	TTAAGTAAAT TATATTGTAA TAAAAAGGTA GATAAACCAT CGCCAACAAA AGTGTGACAG ACACACTAAA AGCCCTCCAA TCATTCTCAA AGCTGACTCC TTTTTTTTCT TTTTCCTTTT AATTTCAAAC AGCTCCTTGA CACTGCTTTT CATGTTCAAA TGGTAAAGGA CCTCTTCCCC TTCCTCCCCT ACACATACAG G

- (2) INFORMATION FOR SEQ ID NO:948:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 312 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

GAATTCGGCC TTC	ATGGCCT ACAAAAGGCA	ACAAACAAGA	TTAACATGGA	ATTATAAAAA	60
TCACTCAATC CAA	AATAAGG CAGAAGAAGT	GGAAAAGGGA	GATGAAGATC	AGATGGAACA	120
AAGAATATTA CTA	GAAATGA CTATGTTTTA	TAATGCAAAA	TAGTTCAGTA	CAGGAGAAAG	180
ATACAATAAT TTG	AGTGCAT ATGAACTTAA	AAGAGAATTT	CAAAATATAT	GAAGCAAAAA	240
TTGACAGAAC CCA	AAAGGCA ACAAACAAGA	TTAACATGGA	ATTATAAAAA	TCACTCAATC	300
CAATATCTCG AG					312

- (2) INFORMATION FOR SEQ ID NO:949:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 291 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

GAATTCGGCC	TTCATGGCCT	ATAGGCCATG	AAGGCCGGGA	GCCTCAAGAA	AAATTAGCAG	60
		CTATTTAGGG				120
AAAAATTCCA	TGTCTTCAAA	AATAATTCTT	CCCTCTCAAT	CTCTCTGAAT	ATCTCATAAG	180
AGTATTCAGG	CCACAGAAAT	AACTACCATT	TAGCCACTCA	GAGGCTTATA	GTAGTTCTAC	240
TAACTTTAAC	ATTTGGCAAC	CAAAATTACT	CTAAGAATCA	TCACCCTCGA	G	291

- (2) INFORMATION FOR SEQ ID NO:950:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 240 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

GAATTCGGCC	TTCATGGCCT	AGATGGGCAT	TCTGTTTATC	TTACTAGTAG	TACGCAGGGT	60
ATGTTGAAAT	CTCCAACTGT	GATGGTGGAC	CTGTCAACTT	CTCCCTGTGG	TTTTATCAGT	120
TTTTCCTGGG	TATTTTGAGG	CTATTCTGAT	AGGTACATAA	AATACAAAAA	TTGCTATATC	180
CTCCTAATTA	ACACTTATTA	TCAAATTGTT	ACTAATGCTT	TCTGTTCCTA	GGCCATGAAG	240

- (2) INFORMATION FOR SEQ ID NO:951:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 404 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

60	AGGGTGCAAG	CTCTGCCTCC	TCACTGCAAC	AGATCTGAGC	TTCATGGGCT	GAATTCGGCC
120	ACCACGTTGG	GGCGTGTGCC	TGAGACTACA	CCCAAGTAGC	GCCTCAGCTT	CCATTCTCCT
180	TGTGAGGTAG	GAGTGTCAGG	TTTAAACCCT	AGCTTTTTTT	TATTTTTAGT	CTAATTTTTG
240	GTTGCATTCA	ACTAATTCTT	TGAGTACTTA	TGACAGCTTG	GTAGTGTTGT	TAGAAGAAAG
300	CAGAATCAGC	GAATAGGGAA	AGGCAATTAG	ATACATTTAT	GTAGTTGTGT	CTATAATATG
360	TACTTTTTTC	AAGCCATCAT	AAGTCATGGA	ATGTTTGCTG	GGAGTTAGAG	AGATACTAAC
404		CGAG	GCGTTCAGCT	AGTGGGTGTG	ATAAGGCCTT	TTCCTTCCTC

- (2) INFORMATION FOR SEQ ID NO:952:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 382 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

GAATTGGCCT	TCATGGCCTA	GAAAAATÇAT	GTGGGAAAAC	CACTGCTGAA	AATGGATTTA	60
AATTCAGAAC	AGGCGGAACA	ACTGGAAAGA	ATCAATGATG	CTCTTTCCTG	TGAATATGAG	120
TGCCGCCGAC	GAATGTTAAT	GAAACGATTA	GATGTGACTG	TACAGTCCTT	TGGATGGTCT	180
GATAGAGCAA	AGGTAAAAAC	AGATGATATA	GCAAGAATTT	ATCAGCCTAA	GCGTTATGCT	240
TTGTCACCCA	AGACAACGAT	TACAATGGCA	CATCTACTTG	CTGCTCGTGA	AGATCTATCC	300
AAGATCATTA	${\tt GGACAAGTAG}$	TGGCACCAGC	CGGGAGAAGA	CCGCATGTGC	CATTAATAAG	360
GTGCTGATGG	GAAGGGCTCG	AG				382

- (2) INFORMATION FOR SEQ ID NO:953:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 268 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

GAATTCGGCC TTCATGGCCT	AGTCCCTCTT	CCACTGCATT	TCGGCTTCAT	ACATGCACAT	60
GATGTCCTCC TCCTTGCACT	CAGTGATGTC	TGGCACGCGG	CGGTACTGCC	GGTGGTAGTA	120
GTAATACCTG TTCTTTGCGT	GCTGCCGCTC	TATAAATTCT	CTCACGAGGG	TCACGGGTCG	180
GTCCACGATG AGGTCGAACG	CTTTCATCAT	GTAGACGATG	GGATTGGGCT	GCACCGGCGT	240
GCGGCGCGG GGCTCAGGCT	CGCTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:954:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 260 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

TGATTTTTT	AAGTGTGAGG AGGGAATCAG TGCCTCTCGG AAGTCGTTTT AATTAGAATG TTCTTAAACG TGTCTTCATT GGCTCCCAGA TTTGCCGTAG AAACCAAGCA TAAAACAGAA AGGCCCATAG ATTGTACTTT TTGAGCTGTT TGAATTTGTA ACAACTCGAG	120 180 240 260
(2) INFORMA	TION FOR SEQ ID NO:955:	
(i) ;	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 129 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:955:	
	TTCATGGCCT AATCCGAGTG TTTCGCGCAC GTCCTAAGCT GACAGTCCCT TCCCTGGAGT GGAGTCACTG CTCCTTGTCT TTTTTTCATA ACATACACTC	60 120 129
(2) INFORMA	TION FOR SEQ ID NO:956:	
(i) :	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 404 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:956:	
GATCATAGAC CAATGAGAGT CCCCACTTAA GCCTTTGAGA GAAAGATCTA	GGAAATGAAA GACTGATACT TGCTACCACA AAAANANACT TAAGCACATA AGTATAAAGC AATTAGACAA TGAAGTCTAC AAAACAACAC GTTAACAACA ATCAAAATCT TACATGTCAA TACTAACCAT GAATATAAAT GATCTAAGCC AAAGCATACA GTGGCAAACT GGATAAAGAG ATAAGACCCA ACTGTCTGCT GACCCATCTT GCATGTAGTG ACACCCACAA GCTGAAAGTA ATGAGATGGA TCATGCAAAA GGAAAACAAA AAAGAGCAAG TATCACTATT CTTATATCAG TTTTAAACCA ACAACTATCA AGAAGAACCT CGAG	60 120 180 240 300 360 404
(2) INFORMA	ATION FOR SEQ ID NO:957:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 283 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:957:	
AAAATTCCCT TACTAGTAAA TAGAATTTAA	TTCATGGCCT AGACTCTCTT TATACAATTC ATCAAGGTTA AACAAAACAT TAAAAATAGG GTAATAAAAT AGATGAAATT TGTATCACTC AATTTGGTGA AACTATAGGTT CATATTTATA TACAAATAAT ACAGTCTGTA AAAACAGTCT ATAAGCTATC TAAACGTGTT AAAATTTTAA ATCAGGACCT GATTTGTTTT AAATGTCACA TTGAATTCTA GACCTGCCTC GAG	60 120 180 240 283

121	INFORMATION	FOD	CEO	TD	MO. GEP.
(4)	THINKINGTION	FUR	SEQ	עג	NO:338:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

CTCGAGGACC	TGGTCGTGAC	CAACTATAAG	ATGGGGGGGC	GACATTGCCA	ATGGGGTACT	60
TCGGTCCTTG	GTGGACGCAT	CTAGCTCAGG	TGTGTCAGTA	CTGAGCCTGT	GTGAGAAAGG	120
TGATGCCGTG	ATTATGCAAG	AAACAGGGAA	${\tt AATCTTCAAG}$	AAAGAAAAAG	AGATGAAGAA	180
ACGTATTGCT	TTTCCCACCA	GCATTTTGGT	AAATAACTGT	GTATGTCACT	TCTCCCCTTT	240
GAAGAGAGAC	CAGGATTATA	TTCTCAAGGA	AGGTGACTTG	GTAAAAATTA	GGCCTCTTTG	300
GCCGAATTC						309

- (2) INFORMATION FOR SEQ ID NO:959:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 149 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

GAATTCGGCC	AAAGAGGCCT	AGATTGAATT	CTAGACCTGC	CTCGGACTAC	TGCAAGTGCT	60
TAAAGGCATT	ATTTCATAGA	CCTTACAACT	ACCCATATAA	CATTATTATC	TTCATTTTAC	120
AAATGAGGAT	AATAATGTTA	TATCTCGAG				149

- (2) INFORMATION FOR SEQ ID NO:960:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 455 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

GAATTCGGCC	AAAGAGGCCT	ACACCGTAAT	ACTATAATAC	TATATAATCT	GTTTGTTAAT	60
TTTCTGAGAA	TAATAACTCA	ATGGAGTAAC	TCTTTAATAG	GCATCTTTTC	CTTATAAAAA	120
ATATTGTAGA	TTGGCTCTCT	GCAAGCTAAT	TTCTTTTATA	TGGTTAATAT	TTTAGTGTAC	180
ATTAAGAGCT	TAGAGTTCTT	TTTGTAATCA	AGCTTGCTAC	AGAAGCTGTG	CTTTATTTAT	240
TTCATAGTAA	TTTCCTCTAG	TGGGTCATTG	TATAAACCCT	GATCATTTTT	GTATGTCTAT	300
TCCTTTTCTT	GCGAAGTGGG	CAGCTTGTTT	AGCCATGGTG	TTTTGGCTTC	AATAGTGAGG	360
TCTCTATTTG	GGAATCTCTG	AATTTCACAG	GAATGAGTAG	AACTATATTT	AACAATGAAA	420
AAAATAGTAT	TAGATTTTAG	GGCAGCTGGC	TCGAG			455

- (2) INFORMATION FOR SEQ ID NO:961:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

GAATTCGGCC A	AAAGAGGCCT	ACCCTGTCTT	TATGCTCCAA	TGCTTCTTTC	TCCAGATATG	60
AAAGGAGATG (	CTCTCTATCA	AATGGCCCTG	TGGTGGACTT	TGATGTCTGG	TTCTTCTGCC	120
GGAACCCTGC T	rggctttttg	CTGTAGCTCC	ACATTCCTGT	GCATTGAGGG	GTTAACATTA	180
GGCTGGGAAG A	ATGACAAAAC	TCTCGAG				207

- (2) INFORMATION FOR SEQ ID NO:962:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 247 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

GAATTCGGCC	AAAGAGGCCT	ACTGTAGTAT	TTAAATATCT	GTTACAGGTT	TCCAAGGTGG	60
ACTTGAACAG	ATGGCCTTAT	ATTACCAAAA	CTTTTATATT	CTAGTTGTTT	TTGTACTTTT	120
TTTGCATACA	AGCCGAACGT	TTGTGCTTCC	CGTGCATGCA	GTCAAAGACT	CAGCACAGGT	180
${\tt TTTAGAGGAA}$	ATAGTCAAAC	ATGAACTAGG	AAGCCAGGTG	AGTCTCCTTT	CTCCAGTGGA	240
TCTCGAG						247

- (2) INFORMATION FOR SEQ ID NO:963:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 472 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

GAATTCGGCC	AAAGAGGCCT	ACAAGAACAT	GAAACATCTG	TGGTTCTTCC	TTCTCCTGGT	60
GGCAGCTCCC	AGATGGGTCC	TGTCCCAGGT	GCAGCTGCAG	GAGTCGGGCC	CAGGACTGGT	120
GAAGCCTTCG	GAGACCCTGT	CCCTCACCTG	CGCTGTCTCT	${\tt GGTGGCTCCA}$	TGAATAGTCA	180
CTACTGGAGC	TGGGTCCGGC	AGCCCCCAGG	GAAGGGACTG	GAGTGGATTG	GATATATCTC	240
TGACAGGGGG	AGCACCAACT	ACAACCCCTC	CCTCAGGAGT	CAACTCACCA	TATCACTAGA	300
AACGTCCAAG	AACCAGTTCT	CCCTGAATTT	GTTCTCCGTG	ACCGCTGCGG	ACACCGCCGT	360
ATATTACTGT	TCTCGTGGGA	CATCCCCCCC	CCCCTCCTAC	TACTACTCCA	TGGACGTCTG	420
GGGCAAGGGG	ACCACGGTCA	CCGTCTCCTC	AGGGAGTGCA	TCCACCCTCG	AG	472

- (2) INFORMATION FOR SEQ ID NO:964:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 303 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

GCTCGGCTCG (	CTGCAACCTC	TGCCTCCCAG	GTTCGAGCGA	TCTTCCTGCC	TCGGTCTCCC	60
AGGTAGCTGG (	GACTACTGGC	GTGCGCGACC	ACGCCCAGCT	AATTTTTTGT	ATTTTTAGTG	120
GAGACGGGGT T	FTCACCATGT	TGGCCAGGAT	GGTCTCAATC	TCTTGACCGC	GTGATCTGCC	180
TGCCTCGGCC T	CCCAAAGTG	CTGGGATTAC	AGGCTTGAGC	CACCGCATCC	AGCCAACATT	240
TTTCAAATAG A	AAAATCTGAA	$\operatorname{GCTAAAATCA}$	CCCCTAAAGG	ACAAATAACA	GGACTATCTC	300
GAG						303

- (2) INFORMATION FOR SEQ ID NO:965:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 281 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

GAATTCGGCC	TTCATGGCCT	ACTAGATTAT	GGATTTTTTT	ATTTCAATGG	AAGTGAAGTT	60
CAAAGATGCC	AGAGTGGTAC	AGTTCGAACA	AACTGCTTGG	ATTGTCTTGA	TAGAACAAAT	120
AGTGTGCAGG	CATTTCTTGG	CTTAGAGATG	CTAGCTAAAC	AGTTGGAAGC	TCTTGGTTTA	180
GCTGAAAAGC	CTCAGTTGGT	GACTCGCTTT	CAAGAAGTTT	TTCGGTCAAT	GTGGTCCGTG	240
AATGGTGATT	CAATCAGTAA	GATATATGCA	GGAAACTCGA	G		281

- (2) INFORMATION FOR SEQ ID NO:966:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 454 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

GAATTCGGCC	TTCATGGCCT	AGACGTGATG	TGTTGAGAGA	AGAATGTTCT	AGGCAGAGGC	60
AACAGCAGAT	GCAAAGGTCT	GAAGGGGAGA	CAGACCGAGC	TAGAAAAGCA	TGGCACATCA	120
GTGATCTAAG	TTCGTGTGGT	TTCCTAAGGT	TGGAACCTAG	GGTGCAAACT	GAGGATGGGC	180
AGATGAGGTG	GAAGAGGAAG	AGCAGACCCA	GGTCACAAAG	ATCTTTTGTG	CTAAGGATTT	240
TTAAGCAGGT	AGGAGGAGAG	AGAATATGAG	CCTTGGGATT	TGAACTGCTG	TGGGTGTACA	300
GAAAAAGAGA	AACTCAACGA	GAGGTTTAGG	TTTAGGGACG	TGGTAGGCTT	TTGCAGTAAG	360
GGACAAGGAC	AGAAGGCTCA	TCTGAGGATG	GGAGGGACAC	TTTAGAGGCA	AATCCATAGG	420
ATGCAGTGGC	TGAACAGAAA	AGGTGAATCT	CGAG			454

- (2) INFORMATION FOR SEQ ID NO:967:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 322 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

GAATTCGGCC TTCA	TGGCCT AGTCATTTAA T	TTTAACTTAG CAAAACT	CCA ATAGTGTAAG	60
TTAACAGATT TTGG	AAACTG GTTTTAAGTA G	SATGTATTAT AACATAA	AAC AAAGCTAGCC	120
ATTATCAAGT TATT	TCCTTG TTAGCTATTT T	TTACAGCATG TGCATGT	TAG GTAGTCATCG	180
TGAAAGCAAG AATC	TTAAGT TAAATACATG T	TTTTTTTGT TTGTTTG	TTT TACTGCTGTG	240
CTGTATAATA CATG	ATGCTG TTAGCAGCGG A	ACGTATCAG AGACACG	GCA CCAAAGTATG	300
TTACTGTCGG CGAA	AACTCG AG			322

- (2) INFORMATION FOR SEQ ID NO:968:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 478 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

GAATTCGGCC	TTCATGGCCT	AGACTGCTGG	CATATCCACC	CCACCTGTGC	TGCTGCCCCC	- 60
GCCAATCCAT	CAGGGCAGCT	CCGACTCCTG	CAGCACCCAC	CGCCCAGGAC	GTCAGCTACT	120
CAGGTTTTCT	GGCTGCTGGG	GTTCCGCACG	AATGGGCCCT	TCTTTTGGGA	AAATGCCAGG	180
GAAGGGGAAC	GGCTGGGCTC	GGGCGCCACA	GCTTGTCCCT	CCAGCCAGCA	GGCACAGATG	240
TATGGCGCAG	GAGGGACAAC	TGGCCCCTGT	GGCCAGCCCC	AGAGAGACGG	GCCCTTTCTT	300
TGGGACCCTG	GCCTCAGAGG	CCTGCGTGTC	ACAGCTCAGG	GTCTGGCTGG	GCAGGGGCAA	360
AACCTGCCTT	ATTTGCCAGA	TGTCCCAGAA	GTACACAGGA	GCAGACGCAC	CACTTCGATG	420
GCTATTTTAG	GAGGCTGGTG	ACAAGCAAGG	CATGGTGGCA	GGAAGCCAGG	CCCTCGAG	478

- (2) INFORMATION FOR SEQ ID NO:969:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 484 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

CTCGAGGTCC	CTGTCCTGCT	CAGTTTCTCT	TCAATGTGGA	AGTCCTGGGA	GGTCAGTCTC	60
ATGAGAATAA	GGTGCTGTAC	TTTCACAGCC	TTCTCAGACT	TTTCTGAGGA	TGGCCTTACA	120
CTTGCCAGCT	AGTGGAGTGA	GCAGAACTCC	TCCTGGTTTC	TGTGGCTGTT	CTCAGAATGC	180
CCTAGTTCAC	TTTCCAGTAA	${\tt TACTTTTTG}$	GGAACATTTT	${\tt GTGTTTCTCA}$	TTTTCTCAGG	240
TCCCCCAGGC	ACACCATCTT	TCCTCTGCTT	CCTCTCACAC	AGGTGCTGAT	ACTGTGTAGG	300
TTTGGGGCTG	TTGTTCTGGC	CCACTCCCTG	ATATTTTCTG	GGTTTGTCAC	CTAGTTTTCT	360
TAAAAGTATC	ATCTACATGG	TTTTGGTTTC	ACTATCTATT	CTGTCTTTAT	TTGAACACTA	420
GGGGAAATTC	ATTATGCCAA	TCTCACACAT	TGTGTGATTC	CATTAGGCCA	TGAAGGCCGA	480
ATTC						484

- (2) INFORMATION FOR SEQ ID NO:970:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 540 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

GAATTCGGCC	AAAGAGGCCT	AGGCAAAATG	AAAATACTTG	TGGCATTTCT	GGTGGTGCTG	60
ACCATCTTTG	GGATACAATC	TCATGGATAC	GAGGTTTTTA	ACATCATCAG	CCCAAGCAAC	120
AATGGTGGCA	ATGTTCAGGA	GACAGTGACA	ATTGATAATG	AAAAAAATAC	CGCCATCATT	180
AACATCCATG	CAGGATCATG	CTCTTCTACC	ACAATTTTTG	ACTATAAACA	TGGCTACATT	240
GCATCCAGGG	TGCTCTCCCG	AAGAGCCTGC	TTTATCCTGA	AGATGGACCA	TCAGAACATC	300
CCTCCTCTGA	ACAATCTCCA	ATGGTACATC	TATGAGAAAC	AGGCTCTGGA	CAACATGTTC	360
TCCAGCAAAT	ACACCTGGGT	CAAGTACAAC	CCTCTGGAGT	CTCTGATCAA	AGACGTGGAT	420
TGGTTCCTGC	TTGGGTCACC	CATTGAGAAA	CTCTGCAAAC	ATATCCCTTT	GTATAAGGGG	480
GAAGTGGTTG	AAAACACACA	TAATGTCGGT	GCTGGAGGCT	GTGCAAAGGC	TGCACTCGAG	540

- (2) INFORMATION FOR SEQ ID NO:971:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 289 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

GAATTCGGCC	TTCATGGCCT	AGCCAGTCTC	AGCACTTAAA	CAACCAGGTG	TTGAAGGACT	60
ATGTTCCAAA	GAACAGAAGA	GAGTATGGTT	TGCAGATGGT	ATATTGCCCA	ATGGTGAAGT	120
TGCAGATACA	ACAAAATTAT	CATCTGGAAG	TAAAAGATGT	TCTGAAGACT	TTAGTCCTCT	180
CTCACCTGAT	GTGCCTATGG	TAAGGAATTC	AAAGAATACT	TAATTGACTA	AACAAAATTT	240
${\tt TATTTCGTAG}$	ATAATTCCTG	GTGTGATTAT	TAGAGTGCTT	TTTCTCGAG		289

- (2) INFORMATION FOR SEQ ID NO:972:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 418 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

${\tt GAATTCGGCC}$	TTCATGGCCT	AGAGCTTGGG	AGGTTGAGGC	TGCAGTGAGC	TATGAGCTGC	60
ACCACTGTAC	TCCAGCCTGG	GTGACAGGGC	AAGACTCTGT	CTCAAAAAAC	AAAAACAACA	120
ACAAAAACTT	TATTCCTAAA	AAGTGCTGAC	CCAGAGATAA	GAAGCAAGCA	CATGGTTGGT	180
AAAATGACAT	CAGTGAGCTT	GCTTTATGCA	GGGTTGCCCC	AAACCTTCAA	TTTGTAAAAC	240
TCAAAATATC	TGGAAAGCTT	GGTGAGGCGA	GGCGGGACTG	TAACTCAGCA	CTCACCGCAG	300
GGTGAGACCC	TTAGGGCAGC	GGGTGCTACA	CTGAACAAAG	CGGTGAACAG	CCCCCTCGTG	360
AGAGGGGGTT	CTTGGCAGAT	GACGCCAGCA	GCTGACAAAC	AGGCAAGTGC	AACTCGAG	418

- (2) INFORMATION FOR SEQ ID NO:973:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 276 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

GAATTCGGCC TTCATGGC	CT AGATTTGTAA	AAGATTTTCC	TAGATTTACT	GTGTTCTGGA	60
TCTAGCTTGA ACGTGAAT	GT TTGTATAGTA	CGTTTTCTTA	ATATTTTTTA	GTATTCATAG	120
TATATAATCA TACTAAAC	CTT GAGAAACTGG	AAGAATCAAG	TCTTCCTCAG	TTCTGTTTAG	180
ACTTTCTAGT TTTTTTT	AG GATACTTCCA	TATCTTCTGT	AAGCTACACA	GTGAGCTTCA	240
TTTTTGCACA GTTATAAT	AC ACTCTCGAAT	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:974:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 379 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double.
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

GAATTCGGCC	TTCATGGCCT	AGGGTTCGAT	GATAAGCACA	GGCGGCAGCT	GGATTGCAAG	60
TGGAGTGGTA	ATGGCCAGAA	CAGCCTCTTT	CTGTTTTGCA	${\tt TTTAGTCGAG}$	GATCCAACTG	120
TTCATCCCAT	TGTCTGTTAG	GACTCCATGG	TATGGTGGGA	GTCATACTGA	TGTCTGGAAA	180
CAAAACCCCA	TTGTCCTTGA	TCCTGTCTAG	TGCATAGTGC	ATTTCACAGA	GGGGTAATCG	240
ATTTAATTGA	AACTGAAGTT	CAACCTGTGT	GTCACAGTCA	GGCCGAAGAT	TAAGTTCTTC	300
ACAGCATTCC	CTAGATAGCC	TTAAAAATAT	ATATTCCTTT	GTTTTTTCTT	CAATAGTAGC	360
TTCCTAGACC	TGCCTCGAG					379

- (2) INFORMATION FOR SEQ ID NO:975:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 417 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

GAATTCGGCC	TTCATGGCCT	AAGAGAAAGA	GAGTGAGAGA	GAGAGAGAAA	GAGAGAGA	60
GATGCTGTTG	AATCAGAAAC	AGATCAACAG	CCCAAAGATT	TTCCTGTCCC	TGGAGTGCCA	120
GCCCCAGGAA	GCTCCAGGGC	TGAGTGGTCA	GGAGCCAGTT	TCTCCAGCCC	CTCCTCCCCA	180
CAACCCCTAG	TGGGGAGGGG	CAGCTGTCCA	TTTGCCCAAA	GTATTAATGC	AACTGAAGCT	240
GTGATATTTC	CAACGACTGT	AGGAGGAAAA	ATTAAGGGGA	GAGAGGAAAA	CAAAACCAAC	300
CAACCCCTAA	AATCATTTTC	TTATTGTACA	TAACGACCTC	ATTCTCCTGT	ATATGCGGAA	360
GATATAACCT	TATATTTGGT	AAGTGTTTCT	TGTGCTATTT	TATCACGCGA	CCTCGAG	417

- (2) INFORMATION FOR SEQ ID NO:976:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 154 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

GAATTCGGCC	TTCATGGCCT	ACACAGAAAA	ATTTCAACAA	TAAAAGTTCT	TAATTATGGG	60
AAATAGTTAC	ATGTGTGTTA	TATCATTTAT	GGCTCATTTT	GTATTTTTAT	TTAAAAGTAT	120
TAAAATCCCA	ACAGTAACAG	CAATACAACT	CGAG			154

- (2) INFORMATION FOR SEQ ID NO:977:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 252 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

GAATTCGGCC	TTCATGGCCT	AAATTGTTCT	TTGCTCAAAT	AAACTGTTAA	ATTTATCTTG	60
GCAGACTCTA	TTTTGATCCC	CAAATTTGAT	TTAGATTTGG	GGCCATTAAA	TTTCACTATT	120
TAATAATAAC	CCTACTGGAT	GAGAATAAGT	GTTTCTCAAT	TTCTGGTGAT	ATGGTTTGGC	180
TGTGTCCCCA	CCCAGAATCT	CATCTTGAAT	TATATTCCCC	ATAATCCCCA	CGTGTCAACG	240
GCAGGACTCG	AG					252

- (2) INFORMATION FOR SEQ ID NO:978:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 251 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

GAATTCGGCC	TTCATAGCCT	AGTTTAGTTC	TCAGAATTCT	TCATATATTT	TGGCAGCAGT	60
TTTTCCATCA	${\tt GATTATTTTG}$	TAAATATTTT	CTCCCAGTCT	GTGACTTGCT	TTTTCCATTC	120
TCTTAACAGT	${\tt GTCTTTCACA}$	CAACAGAAGT	TTTTAATTTT	AATGAGGCTC	AACTTAATTT	180
TTTTTTCATT	AGTAGATTGT	GCTTTTGGTT	TTGTATCTAA	GAAGCCATCA	TTGAACCCAG	240
GATCGCTCGA	G					251

- (2) INFORMATION FOR SEQ ID NO:979:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 534 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

GAATTCGGCC	TTCATGGCCT	AGAAGGCTTC	TGAATAATTT	CTCAAAACTA	NCTTTCCATT	60
TNAGTACACG	ATTTGATAAA	CATAGCACAT	TAGATAGGTA	TTTAGCAATT	TCTTCTACCA	120
ACTACACTTT	GCCCTCACTA	AGGGTTAGAG	TATGATTTGA	AACAATTTCT	ACATATAAAG	180
CATCTTTAAA	${\tt TAAGTTTGT}$	GTTCACTGAA	${\tt CTGAGACTTC}$	TTTCACTTAT	GTACCTATGG	240
AAGTTAATCT	GAGCATACAC	ATATATACAT	ACTTGCATAC	ATATGTGTAC	ATATGTTTTT	300
TAAGTAAGTN	ACTTTTACCA	TTAGAATAAA	CCTAGACACT	ACAGGGACAA	CTCTGGGGAA	360
CAGGGCGGTC	TGCCTTAACA	ACCCTTCTCT	${\tt AGGTTGAGGA}$	AGGCAGGTAT	AGTTCACTGA	420
AGGATGTGAT	${\tt GAGGCTGTAG}$	TAAGTCTTCT	CATCATCTGT	TAATCCTGCG	TTGCCTGGTC	480
TCACCACCAC	AGCTACGTGC	ACATCTGCTT	CCTCAGCAGC	ACTGGCCTCT	CGAG	534

- (2) INFORMATION FOR SEQ ID NO:980:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 223 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

GCTCGAGTGT	CGTGCTATCT	CTAAATTGTG	ATCACTAAGA	ACCGCTGCGG	AAACAGTAAC	60
TGTTTCTTTT	ATTTTTGACA	TTTTAGTTTG	TAATTTATCC	AATTCTTTCT	TCTTTTGATA	120
AGTCTCCATT	CTCTTTACTT	CACGGGTATT	TTCAAATTCA	TTAATCATTT	TATCACAGTG	180
CCACTTGTTA	GACCCTAATG	AACGATGTCA	CCCTCTTATC	AAA		223

- (2) INFORMATION FOR SEQ ID NO:981:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

GAATTCGGCC	TTCATGGCCT	AATTACTTGA	CCCGTAATAG	GGTTGTGGCC	GTTTTCTGAT	60
GCCTAAGTAT	TATACAGAGC	CCACAATGGC	CAGTTTACTA	CCAGAAAGGG	CTTCAGTAAG	120
ATATTCTTGG	ACTTGATACT	TTCTTCAGAT	CCTCTTTGTG	CCAAGATAAT	TTATCCAGTC	180
ATTGGGAATA	GTAAGTTTCT	GTGTAACCCA	TCTCAATTAT	AGAAGCAAGT	TCAGCTTTAT	240
GTATTTGTAT	GGGGAGTTGA	AGATTCAGAT	AGAGGTATTA	AGATGTGTGG	CATTTACTTA	300
AACCATCACA	TTTTTTTCTT	TCTACGCCCC	CTTGCCTGTA	AAACACCTGG	GAAGTTCCAC	360
TGGTGTCATC	CATCCTGATG	CTTCAGACCA	CCCTCCCTTC	TTCACAGACC	GTGTCACTTT	420
GCCTGTGGGT	GGGGGCTAGC	CAGCCACCAC	CCTCTTTTCT	GTGCTGCCAG	CCAATCTCGA	480
G						481

- (2) INFORMATION FOR SEQ ID NO:982:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 293 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

60	CCCCTTTCCC	ATTTTTTTT	GTTTCTTCTG	TGCCCCCAGT	CTCCTCCCTC	TCCGTGTCCC
120	CCCTCCCTCC	AAAACGGTTC	CAGCACAGGT	TCCCTTGGTT	TCCGCATTCT	TCCCTCCCTC
180	TGTGTGTGTT	CTTTTCTTTG	GTTGCCTTCT	CTCACGTCAT	GGATCACCAG	CTGCCTTCAT
240	CCCTCCCTCT	GGCCCTCCCT	TTTTCTTTTT	CTCCTCTCCC	ATTTTTCTTC	TATTTAAGTT
293	GAG	AGCCGGACTC	GTTTGCAAAC	TGTGCTATGA	AACTGGAGGA	TCTGCCATGT

- (2) INFORMATION FOR SEQ ID NO:983:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 334 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

GGTGAGGATG GTGGCTGT	G TTGTGTTGGT	GGCTGTGATG	GTGAAGGTGG	CTGTGGTGGG	60
GATGGTGACT CTGATGCT	AA TGTTGGTTGT	GGTGATGGAG	GCAGCTGTGG	CAAGGATGGT	120
GACTTTGGTG GAGAAGGT	G CCATGTTGGG	GCTAGTGGCT	GTGGTTGTGG	TGATGGCCAT	180
GGTGAGGATG GTGTTAAA	G TGGCTGTGAT	GAAGATGGTG	ACTGGGGTAG	AAATGGTGAC	240
TGTGATGGTA ATGTTGGCT	TG TGGTGATGAA	GGGTAGTTAT	GGTGAGGATG	ATGACTATGG	300
TGGTGAAGGG GCCATAGTG	G CAACGGCACT	CGAG			334

- (2) INFORMATION FOR SEQ ID NO:984:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 631 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

GAATTCGGCC	TTCATGGCCT	AGGGAAAGAG	TAGGGGTGGA	GGGGTAGGAG	GATTTACTCT	60
TCCAGCGAGA	GCTACGCGCA	TCCCATCCTC	CCCCTCCCCC	CTACCCGGGC	TCCGGCNTGG	120
AGGCGGGGCG	TGGCCGGCCT	GCTTTGGGAG	GGGAGGGGCT	TCCCTTACAG	TGCTGGGCTC	180
TGCCAGGACG	GCTGTGGGGT	CGCCTTACCT	CGGGGTATCC	ACTCTGCAGT	CGACCAGTTC	240
CCGCCAGGAG	CAAAGGGTAG	GAAGGAGAGC	AGGATCTGCT	GTAGGAACGC	AGCTACCGCG	300
CCACTATCAC	GAAGAAACAG	CAGGCTCGGG	GCACGAGACG	AACTGGAGAC	CGCGCTGCCT	360
AGCTGGGTAA	CCTGGGAAGC	AGAGGGTAAT	AAGTGGCGCC	TTAAGATAAC	CCTGTAGCAG	420
CAGCAGTGGC	GGCCAAAGGA	GGCTGCTCAG	GGAACAAGCG	GCTGŢAGTAG	TCTGTGGGGC	480
GACTGGAGTG	ACCGAAGCCA	AGGCAGTTTA	GTGCCTCTCG	TGTTCTTATT	TTTTAACCTC	540
TGACTATGCA	ATTCTGAAAC	CTCCCCCATT	CGGGGGACCA	GACAGCCTGA	TAGACACCTT	600
CCACTCTCCT	TCCTCCCGCC	GTGGTCTCGA	G			631

- (2) INFORMATION FOR SEQ ID NO:985:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 324 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

GAATTCGGCC	AAAGAGGCCT	ACTGCCTCGG	TTTCTACCTT	TGCCAAATGA	GTTGATAGAT	60
TATCGCTTTT	TTTCCAGCTG	TCATACTCTA	GGAGTCTGAA	TTGTAAAATĊ	AAAGAAGCAT	120
TTCCCAGAAA	AGTTTTTGTC	AAAAATTTGA	TTTACATAAC	CTCAGAAATG	TGTATTGCTT	180
TAAAAATTAT	AAAGTTCATG	GAGCATACCA	AGCAGCCTGT	ATACCATTTC	TAAACCAACT	240
ACTCCCCTGC	AAGATAGATC	TCTTTTTTAT	AGACAGAAAA	TAAATTCAAA	GAGGTTTGTT	300
ACTTGCCCAA	GGCCACCACT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:986:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 239 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GAATTCGGCT	TTCATGGCCT	AAAATGTTTT	TCAATTAAAG	ACTTAAATAT	TACACTTTTA	60
AAACTTTTTA	TTATGGAAAT	СТААААААА	TTCACCAAAT	GAGAGAGAAC	ATTACAATGA	120
ACCACCACAT	ACCCATCACC	CATTTTCAAC	AATTATCAAC	ACATGGCCTA	TCTTGTTTCC	180
TCCATACCTT	CAGACACCCT	CCGTCCACAA	ACTGGGTTAT	TCTGAAGCAA	GCCTTCGAG	239

- (2) INFORMATION FOR SEQ ID NO:987:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 695 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

AAAAGTTCAG	GGACTTTGCA	CCCTGTGGGG	TACTCAGATG	TCCAGCCGCA	CTCTCTACAT	60
TAATAGTAGG	${\tt CAACTGGTGT}$	CCCTGCAGTG	GGGCCACCAG	GAAGTTCCGG	CCAACTTTAA	120
CTTTGCTAGT	GATGTGTNGG	ATCACTGGGC	TGACATGGAG	AAGCTGGCAA	GNGACTCCNA	180
AGCCCACCCC	TGTGGTGGGT	GAATGGGAAA	GGGAAAGAAT	TAATGTGGAA	TTTCAGAGAA	240
CTGAGTGAAA	ACAGCCAGCA	NGCAGCCAAC	TTCCTCTCGG	GAGCCTGTGG	CTTGCAGCGT	300
GGGGATCGTG	TGGCAGTGAT	GCTGCCCNGA	ANGCCTGAGT	GGTGGCTGGN	GATCCTGGGC	360
TGCATTCGAG	CAGGTCTCAT	CTTTATGCCT	GGAACCATCC	AGATGAAATC	CACAGACATA	420
CTGTATAGGT	TGCAGATGTC	TAAGGCCAAG	GCTATTGTTG	CTGGGGATGA	AGTCATCCAA	480
GAAGTGGACA	CAGTGGCATC	TGAATGTCCT	TCTCTGAGAA	TTAAGCTACT	GGTGTCTGAG	540
AAAAGCTGCG	ATGGGTGGCT	GAACTTCAAG	AAACTACTAA	ATGAGGCATC	CACCACTCAT	600
CACTGTGTGG	AGACTGGAAG	CCAGGAAGCA	TCTGCCATCT	ACTTCACTAG	TGGGACCAGT	660
GGTCTTCCCA	AGATGGCAGA	ACATTCCTAC	TCGAG			695

- (2) INFORMATION FOR SEQ ID NO:988:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 314 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

GAATTCGGCC	TTCATGGCCT	ACTCAGAACA	ATCACTGCAT	ATCCCATCTT	AAAGGCAAAA	60
CCCAAACCAG	AAAAACCCCA	CTCAGGTCTT	GCTGACCCAA	CACTACAGTC	ACTGTATTTG	120
AGACCCCTTT	TTCTTGAAAA	${\tt AGGGACTTCA}$	CTTTTTTGAG	CAGCATTCTA	TGGTTCTTTC	180
CACACAGCAA	TTGACGCATC	TCACGGCACT	GCTCTCTGCT	GGGCAGAGAG	CAAACACAGA	240
CAGCCACCAT	CCCCATATTC	${\tt GTAGTAAGAG}$	AAACTCCAGA	AACGCAGCCA	CCGTCCCCCT	300
AGACCTGCCT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:989:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 687 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

GAATTCGGCC AAAGA	GGCCT AGGAGCTCCC	CCATGGATCA	TGGCGTTAAT	GTTTACAGGA	60
CATTTACTAT TCTTA	GCATT ATTGATGTTT	GCTTTCTCTA	CTTTTGAGGA	ATCTGTGAGC	120
AATTATTCCG AATGG	GCAGT TTTCACAGAT	GATATAGATC	AGTTTAAAAC	ACAGAAAGTG	180
CAAGATTTCA GACCC	AACCA AAAGCTGAAG	AAAAGTATGC	TTCATCCAAG	TTTATATTTT	240
GATGCTGGAG AAATC	CAAGC AATGAGACAA	AAGTCTCGTG	CAAGCCATTT	GCATCTTTTT	300
AGAGCTATCA GAAGT	GCAGT GACAGTTATG	CTGTCCAACC	CAACATACTA	CCTACCTCCA	360
CCAAAGCATG CTGAT	TTTGC TGCCAAGTGG	AATGAAATTT	ATGGTAACAA	TCTGCCTCCT	420
TTAGCATTGT ACTGT	TTGTT ATGCCCAGAA	GACAAAGTTG	CCTTTGAATT	TGTCTTGGAA	480
TATATGGACA GGATG	GTTGG CTACAAAGAC	TGGCTAGTAG	AGAATGCACC	AGGAGATGAG	540
GTTCCAATTG GCCAT	TCCTT AACAGGTTTT	GCCACTGCCT	TTGACTTTTT	ATATAACTTA	600
TTAGATAATC ATCGA	AGACA AAAATACCTG	GAAAAAATAT	GGGTTATTAC	TGAGGAAATG	660
TACGAGTATT CCATG	GTCCG TCTCGAG		,		687

- (2) INFORMATION FOR SEQ ID NO:990:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 677 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

GAATTCGGCC	AAAGAAGGCC	TAGAGCCCTT	CTGTCCCTTC	TACCATGTGT	GGATGCAGTG	60
AGAAGGCACC	GTATCTCTGA	AGCAGAGAGC	CCGCCCTGGA	CACTGGATCT	GCTGGCACCT	120
TGATCTTGGA	CTTCCCAGCC	TCTAGAACTG	TGAGAAATAA	${\tt TTTTTTGTTG}$	TTTACAAATT	180
ACCCAGGCTA	AGGTGTTTCA	TTGTAACCTG	AATGGACCAA	GCTGGTGTGA	CCCTGTTGGA	240
AAACTGGCAG	TATCTACCAA	AAGCCGAACA	TACGTATAAA	CTGATCCAGC	AGTTCCACTC	300
CTGGGTATGT	ACACCACAGA	AAGCTATGTC	CACCGAGACA	TTGGCAAGAA	TGTTTCTAAC	360
CACACGCTGA	CTGTAGCCCC	AAACCTGAAA	CAACCCAAAT	GTCCATCCAC	CAACCCAAAT	420
GTCCATCCAC	AGTTGAAGCT	ACAGTGAAGT	CACAGGGTCG	AATACTACTG	CACAGCAACG	480
AATATGAATG	AAAATATCGC	TATGCACAGC	AACATGGATA	AATTTCACAG	ACATGAGGTC	540
AAGCAAAAGA	GGTCAGAGTC	CTCATCATCA	AGAGAGAATT	CATTGTATGA	TTCTCTTCCT	600
ACAAAAAGTA	CAGAAATAAG	CAAAACTGAT	CCATGGTGTT	AGAAGCCAGG	GGAACAGTTA	660

ACAAGGGAGC ACTCGAG 677

- (2) INFORMATION FOR SEQ ID NO:991:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 445 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

GAATTCGGCC	AAAGAGGCCT	AAGAAGCTGC	TTCCTCCTGG	GAACAACCGC	CTCCCGCTCC	60
TAGCAGGTTG	CTACTGCCCC	GAACCCGCGC	TGCAGGGAAC	AGCGGGGCAA	ACAAAACCAA	120
TAGAGCCATG	GCGACTCCCT	CTGCTGCCTT	CGAGGCCCTT	ATGAATGGTG	TGACAAGCTG	180
GGATGTACCC	GAAGATGCTG	TTCCATGTGA	ACTGCTTCTT	ATTGGAGAGG	CTTCATTTCC	240
TGTGATGGTG	AATGACATGG	GCCAGGTCCT	CATTGCTGCC	TCCTCCTATG	GCCGTGGCCG	300
CCTGGTGGTC	GTGTCCCATG	AGGACTACTT	GGTGGAAGCC	CAGCTCACGC	CCTTTCTCCT	360
GAACGCAGTG	GGGTGGCTTT	GCTCTTCCCC	TGGGGCTCCC	ATTGGTGTAC	ACCCATCCCT	420
GGCACCTTTG	GCCAAAATCC	TCGAG				445

- (2) INFORMATION FOR SEQ ID NO:992:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 392 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

GAATTCGGCC	TTCATGGCCT	ACTGTGATTT	AAAATCTTGC	TGTGTGGCTT	GGGTTGTTTG	60
TGTTGGTTCC	AAACCCTGAA	TCTTTTGGGG	TCTTCAATTT	GTGGGCATGT	CAGTGGAAAT	120
TCTAAGCTTT	GTTTAATGGT	GTGTGTGTGT	CTGTCTGTCT	CTGTGTGAGT	GTGTTTAGAA	180
ATTGGCTTCT	CTGGGTTCCT	CGCTCGTCTT	CTGGAAGGTG	GGGTTATAGA	CATGCTGGTG	240
AATTCTGAAT	GTTTTATAAA	TTAGACTATT	AACGGAGTTA	AATTGAAGAA	ACCTTCTGTC	300
ATAAGACCTT	CCAGGAATTC	CATTCCAAAT	GAGGAAATGC	ATAAAGACTT	GTCCACTTGG	360
CAAACATTGG	GTGTTTGGGA	GGTGGACTCG	AG			392

- (2) INFORMATION FOR SEQ ID NO:993:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 359 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

GAATTCGGCC TTCATGGCC	T AGGCGGCTCC	CTTGGTCCTG	GTGCTGGTGG	TGGCTGTGAC	60
AGTGCGGGCG GCCTTGTTC	C GCTCCAGTCT	GGCCGAGTTC	ATTTCCGAGC	GGGTGGAGGT	120
GGTGTCCCCA CTGAGCTCT	T GGAAGAGAGT	GGTTGAAGGC	CTTTCACTGT	TGGACTTGGG	180
AGTATCTCCG TATTCTGGA	G CAGTATTTCA	TGAAACTCCA	TTAATAATAT	ACCTCTTTCA	240

TTTCCTAATT GACTATGCTG AATTGGTGTT TATGATAACT GATGCACTCA CTGCTATTGC

CCTGTATTTT GCAATCCAGG ACTTCAATAA AGTTGTGTTT AAAAAGCAGA AACCTCGAG

300

359

TCTGGCATCT TGGCAGCCCT GAGTGCCATG ATCTCTCTAG AAATTCCGCA AGTCAACATC 120 ATGACAAAAA TGGATCTGCT GAGTAAAAAA GCAAAAAAGG AAATTGAGAA ATTTTTAGAT 180 CCAGACATGT ATTCTTATT AGAAGATTCT ACAAGTGACT TAAGAAGCAA AAAATTCAAG 240	(2) INFORM	ATION FOR SEQ ID NO:994:	
GAATTCGGCC AAAGAGGCCT AGACTGTCAG CTGTGAGTGG CCAGTACAAC AAATGCTTTG GCTTTCAGTT GTCATTCTGA TGTCTTGCAA CATATCATCG TGTTTGATTC TCGAG  (2) INFORMATION FOR SEQ ID NO:995:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 633 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:  GAATTCGGCC AAAGAGGCCT AGTGGAGACA AAAGCATGTG ATCCCAATTT GCTGGGATAT CCTCTCCTGC ACTTTCATCTG GAACAGCTGG AGCCAGCCCAC CACATACCAG TCACCCTTGCA AAGAAAGGAT GGCTAGGGTA AAACAAGACG AGCAACTCCC TGGAATCCAG CCTCTCCTGC ACTTTCATCTG GAACAGTCTG GAAGAGCAAG GACAACTCCC TGGAATCCAG CCTCTCTGCTG AAAGAAAGAG CCTACGACGGC AGGAGATATC TAAACAAGACG AGCAACTCCC TGGAATCCAG CCCTTGCTG CATTTCAAACA CCTTCACTGG GAAGAGACG AGCAACTCCC TGGAATCCAG CCCTTGCTG AAGAAAGAGA ACTTCAGAGT TAAACAAGACG AGCAACTCCC TGGAATCCAG CCTCTGCTGCT GATTANAACTG CACAGCCCC GGGGAGATGT TGAACATGG AGGGTCGAAT 360 CCCTTGCTGCT GAAGAGGAGA ACTTCAGCAT TCCCACCCTTC TTCAACATGC AGGGTCAAAT 420 CCCTTCTGGTC ATTANAACTG CACAGCCCC GGGGAGATGT TGAACATGC AGGGTCCAAT 420 CACACACCACC TGTTCCTCCT CATCCAAGGT GGCCATTGGAG TTCCTTGGTG TAATCAAAGCTAGC AAGCCTTCT CACACCGCC TGTTCCTCCT CATCCAAGGT GGCCATTGGAG CGCTCCTTGT TAAACATGCCTCC CAACACCGCC TGTTCCTCCT CATCCAAGGT GGCCATTGGAG CGCTCCTTGT TGAACTTGC CAACGCCCTTGCT TCCCTCCAGAT GGCCATTGGAG CGCTCCTTGT TGAACTTGC CAACGCCCTTGCT CCTCCAAGAT GGCCATTGGAG CGCTCCTTGT TGAACTTGC CAACACCGCC TGTTCCTCCT CATCCAAGGT GGCCATTGGAG CGCTCCTTGT TGATCTTGC CAACTCAACG CTCTTCTCCCCCAAGAT GAGCCTTCC CAACACCCCC CAACACCACC TGTTCCTCC CATCCAAGAT GAGCATCC CAACACCACC CAACACCACC TGTTCCTCC CATCCAAGAT GAGCATCC CAACACCACC CAACACCACC TGTTCCTCC CATCCAAGAT GAACTCCCC CAACTCTTGC CAACACCACC TGTTCCTCC CATCCAAGAT GAGCATCACACAC CAATACCACC (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:  GAATTCGGCC AAAAGGGCCT AGTTGATTCT CAGTTCATAG AAATTCCACA AGTCAAACTC 120 ATGACAAAAA TGGATCTGCT GAGTAAAAAA GACAAAAAAAG AAATTCAACAAAAAACACAAAAAACCAAAAAAACGAAAAAAACACAAAAAA	(i)	(A) LENGTH: 115 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
GAATTCGGCC AAAGAGGCCT AGACTGTCAG CTGTGAGTGG CCAGTACAAC AAATGCTTTG GCTTTCAGTT GTCATTCTGA TGTCTTGCAA CATATCATCG TGTTTGATTC TCGAG  (2) INFORMATION FOR SEQ ID NO:995:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 633 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:  GAATTCGGCC AAAGAGGCCT AGTGGAGACA AAAGCATGTG ATCCCAATTT GCTGGGATAT CCTCTCCTGC ATTTCAAACA CCTTCACTCA GTGTCAGCCA CAGCGGCCAC CACATACAG 120 CTGGCCCCGA CCTTCTCTG GAACAGTCTG GAGATCACAG GTCAGGGTGG AAGGCCTGGT 180 CCTCTCTGA AAGAAAGGAT GGCTAGGGGT AAACAGAACG GACACTCCC TGGAATGCAG GGAGCCAGA AGGGCAGCCA GAGCAGCCCC GAGAAAGAGA GACACTCCC TGGAATGCAG GGAGCCAGA AGGGCAGCCA GAGCAGCCCC GAGAGAGA	(ii)	MOLECULE TYPE: cDNA	
GCTTTCAGTT GTCATTCTGA TGTCTTGCAA CATATCATCG TGTTTGATTC TCGAG  (2) INFORMATION FOR SEQ ID NO:995:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 633 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:  GAATTCGGCC AAAGAGGCCT AGTGGAGACA AAAGCATGTG ATCCCAATTT GCTGGGATAT CCTCTCTCGC ATTTCAAACA CCTTCACTCA GTGTCAGCCA CAGGGGCCAC CACATAGCAG CTGGCCCCGC ACCTTCTCTG GAACAGTCTG GAGATGCAG GTCAGGGGG AAGGCCTGGT TCACCCTTGA AAGAAAGGAT GGCTAGGGGT AAACAAGAGAC AGCACTCCC TGGAATGCAG CGGGCCCAGA AAGGCAGCCC AGGAAGAGAA ACTCAGCACAG GGTTCCTTT CCTTCTGGTC ATTANAACTG CACAGCCCCC GGGAGAGTT TGAACATGCA GGTTCCTTT 300 CGCTGGCCC GAGGAAGGAA ACTCAGCAT CCCACCCTTC TTCAGCATCT CATGGACTT 420 CGCTGGCCC GGAAGGAGA ACTCAGCAT CCCACCCTTC TTCAGCATCT CATGGACTT 420 CAACACCGCC TGTTCCTCCT CATCCACGAT GCCCACCTTC TTCAGCATCT CATGGACTTT 420 CAACACCGCC TGTTCCTCCT CATCCACGGT GGCGTTCCAC CAATACTCCC CCACCTTGCT 600 CAACACCGCC TGTTCCTCC CATCCACGGT GGCGTTCCAC CAATACTCCC CCACCTTGCT 600 CAACACCGCC TGTTCCTCC CATCCACGGT GGCGTTCCAC CAATACTCCC CCACCTTGCT 600 CAGGTTCACC AAAACGCACT TCCCCGGGTC GGGGTTCCAC CAATACTCCC CCACCTTGCT 600 CAGGTTCACC AAAACGCACT TCCCCGGGTC GGGTTCCAC CAATACTCCC CCACCTTGCT 600 CAGGTTCACC AAAACGCACT TCCCCGGGTC GAG (2) INFORMATION FOR SEQ ID NO:996:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:  GAATTCGGCC AAAAACGCACT AGTTGATTCT CAGGTTCATC CAAGTTATT TTTATT TCTGGCACT TGCGAGCCCT GAGTGCAAAA AGACTCT CAAGTTATT TTTATT TCTGGCACT TGCGAGCCCT GAGTGCAAAAA GCAAAAAAAAAA	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:994:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 633 base pairs  (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:  GAATTCGGCC AAAGAGGCCT AGTGGAGACA AAAGCATGTG ATCCCAATTT GCTGGGATAT (CTCTTCCTGC ATTTCAAACA CCTTCACTCA GTGTCAGGCC CAGCGGCCAC CACATAGCAG TCGCCCCCC ACTTTCCAACA GTGTAGAGCA GTCAAGGCC CACATAGCAG 180 TCACCCTTGA AAGAAAGGAT GGCTAGGGGG AAACAAGACCC TAGAAACCCC TGGAATGCAG GAGGCAACA AGGGCAGCCG AGGATAAGGC TCTGCCTCCC CACAGGGGAG GGTTTCCTTT 300 CCCTCTGGGTC ATTANAACTG CACAGCCCCC GGGGAGATGT TGAACATGGC AGGGTCGAAT (CCCTCTGGGCT TGCCTGCAGC CTCCTCTCAGCATCT CATGGACTTT 420 CAGCTCATGG CTCTGTGGCT TGCCCTGCAG CTCTTTGTAACATCT CATGGACTT 420 CAACACCCCC TGTTCCTCCT CATCCACGGT GGCCATGGAG CGCTCCTTGT TGATCTTGTC AAATGTCGATG GGCCTTCTCC CCTCCAGGAT GGCGTTCCAC CAATACTCGC CCACCTTGC AAATGTCGATG GGCCTTCTCT CCTCCAGGAT GGCGTTCCAC CAATACTCGC CCACCTTGCT AAATGTCGATG GGCCTTTCTC CCTCCAGGAT GGCGTTCCAC CAATACTCGC CCACCTTGCT AAATGTCGATG GGCCTTTCTC CCTCCAGGAT GGCGTTCCAC CAATACTCGC CCACCTTGCT (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE GAGGCCCT AGTTGATTCT CAGTTCATGA TAGAACATC TAGAACATC TAGAACATC TAGAACATC AGGAACATC TAGAACATC AGGAACATC AGTCAACATC AGGAACATC AGGAACATC AGGAACATC AGGAACAATC AGGAACAATC AGGAACAACAC AGGAACAACAC AGGAACAACAC AGGAACAACAC AGGAACAACAC AGGAACACAC AGGAACAACAC AGGAACAACAC AGGAACAACAC AGGAACAACAC AGGAACAACAC AGGAACACAC AGGAACAACAC AGGACAACACAC AGGAACAACAC AGGAACAACAC AGGAACAACAC AGGACAACACAC AGGAACAACAC AGGACAACACAC AGGACAACACAC AGGACAACACAC AGGACAACACC AGGACAACACAC AGGACAACACC AGGACAACACC AGGACACACC AGGACAACACAC AGGACAACACAC AGGACAACACC AGGACACACCACACACA	GCTTTCAGTT	GTCATTCTGA TGTCTTGCAA CATATCATCG TGTTTGATTC TCGAG	
(A) LENGTH: 633 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:  GAATTCGGCC AAAGAGGCCT AGTGGAGACA AAAGCATGTG ATCCCAATTT GCTGGGATAT 60 CCTCTCCTGC ATTTCAAACA CCTTCACTCA GTGTCAGCCA CAGCGGCCAC CACATAGCAG 120 CCTGGCCCCGC ACCTTCTCTG GAACAGTCTG GAGATGCAG GTCAGGGTGG AAGGCCTGGT 180 TCACCCTTGA AAGAAGGAT GGCTAGGGGT AAACAAGACA GTCAGGGTGG AAGGCCTGGT 180 CCTTCTGGTC ATTANAACTG CACAGCCCCC GGGGAGATGT TCAACACTGGC AGGCAGACTCCC TGGAATGCAG CGGTGGCCTC GGAAGGGAA ACTTCAGCAT CCCACCCTTC TTCAGCATCT CATGGACTTT 40 CGCTGGGCCTC GGAAGGGAA ACTTCAGCAT CCCACCCTTC TTCAGCATCT CATGGACTTT 420 CAGCTCATGG CTCTGTGGCT TGCCCTGCAG CTTCTGGTG TAGTCCAAGAG TAAGCCTGTC 480 CAACACCGCC TGTTCCTCCT CATCCACGGT GGCCATGGAG CGCTCCTTGT TGATCTTGTC 540 AATGTCGATG GGCTTTCTC CCTCCAGGAT GGCGTTCCAC CAATACTCGC CCACCTTGT TGAACATGTC AAAACGCACT TCCCGGGCT GAG  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:  GAATTCGGCC AAAGAGGCCT AGTTGATTCT CAGTTCATGG TGGAGTCATT CAAGTTTATT 60 TCTGGCATCT TGGCAGCCCT GAGGACAAAAAGAG AAAATTCAGCA AAATTCAACTCCT CAGGACAACAAAAA TGGACTAAAAA GCAAAAAAGA GAAAAAAGAA AAATTCAAAC 340 CCAGACATGT ATTCTTTATT AGAAGATTCT ACAAGTGACT TAAGAGCAA AAAATTCAAA 3ATTTTAAAA TGGACAAAAA TGGACTAAAAAA GCAAAAAAGAAAAAAAAAA	(2) INFORMA	ATTOM FOR SEQ ID NO:995:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:  GAATTCGGCC AAAGAGGCCT AGTGGAGACA AAAGCATGTG ATCCCAATTT GCTGGGATAT 60 CCTCTCCTGC ACTTCAAACA CCTTCACTCA GTGTCAGCCA CAGGGGCCAC CACATAGCAG 120 CCTGCCCCCG ACCTTCTCTG GAACAGTCTG GAGATGCAAG GTCAGGGTGA AAGCACTGCT 180 TCACCCTTGA AAGAAAGGAT GGCTAGGGGT AAACAACACA GACAACTCCC TGGAATGCAG 240 GGAGCCAAGA AGGGCAGCCG AGGATAAGGC TCTGCCTCC CAACGGCGAG GGTTTCCTTT 300 CCTTCTGGTC ATTANAACTG CACAGCCCCC GGGGAGATGT TGAACATGCA AGGATCCAT 360 CCTTCTGGTC ATTANAACTG CACAGCCCCC GGGGAGATGT TGAACATGCA AGGATCATT 420 CAACACCGCC TGGAGGGAGA ACTTCAGCAT CCCCACCCTTC TTCAGCATCT CATGGACTTT 420 CAACACCGCC TGTTCCTCCT CATCCACGGT GGCCATGGA CGCTCCTTGT TGATCTTGTC 480 CAACACCGCC TGTTCCTCCT CATCCACGGT GGCCATGGAG CGCTCCTTGT TGATCTTGTC 540 AATGTCGATG GGCTTTCTC CCTCCAGGAT GGCGTTCCAC CAATACTCGC CCACCTTGCT 600 CAGGTTCACC AAAACGCACT TCCCGGGCTC GAG 633  (2) INFORMATION FOR SEQ ID NO:996:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 462 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:  GAATTCGGCC AAAGAGGCCT AGTTGATTCT CAGTTCATGG TGGAGTCATT CAAGTTTATT  60 TCTGGCATCT TGGCAGCCCT GAGTGCCATG ATCTCTCTAG AAATTCCGCA AGTCTAACATC 120 ATGACAAAAA TGGATCTGCT GAGTAAAAAA GCAAAAAAAGG AAATTCAGAA ATTTTTAGAT 180 CCAGACATGT ATTCTTTATT AGAAGATTCT ACAAGTGACT TAAGAAGCAA AAAATTCAAG	(i)	(A) LENGTH: 633 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
GAATTCGGCC AAAGAGGCCT AGTGGAGACA AAAGCATGTG ATCCCAATTT GCTGGGATAT  CCTCTCCTGC ATTTCAAACA CCTTCACTCA GTGTCAGCCA CAGCGGCCAC CACATAGCAG  CTGGCCCCGC ACCTTCTCTG GAACAGTCTG GAGATGCAAG GTCAGGGTGG AAGGCTGGT  CCCCTTGA AAGAAAGGAT GGCTAAGGGT TAAACAAGACG AGCAACTCCC TGGAATGCAG  GGAGCCAAGA AGGCCAGCCG AGGATAAGGC TCTGCCTCCC CAACGGCGAG GGTTTCCTTT  300  CCTTCTGGTC ATTANAACTG CACAGCCCCC GGGGAGATGT TGAACATGGC AGGGTCGAAT  CCGTGGCCTC GGAAGGGAGA ACTTCAGCAT CCCACCCTTC TTCAGCATCT CATGGACTTT  CAGCTCATGG CTCTGTGGCT TGCCCTGCAG CTTCTGGTGG TAGTCAAAGG TAAGCCTGTC  CAACACCGCC TGTTCCTCCT CATCCACGGT GGCCATGGAG CGCTCCTTGT TGATCTTGTC  CAACACCGCC TGTTCCTCCT CATCCACGGT GGCCATGGAG CGCTCCTTGT TGATCTTGTC  CAGGTTCACC AAAACGCACT TCCCGGGCTC GAG  (2) INFORMATION FOR SEQ ID NO:996:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 462 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:  GAATTCGGCC AAAGAGGCCT AGTTGATTCT CAGGTTCATG TGGAGTCATT CAAGTTTATT  TCTGGCATCT TGGCAGCCCT GAGTGCCATG ATCTCTTAG AAATTCCGCA AGTCAACATC  ATGACAAAAA TGGATCTGCT GAGTGAAAAAAG AAAATTCAAG AATTTTAGAT  180  CCAGACAGTT ATTCTTTATT AGAAGATTCT ACAAGTGACT TAAGAAGCAA AAAATTCAAG  240	(ii)	MOLECULE TYPE: cDNA	
CCTCTCCTGC ATTTCAAACA CCTTCACTCA GTGTCAGCCA CAGCGGCCAC CACATAGCAG CTGGCCCCGC ACCTTCTTG GAACAGTCTG GAGATGCAAG GTCAGGGTG AAGGACTGGT 180 TCACCCTTGA AAGAAAGGAT GGCTAGGGGT AAACAACAGCA AGCAACTCCC TGGAATGCAG GGAGCCAAGA AGGCCAGCCG AGGATAAGGC TCTGCCTCCC CAACGGCGAG GGTTTCCTTT 300 CCTTCTGGTC ATTANAACTG CACAGCCCCC GGGGAGTGT TGAACATGGC AGGGTCGAAT GCCTGGCCTC GGAAGGGAA ACTTCAGCAT CCCACCCTTC TTCAGCATCT CATGGACTTT 420 CAGCTCATGG CTCTGTGGCT TGCCCTGCAG CTTCTGGTGG TAGTCAAAGG TAAGCCTGTC 480 CAACACCGCC TGTTCCTCCT CATCCAGGGT GGCCATGGAG CGCTCCTTGT TGATCTTGTC 540 AATGTCGATG GGCTCTTCCT CCTCCAGGAT GGCGTTCCAC CAATACTCGC CCACCTTGT TGATCTTGTC 540 CAGGTTCACC AAAACGCACT TCCCGGGTC GAG (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:  GAATTCGGCC AAAGAGGCCT AGTTGATTCT CAGTTCATGG TGGAGTCATT CAAGTTTATT 60 TCTGGCATCT TGGCAGCCCT GAGTGCAAF ATCTCTCTAG AAATTCCGCA AGTCAACATC 120 ATGACAAAAA TGGATCTGCT GAGTGCAAF ATCTCTCTAG AAATTCAGAA ATTTTTAGAT 180 CCAGACATGT ATTCTTTATT AGAAGATTCT ACAAGTGACT TAAGAAGCAA AAAATTCAAG 240	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:995:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 462 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:  GAATTCGGCC AAAGAGGCCT AGTTGATTCT CAGTTCATGG TGGAGTCATT CAAGTTTATT  TCTGGCATCT TGGCAGCCCT GAGTGCCATG ATCTCTCTAG AAATTCCGCA AGTCAACATC  ATGACAAAAA TGGATCTGCT GAGTAAAAAA GCAAAAAAGG AAATTGAGAA ATTTTTAGAT  180 CCAGACATGT ATTCTTTATT AGAAGATTCT ACAAGTGACT TAAGAAGCAA AAAATTCAAG  240	CCTCTCCTGC CTGGCCCGC TCACCCTTGA GGAGCCAAGA CCTTCTGGTC CGCTGGCCTC CAGCTCATGG CAACACCGCC AATGTCGATG	ATTTCAAACA CCTTCACTCA GTGTCAGCCA CAGCGGCCAC CACATAGCAG ACCTTCTCTG GAACAGTCTG GAGATGCAAG GTCAGGGTGG AAGGCCTGGT AAGAAAGGAT GGCTAGGGGT AAACAAGACG AGCAACTCCC TGGAATGCAG AGGGCAGCCG AGGATAAGGC TCTGCCTCCC CAACGGCGAG GGTTTCCTTT ATTANAACTG CACAGCCCCC GGGGAGATGT TGAACATGGC AGGGTCGAAT GGAAGGGAGA ACTTCAGCAT CCCACCCTTC TTCAGCATCT CATGGACTTT CTCTGTGGCT TGCCCTGCAG CTTCTGGTGG TAGTCAAAGG TAAGCCTGTC TGTTCCTCCT CATCCACGGT GGCCATCGAG CGCTCCTTGT TGATCTTGTC GGCTCTTCTC CCTCCAGGAT GGCGTTCCAC CAATACTCGC CCACCTTGCT	120 180 240 300 360 420 480 540 600
(A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:  GAATTCGGCC AAAGAGGCCT AGTTGATTCT CAGTTCATGG TGGAGTCATT CAAGTTTATT  TCTGGCATCT TGGCAGCCCT GAGTGCCATG ATCTCTCTAG AAATTCCGCA AGTCAACATC 120 ATGACAAAAA TGGATCTGCT GAGTAAAAAA GCAAAAAAGG AAATTGAGAA ATTTTTAGAT 180 CCAGACATGT ATTCTTTATT AGAAGATTCT ACAAGTGACT TAAGAAGCAA AAAATTCAAG 240	(2) INFORMA	ATION FOR SEQ ID NO:996:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:  GAATTCGGCC AAAGAGGCCT AGTTGATTCT CAGTTCATGG TGGAGTCATT CAAGTTTATT  TCTGGCATCT TGGCAGCCCT GAGTGCCATG ATCTCTCTAG AAATTCCGCA AGTCAACATC  ATGACAAAAA TGGATCTGCT GAGTAAAAAA GCAAAAAAGG AAATTGAGAA ATTTTTAGAT  180  CCAGACATGT ATTCTTTATT AGAAGATTCT ACAAGTGACT TAAGAAGCAA AAAATTCAAG  240	(i)	(A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
GAATTCGGCC AAAGAGGCCT AGTTGATTCT CAGTTCATGG TGGAGTCATT CAAGTTTATT  TCTGGCATCT TGGCAGCCCT GAGTGCCATG ATCTCTCTAG AAATTCCGCA AGTCAACATC  ATGACAAAAA TGGATCTGCT GAGTAAAAAA GCAAAAAAGG AAATTGAGAA ATTTTTAGAT  CCAGACATGT ATTCTTTATT AGAAGATTCT ACAAGTGACT TAAGAAGCAA AAAATTCAAG  240	(ii)	MOLECULE TYPE: cDNA	
TCTGGCATCT TGGCAGCCCT GAGTGCCATG ATCTCTCTAG AAATTCCGCA AGTCAACATC 120 ATGACAAAAA TGGATCTGCT GAGTAAAAAA GCAAAAAAGG AAATTGAGAA ATTTTTAGAT 180 CCAGACATGT ATTCTTTATT AGAAGATTCT ACAAGTGACT TAAGAAGCAA AAAATTCAAG 240	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:996:	
Simple denoting and an armount of the second	TCTGGCATCT ATGACAAAAA CCAGACATGT	TGGCAGCCCT GAGTGCCATG ATCTCTCTAG AAATTCCGCA AGTCAACATC TGGATCTGCT GAGTAAAAAA GCAAAAAAGG AAATTGAGAA ATTTTTAGAT ATTCTTTATT AGAAGATTCT ACAAGTGACT TAAGAAGCAA AAAATTCAAG	120 180

TACGATCAGT	CAGATGAAGA	AAGCATGAAC	ATTGTATTGC	AGCATATTGA	TTTTGCCATT	360
CAATATGGAG	AAGACCTAGA	ATTTAAAGAA	CCAAAGGAAC	GTGAAGATGA	GTCTTCCTCT	420
ATGTTTGACG	AATATTTTCA	AGAATGCCAG	GATGTACTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:997:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 548 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

GAATTCGGCC	AAAGAGGCCT	AGCTGGTAAC	ACATGTGAAC	TCAGGTAAAG	TCATCGAGCA	60
TTTTACTGAC	TCTATTCCTC	AATAAAGTAC	TGGGAAAAA	CTCATAAGAA	TGACAAAAAC	120
		CAGAAGCCTC				180
		AATCCGTGGA				240
		GTTGGAATCT				300
		AAAACTGGGC				360
		CATGGCTTTC				420
		AAACATCTCC				480
CACCACAGAC	GTGAAATGGC	ATCTGTCATC	TTTAGCGCCA	CCTTATGTCA	AGGGAGTTGA	540
TTCTCGAG						548

- (2) INFORMATION FOR SEQ ID NO:998:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 572 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

GAATTCGGCC	AAAGAGGCCT	AGTTTCCCTT	TCTGTATTTT	ACTACTAAAT	TAGAAAGCAC	60
TGGTTATGTA	ATAAGTTACT	ACATTGCTTT	GGTTGAGTAA	AAACAAGAGT	ATATATTTT	120
CTTGTTTCTT	ATTTNCTAAA	CCCTTAACTC	CTGCTGAGGT	CATAACAACC	TCAGTCTAAG	180
CTCTGTGTCC	ATCATACTGT	TAACTTAAAC	AAATGGGTGG	TGGGGGTGGG	AAGGGTAATA	240
CAGTCCTGCC	ATTGCCTACC	AGTAGGAGAG	TCCAAACAGA	ACACTCTTTT	GAGTAGCAAT	300
TATTTAATTT	GCCCAGTCAA	GGCACCGTGT	TTATATACTA	TTTCACATTG	AATTTGATTA	360
TGCCCTACAG	ACCTGGCTGG	TCAAGGATTT	GATATACACA	TATTGGCTTG	GGATTCGAGC	420
TTTCTTTTTT	AATAAATTAA	TATATTTAAA	ATATATTATA	TATATACATA	TATACATAGC	480
TATATCTGTA	TATATATTGG	GTATGTTTTA	AGGATTTTTT	CGCATGAGCG	CAGCTGTTGC	540
GATAAATTGA	CCGATTGGGA	GGTATTCTCG	AG			572

- (2) INFORMATION FOR SEQ ID NO:999:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 629 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

GAATTCGGCC AAAGAGGCCT	AGAGGGGAGC	ACGTCTTTTC	CTTGAGTGTA	ATTCACTAAT	60
GACTGTGGTT CCAAGGAGGT	GCGACCTTTA	AAGGGAATTG	GCCCTTCTTT	GAAGGCAGGT	120
GAGAATCTAG TCTCAGTGAC	AACCCAGCCT	GATTTGGAAG	GGGGGAGTCA	TAAGGGTTTT	180
CGCCCAGCAC ACCAGGGTTG	CAGCCTGCGC	AAGACCTTCC	ATAGCTATTT	CTGCCGGCTT	240
GCTTCCTTCC CTTCCCAGCC					300
TCCTCCCACT GGAGGCTGCC					360
GGGGTCACCC AGGCGTGAAG					420
GCGTCTCTCT GGGAATCCTG					480
CCAGTGCTGC TCTGAGAAGA					540
TCTCCCTCCA GCTAAAGCTA	GAGGGACCTC	ATTATGTGTC	TTACAAGATG	TACCCTAAAC	600
CGTCGATTGA ATTCTAGACC	CGCCTCGAG				629

## (2) INFORMATION FOR SEQ ID NO:1000:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 568 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

GAATTCGGCC AAAGAGGCCT	ACCTGTATGC	TATTAACACT	CACCACAGCA	GAGAGCTGAG	60
GATTGTGGTT GCAATTCGGA	ATAAACTGCT	TCTGATCACA	AGAAAACACA	ACAAGCCAAG	120
CGGGGTCACC AGCACCTCAT	TGTTATCTCC	CCTGTCTGAG	TCACCTGTTG	AAGAATTCCA	180
GTACATCAGG GAGATCTGTC	TGTCTGACTC	TCCCATGGTG	ANGACCTTAG	TGGATGGGCC	240
AGCTGAAGAG AGTGACAATC	TCATCTGTGT	GGCTTATCGA	CACCAATTTG	ATGTGGTGAA	300
TGAGAGCACA GGAGAAGCCT	TCAGGCTGCA	CCACGTGGAG	GCCAACAGGG	TTAATTTTGT	360
TGCAGCTATT GATGTGTACG	AAGATGGAGA	AGCTGGTTTG	CTGTTGTGTT	ACAACTACAG	420
TTGCATCTAT AAAAAGGTTT	GCCCCTTTAA	TGGTGGCTCT	TTTTTGGTTC	AACCTTCTGC	480
GTCAGATTTC CAGTTCTGTT	GGAACCAGGC	TCCCTATGCA	ATTGTCTGTG	CTTTCCCGTA	540
TCTCCTGGCC TTCACCACCG	AACTCGAG				568

## (2) INFORMATION FOR SEQ ID NO:1001:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 543 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

GAATTCGGCC	AAAGAGGCCT	AGTAATACTT	AAAGTGCAAT	TGTTCCAAGG	CTTTTGTTTC	60
CATCATCACA	AATATTATAA	AGAAAGAGCT	ATGTTTAGGG	TGAAGAAGAT	ATGGCACAAG	120
TAATATGTAA	AGAACTTATG	ACTTTCGCAT	CCTCTAGCAA	ACAGTAAGCT	GCCTGTACAG	180
CTGCACACAG	ACGGACTTTA	CACAACAAAC	TCTGGAACTT	CATCATGAGT	GAGATCCAGA	240
GAAAAGTATT	TGCTGGTTCT	TTTGACTGGA	AAAGCATCTT	GGATGTTGAT	GCACTGCTGG	300
GCCAAGCAAC	TGTTGCAATA	GAGGCCTTCC	TCATCCAGTT	CATGGCCACA	TCCAAAGGTG	360
TAACTCTGAG	CAGTGTCCTG	ACACAGACCT	GCAATGCGCA	GGAAGTCTTT	CTGGTAAAGT	420
CTGATGTCAT	CGAGGCTCAA	GCTGTGTCGA	TCAGTGGAGG	TCTTTGGTTT	CCGACATATA	480
GTCTGTGGAA	GAGAATCAGT	ACTCTGGCCA	CGAAGCTTAA	CAACTGTTTC	TGAAGAGCTC	540
GAG						543

- (2) INFORMATION FOR SEQ ID NO:1002:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 592 base pairs
    - (B) TYPE: nucleic acid .
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

GAATTCGGCC AAAGAGGCCT	AATTCCACTT	ACGAATTAAC	ACTGTGTACA	TGGCACCTTT	60
GGGCCCATCT TGCCTTGAAA					120
TCAGGACTGC AAACAGACCT					180
TCTTGTCTCA GCCGGGCTGT					240
AATCAATCTG CCCACCTCCT					300
CCTCCCAGGG CTGCCGGGCT					360
TGGGCTATGC CCCTCGAACA					420
GATATGGAGG GGACAGGAGA					480
CTCTCAAAGA GGCAAGAAAT	CTCTAAGAAT	GAAAGGAGGT	GTTTTGTTGT	TGTTGTTGTT	540
TTTTGTATGT ACTGGGAGGA	AATGGCTAAT	CTTGGGTATG	CACACGCTCG	AG	592

- (2) INFORMATION FOR SEQ ID NO:1003:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 584 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

GAATTCGGCC	AAAGAGGCCT	AGGCTCCGTC	TGTTGGGGGG	CGAACACGCC	GCGGTCCTCG	60
TCGTGTGAAG	TAAGAACTCT	GCTAGAGAGG	AAATGGCTGC	TTCATCATCA	TCCTCCTCAG	120
CTGGTGGGGT	CAGTGGAAGT	TCTGTCACTG	GATCTGGTTT	CAGTGTCTCA	GACCTTGCCC	180
CACCACGGAA	AGCCCTTTTC	ACCTACCCCA	AAGGAGCTGG	AGAGATGTTA	GAAGATGGCT	240
CTGAGAGATC	${\tt NTCTGCGAAT}$	CTGTTTTTAG	CTATCAAGTG	GCATCCACGC	TTAAACAGGT	300
GAAACATGAT	CAGCAAGTTG	CTCGGATGGA	AAAACTAGCT	GGTTTGGTAG	AAGAGCTGGA	360
GGCTGACGAG	${\tt TGGCGGTTTA}$	AGCCCATCGA	GCAGCTGCTG	GGATTCACCC	CCTCTTCAGG	420
TTGATACTGC	${\tt CTGGATGGTC}$	ACCTCTGGTG	CGCAGCAAGT	GCAAAGCCAG	TGGGGGACTT	480
TCTCACAGCT	TACATAGCCA	TCCAGAGATC	CACAGCTACG	TCACTGAATT	GTTAATGCAC	540
ATTTGTACTT	GGTTTCTCTG	TATCTATTCA	CAGGCGAACT	CGAG		584

- (2) INFORMATION FOR SEQ ID NO:1004:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 440 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

60

ACTCCAAATG ATGACATGGT	CTTATTTTAT	CTATTAACCA	TAAGCTTACA	GATTCTAGTG	120
AAGAAAAAC TTTAGGAGGC	TACATGGTCT	ATTGGAGAGT	GTAGGCTCTG	CAGTCAGAAG	180
ATCCCTACCC AGGCTTCTGT					240
CTCCTGAGGC TCTGTTTTCT					300
TCACACATGG AAATCTTATC					360
CATACCATTA ATACTTTACT	TTAGCTATGT	TTGGTATGCA	TGAGTTGATG	AGTGATTAGA	420
GTACTATGAG CGATCTCGAG					440

- (2) INFORMATION FOR SEQ ID NO:1005:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 426 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

GAATTCGGCC	TTCATGGCCT	ACTCAGTTGC	AGATTCTGGC	CAACATGGAC	AGCCAGCTAA	60
AAGAGCTACA	GAGTCAGCAT	ACCCATTGTG	CCCAGGACCT	GGCTATGAAG	GATGAGTTAC	120
TCTGCCAGCT	TACCCAGAGC	AATGAGGAGC	AGGCTGCTCA	ATGGCAAAAG	GAAGAGATGG	180
CACTAAAACA	CATGCAGGCA	GAACTGCAGC	AGCAACAAGC	TGTCCTGGCC	AAAGAGGTGC	240
GGGACCTGAA	AGAGACCTTG	GAGTTTGCAG	ACCAGGAGAA	TCAGGTTGCT	CACCTGGAGC	300
		TTGAAAACCA				360
		ACTGTAGAGA				420
CTCGAG		,				
CICGAG						426

- (2) INFORMATION FOR SEQ ID NO:1006:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 402 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

GAATTCGGCC	TTCATGGCCT	AGAGTAGCCA	GGGAGCTGGA	AGTTCCACAG	ATTGGTTTTA	60
ATAAACAAAC	TCCCTCAATG	ATGAGTGGTC	TTTTGAAGAG	CATGGTTAGA	ACTTGGGATT	120
GTGCTTCTCA	TGACTACAAA	TGTACTTGTA	GCTTAGGTGC	AAAAGGGTAG	GTCAGTGGGT	180
AGCTAACTAC	TGAGGATTGA	TTTTCCTGAC	GCTGGTGTTT	AAGTGTCACC	CAGAACTGGC	240
ATATAAAGTG	GCTCATTCAC	CCAAGTATCT	TCCTTTCCTT	TTTACAAAAT	CCTTGGCTGT	300
TGTGGGGCCT	ACATCTCTTC	ATGATTATTA	TTGCATCTGG	TGTCATGTTT	TTCCAGCTGG	360
TGTACTGCTT	CCCTGTAGGC	TTCTTGATGT	TCACTCCTCG	AG		402

- (2) INFORMATION FOR SEQ ID NO:1007:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 456 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

```
GAATTCGGCC TTCATGGCCT ACTGGTGCCA CGGGAGGCAG ACACCAAGTT CTGGGGTCTC 60
CAGCTGCAGT GGGTGGCGC CAATTGCTTC TCTCTGTCCA GACTAATGAG AACATGGAGA 120
TCACCAGTGC ACTGCAGTTG GAATAGCACG TAAAGAGGGA GCTCGGAAAG AAGCTGGGCA 240
AGCTAAAGGA GCAGAGGCA GCTCAGCCT GGGGGAAAG GCACCAGCCT 240
CTGGGGAGGG GAGTGCTAA GCCAGAGGCA GCTCCAGCC GGGGGAAAG TAAGCCCCAGC 300
ACCCTCCCAGG GCAGTCCTGT GACTGTTCT TGCTTCCCGC CCTCTGACAT TTAGTGGTGG 360
GTTCGTTCTT CCTAGGTCTG GACATCATCA TCCCAGCTG AGTCATGGAG CCTCCCAAAC 420
ATAGGGAAAG AGATGGTGGT ATAAGAGGCT CTCGAG
```

- (2) INFORMATION FOR SEQ ID NO:1008:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 564 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

GAATTCGGCC AAAGAGGCCT	AGGATGGCTG	TGTTTGACGG	GTGTTGCTCG	TGACAGTTGG	60
GGTCCTCCTC AGCATCAGTC	TTGACATGGC	TGCAACTGGG	GGGGTCCTCG	GGATCCTCCC	120
GGAATCTCTT CCTCAGCATI	CGCTCATGAT	AAGGTTTCAG	GTGTCTTGAT	GGTTCAGTCC	180
TGGAGAAACA TAAGCATAAC	CTCTACCCCA	AGTTATTATT	TTACCTATTT	CCCAACTTTC	240
TGTTATCAGG TCTCTCCACC	AAACCAGTTG	TTCTGCTTCT	GTCTTTGCAG	CTGGTTTCTG	300
TAGATGCTGT TCAGCTGCTG					360
TAATAATGCG ATTCAATTGC	TTATGGGGTG	TCCTGTAGTA	CCTGTTTTCC	CCCTTTTGCT	420
TCTGCAACTG CTGTTTCAGG					480
TATATGGGAT ATCAGTAATG	TGTTTAATAT	TCCGTATAGA	GAAAAATTTA	GCTAGAGCTT	540
GAGAATTAGG TTCCAATCCT	CGAG				564

- (2) INFORMATION FOR SEQ ID NO:1009:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 661 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

```
GAATTCGGCC AAAGAGGCCT AGAAAAAGAT GTCATTCCGT AAAGTAAACA TCATCATCTT
GGTCCTGGCT GTTGCTCTCT TCTTACTGGT TTTGCACCAT AACTTCCTCA GCTTGAGCAG
                                                                      120
TTTGTTAAGG AATGAGGTTA CAGATTCAGG AATTGTAGGG CCTCAACCTA TAGACTTTGT
                                                                      180
CCCAAATGCT CTCCGACATG CAGTAGATGG GAGACAAGAG GAGATTCCTG TGGTCATCGC
                                                                      240
TGCATCTGAA GACAGGCTTG GGGGGGCCAT TGCAGCTATA AACAGCATTC AGCACAACAC
                                                                      300
TCGCTCCAAT GTGATTTTCT ACATTGTTAC TCTCAACAAT ACAGCAGACC ATCTCCGGTC
                                                                      360
CTGGCTCAAC AGTGATTCCC TGAAAAGCAT CAGATACAAA ATTGTCAATT TTGACCCTAA
                                                                      420
ACTITIGGAA GGAAAAGTAA AGGAGGATCC TGACCAGGGG GAATCCATGA AACCTITAAC
                                                                      480
CTTTGCAAGG TTCTACTTGC CAATTCTGGT TCCCAGCGCA AAGAAGGCCA TATACATGGA
                                                                      540
TGATGATGTA ATTGTGCAAG GTGATATTCT TGCCCTTTAC AATACAGCAC TGAAGCCAGG
                                                                      600
ACATGCAGCT GCATTTTCAG AAGATTGTGA TTCAGCCTCT ACTAAAGTTG TCGATCTCGA
                                                                      660
                                                                      661
```

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:	
GAATTCGGCC TTCATGGCCT AGGAAAGATT TGACTGCTTC TCTCATGCAG GGGAATAAAG CAAAGGCACG TGCAGAGGGA AGTAGGGGTA GAGAGAGGCA AGTTAGCTTC AGAGAGATTT ATTTGCACCC AGTTCTGTTC TACTCAGCCT GACGTTTTAT CATCTTTTTG AAAAGTGGCG TGAAGTGGTT TGGAACACAT CAGAGGGTGA AGCCGAGCAA ATCTGAAAGA GAGCAGAGGA TTTCATATGA TATCCTATGT GTGCTTTCCC CTTCCTTCTT AGGAGCTGGA AGAGGCAGAA TTGATGTCCA CTCGAG	60 120 180 240 300 316
(2) INFORMATION FOR SEQ ID NO:1011:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 244 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:	
GAATTCGGCC TTCATGGCCT AGAAACATGC TAGACATTTT GAAGAACCAG CAAGAATGTT AGTGTAGCCA ACAGTGAGGC AGGCAAAGGT GAGTAAGGTA GATTAGTTCA GGGAAGAAAA CATAACATTA TTTAATCCAT TGTGGGCCAC ATTGCACTAT GATAACACTA TCATGTCATA GAGTCTCACC ATTGTTTAAG ATGTTTAAAT TTTTTAATAC GAATATATTC TCACACCCCT CGAG	60 120 180 240 244
(2) INFORMATION FOR SEQ ID NO:1012:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 355 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:	
GAATTCGGCC TTCATGGCCT AGCACTTCCC GAGACTCTCT AGCCTTGGAT AAAGAGAGAA TGGATAAAGA TCTGGGATCT GTGCAGGGAT TTGAAGATAC AAATAAATCC GAGAGAACTG AGAGTCTGGA AGGAGATGAC GAGTCCAAGT TAGATGATGC ACATTCATTA GGCTCTGGTG CTGGAGAAAGG ATACGAGCCA ATCAGTGATG ACGAACTACA TGAAATTCTG GCAGGTGATG CAGAAAAGAG GGAGGACCAA CAGGATGAGG AGAAGATGCC AGATCCCTTA GATGTGATAG ATGTGGATTG GTCTGGTCTT ATGCCAAAGC ATCCAAAAGA ACAACGAGGC TCGAG	60 120 180 240 300 355
(2) INFORMATION FOR SEQ ID NO:1013:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 351 base pairs  (B) TYPE: nucleic acid	

(C)	STRANDEDNESS: double	
(D)	TOPOLOGY: linear	

PCT/US98/06956

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

GAATTCGGCC	TTCATGGCCT	ACAGCCTAAA	TGTTTTATTT	CCTGAGAGGC	TGGAATCTGT	60
ATTTGTGGTA	TCAATCAGTC	AACTGAAATT	TATTAAATGC	CTGCTGTGAG	CAAGGCCTAA	120
TGCTGAGGGA	TGTAAAGAAG	AGTGAGAAGC	TAGTCTGGTT	GGGGTNATAT	GACATGGCAA	180
GTCATAGAAT	GAAGAAGCGT	ATTCCTTGTC	ATATGAAAGC	TGCAGATTAG	TGTGGTTCTA	240
AGTAGAGGCC	AGGGTCACTG	GAGTCTAGGA	TTGCAGGGTT	GGCTGGCTTC	CCAGAGGCTA	300
AGAATTTAAT	TTGGATCTTG	AAGATCTGGT	CCAATTCCAA	CANGACTCGA	G	351

- (2) INFORMATION FOR SEQ ID NO:1014:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

GAATTCGGCC	TTCATGGCCT	AGGCCTTGTA	TTTTTTTTTA	TTTTCTGCTA	AATTAGAAAG	60
AAATTTGCTG	TTTCAAATAT	ACTCAAGCTG	TTCAGTTCTT	CAACAAAAAG	TAGGTGACTG	120
AAAACTGTAT	GTTTAACTAT	GCTTAAGTTA	ATATTTATAG	TAATGATAGA	AGCCATTTTA	180
TTGGCAATAT	ATCACTTCCT	GATTTCCACA	CCAGGCATTC	CCACATGCAC	AAACAGGTGT	240
GTGGGAGGAA	GGGAAATGGG	CAAAAATGAT	TTCCTTCAAG	AGGCTACTGA	GAATGAAAAC	300
TCAAAATCTG	CACAAATAGG	GGTGGTGGAA	GGAGAGAAAG	AAAACTCCAT	GCCAGAAATA	360
ACATGCTTAG	CAGAGAGAGA	GAGAGATCTC	GAG			393

- (2) INFORMATION FOR SEQ ID NO:1015:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 262 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

${\tt GAATTCGGCC}$	TTCATGGCCT	AACTCAGTTG	GCTTCTAATT	TGCGTAACAA	GATTAAGGTA	60
${\tt GTATTTTGT}$	ACTATTATTG	GAAGCATGCC	TTCCCTTTTT	CACATTATTA	AATTGTATTT	120
ATATTTGTGC	AATTTTAAAC	TATGTTTTCA	AATAAACTTT	GTCTGCGGCT	TCGAGGTCTT	180
TTCAGGAATC	TTTCAAAATG	GGATTTGGGG	ATCAGAACTC	CTTCTGATCA	AATGGAATCC	240
AATTTGTACT	ACTGGTCTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:1016:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

CAGAATGGGA	CTCCAAGCCT	GNCTCCTAGG	GCTCTTTGCC	CTCATCCTCT	CTGGCAAATG	60
CAGTTACAGC	CCGGAGCCCG	ACCAGCGGAG	GACGCTGCCC	CCAGGCTGGG	TGTCCCTGGG	120
CCGTGCGGAC	CCTGAGGAAG	AGCTGAGTCT	CACCTTTGCC	CTGAGACAGC	AGAATGTGGA	180
AAGACTCTCG	GAGCTGGTGC	AGGCTGTGTC	GGATCCCAGC	TCTCCTCAAT	ACGGAAAATA	240
CCTGACCCTA	${\tt GAGAATGTGG}$	CTGATCTGGT	GAGGCCATCC	CCACTGACCC	TCCACACGCT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:1017:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 355 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

GAATTCGGCC	AAAGAGGCCT	AGTTTAAAGA	AAAAAAAAA	GACCCATCAA	GGGCATAGAA	60
AAGCTTAGGT	GAAGAAACCC	TAAAATGAAT	CCTCATTTAT	CAACTCATTC	ATTTATTGAT	120
${\tt TCATTTGTTC}$	ATTCATTTGT	TCACTCAAGA	AGTATTTGTT	GCCAGACACA	GTACCAACAA	180
AGAAAATAAG	CATCCACTAC	GGCTTTGCAG	AGCTTGGTAC	GCAATGCCTG	GTTCAGAGGA	240
GATATTTGTT	CATCGCTTGC	TTTTAACTGT	ATCACAGCCT	AGGGTGGCAT	GCAGAGGTTT	300
GAATAAGTGC	TGAAACAGGA	CAAGTGAGGT	GCTTATGGAA	ACACACAGGC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:1018:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 502 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

GAATTCGGCC	AAAGAGGCCT	AGAAGGAAAT	TGTCCCGAAT	CCCTGCAGTC	TTTCTGTAGG	60
TTGCGGCACA	ACGCCAGGCA	AAAGAAGAGG	AAGGAATTTA	ATCCTAATCG	GTGGAGGTCG	120
ATTTGAGGGT	CTGCTGTAGC	AGGTGGCTCC	GCTTGAAGCG	AGGGAGGAAG	TTTCCTCCGA	180
TCAGTAGAGA	TTGGAAAGAT	TGTTGGGAGT	GGCACACCAC	TAGGGAAAAG	AAGAAGGGC	240
GAACTGCTTG	TCTTGAGGAG	GTCAACCCCC	AGAATCAGCT	CTTGTGGCCT	TGAAGTGGCT	300
GAAGACGATC	ACCCTCCACA	GGCTTGAGCC	CAGTCCCACA	GCCTTCCTCC	CCCAGCCTGA	360
GTGACTACTC	TATTCCTTGG	TCCCTGCTAT	TGTCGGGGAC	GATTGCATGG	GCTACGCCAG	420
GAAAGTAGGC	TGGGTGACCG	CAGGCCTGGT	GATTGGGGCT	GGCGCCTGCT	ATTGCATTTA	480
TAGACTGACT	AGGGGGCTCG	AG				502

- (2) INFORMATION FOR SEQ ID NO:1019:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 465 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

GAATTCGGCC	AAAGAGGCCT	AATCAAATAG	TAAAGGCTGT	TCTGGCTTTT	TATCTTCTTA	60
GCTCATCTTA	AATAAGTAGT	ACACTTGGAT	GCAGTGCGTC	TGAAGTGCTA	ATCAGTTGTA	120
ACAATAGCAC	AAATCGAACT	TAGGATTTGT	TTCTTCTCTT	CTGTGTTTCG	ATTTTTGATC	180
AATTCTTTAA	TTTTGGAAGC	CTATAATACA	GTTTTCTATT	CTTGGAGATA	TAAATTAAAA	240
GGATCACTGA	TATTTTAGTC	ATTCTGCTTC	TCATCTAAAT	ATTTCCATAT	TCTGTATTAG	300
GAGAAAATTA	CCCTCCCAGC	ACCAGCCCCC	CTCTCAAACC	CCCAACCCAA	AACCAAGCAT	360
TTTGGAATGA	GTCTCCTTTA	GTTTCAGAGT	GTGGATTGTA	TAACCCATAT	ACTCTTCGAT	420
GTACTTGTTT	GGTTTGGTAT	TAATTTGACT	GTGCACGATC	TCGAG		465

- (2) INFORMATION FOR SEQ ID NO:1020:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 243 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

GAATTCGGCC	TTCATGGCCT	AGGATTTCGT	ATGCAAGCTC	TTGTTTCTCA	GGCTGCCTGC	60
AGAAGAAGTC	GCTATAAATT	ATCTGTTGTC	TACATGGTAC	AAGGCCCATT	GACTCATCTG	120
ATGCTTGTTT	TGTTAATTTC	TTTAATATTT	TTATCACGGG	GCAGTGGGAG	GGCTTGGGCT	180
TTTAGCCACA	GCTGTTTTAA	GACTTCTGAT	CTCCTGCCCT	GCAGGAATAG	GTGGCAACTC	240
GAG						243

- (2) INFORMATION FOR SEQ ID NO:1021:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 442 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

CTCCACCGAG	AGCCTGGACA	GTATGAAGGC	TCTGACAGCC	GCCATCGAAG	CTGCAAACGC	60
CCAGATCCAT	$\tt GGCCCTGCCA$	GTCAACACAT	GGGCAATAAC	ACTGCCACCG	TCACCACCAC	120
GACTACCATA	GCCACCGTCA	CCACGGAGGA	CAGGAAGAAG	GACCACTTTA	AGAAAAATCG	180
ATGCCTGTCT	ATCGGGATAC	AGGTGGATGA	TGCTGAAGAA	CCTGACAAAA	CAGGGGAGAA	240
TAAAGCACCC	AGTAAGTTCC	AGTCCGTGGG	AGTGCAAGTA	GAAGAAGAGA	AGTGCTTCCG	300
CAGGTTCACT	CGATCCAACA	GTGTGACGAC	AGCAGTACAG	GCCGACCTGG	ACTTCCATGA	360
TAATCTGGAA	AATTCTCTGG	AATCTATAGA	GGACAATTCG	TGTCCTGGCC	CCATGGCCAG	420
ACAGTTCTCC	CGCGATCTCG	AG				442

- (2) INFORMATION FOR SEQ ID NO:1022:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 274 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

GAATTCGGCC TTCATGGCCT AGATGATCAG	GTTTTTCTGG	ATGGAAATGA	GGTGTATGTA	60
TGGATCTATG ACCCAGTTCA CTTTAAAACA	TTTGTCATGG	GATTAATTCT	TGTGATTGCA	120
GTAATAGCGG CCACCCTCTT CCCCCTTTGG	CCAGCAGAAA	TGAGAGTAGG	TGTTTATTAC	180
CTCAGTGTGG GTGCAGGCTG TTTTGTAGCC	AGTATTCTTC	TCCTTGCTGT	TGCTCGATGC	240
ATTCTATTTC TCATCATTTG GCTCATAACT	CGAG			274

- (2) INFORMATION FOR SEQ ID NO:1023:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 196 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

GAATTCGGCC	TTCATGGCCT	ACTITICCAG	AAACCAAGAG	TGGCTCTACT	GTGGCTATAT	60
TATTATTGTT	ATTATTATTA	TTTTGGAGAT	GGGGTCTCAC	TTTGTCATCC	AGGCTGGAGA	120
GCAGTGGCAC	CATCATAGCT	CACTACAGCC	CCAAACTGCT	GTGCTCAAGG	GATCCTCCTG	180
TCTCAGCCTT	CTCGAG					196

- (2) INFORMATION FOR SEQ ID NO:1024:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 395 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

GAATTCGGCC	TTCATGGCCT	AATCATTTAT	ATAAAGTTTA	AAAACATTTC	AGAACTGAAC	60
TATATATTTT	TAGAAATATC	TGCATATGCC	ACATAAATTT	TTAAAATCAT	AAGAATGCTA	120
AACAGCACAT	TCAGGACAGG	GTGAAGAAAC	AGGCATGCAG	GTTGTGCAGT	AGGAAGCTGG	180
GTAACATTGT	TCCTTATGGC	TTTGTTGTCG	CTTCCAGAAT	TTCATTAAAA	ACTTTTTAAA	240
AAACATGGGC	CCACATTATG	AATTACGTCT	GCTTTTAGAG	TACTAAAAAC	TCCAAGCAAA	300
AACACATGAG	CCACCGGGCA	CGCCTGGCCT	TTATTTTATT	TTTCTACGTT	ATTATTCCTG	360
TTTTCAGAGG	AGGGAATTGT	CAGGGAACTC	TCGAG			395

- (2) INFORMATION FOR SEQ ID NO:1025:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 429 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

GGAGAGCTCT	GGGCCAGCCC	TTCTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	60
CTCTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	CTCTGTGTGT	GTATATATAT	ATATATANAC	120
TTTTCCCTTC	TGGATGCAAT	AGAGCTATTT	TTTTCTCTTT	GGAATTGAGT	GACACCACCA	180
AGATACGTTT	TTGGGTTGAA	TATGTGTGTT	TTTCAAAATT	CAGTCTGGCC	TTTTTTGTTG	240
TTGTTGTTGT	TGTTTTCTTT	AGATGGAGTT	TCACTCTTGT	TGCCCAGTCT	GGAGTGCAAT	300
GGCACTATCT	CTACTCACTG	CTACCTCCGC	CTCCCAGGTT	CAAGCAATTC	TCCTGCCTCA	360
GCCTCCCAAG	TAGCTGGGAT	TATAGGCATG	TGCCACCATG	CCCAGGCAGT	TTTTGTATTT	420
AGTCTCGAG						429

- (2) INFORMATION FOR SEQ ID NO:1026:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 407 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

${\tt GAATTCGGCC}$	TTCATGGCCT	AGAGAACTGG	AGCCAGCTGT	CAACTGCCCC	CGCCCCACCC	60
${\tt AGGCCATTTG}$	GCTTCTGCTA	CCGGCATGCT	GCTCAGGGCT	CTGCCCAAGG	ACAACGACGA	120
GCCCCCTGTG	TCCTCTCCTG	GGTCATCTTC	CATGACCCTG	AGGCAGCGAA	GACAAGCTCG	180
GCAGCTCCCT	${\tt GAGCTGCTTC}$	ACACCAACTA	CCTATGAGTC	TGAGGCCAGC	ATCCAGGCGC	240
TGCCCAGACC	CTGAGAGTCC	CTGGACCATG	ACGTAGCCTG	TGTGTGAAGG	GAGCAAGACA	300
GCCTTGACAG	AAGCACAGAG	AACGCCACTG	GGATTCTTAA	AGACGCGAAG	GGAAAAAGCA	360
CAGAAGATGC	TGGCGCTGCA	TCTCCTCCAG	CACCGAGAGG	CCTCGAG		407

- (2) INFORMATION FOR SEQ ID NO:1027:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 402 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

GAATTCGGCC	TTCATGGCCT	TATAATTAAA	CCTTATTTTT	GCAGATTAGG	AAACTAAGAC	60
GTACTGAGGC	TGGGTGCCTG	GTTCAAGATC	ATATAGCTAA	CATTATTGGA	CATGCAAATC	120
AAGCCCAGAT	TTGTGACTCT	${\tt GAGCTGATGT}$	TAATTCTGTC	ACAATATTGG	TTCTCAAGAT	180
AAATCTTTCC	AGGTGAGGGG	GAAAGGGAAT	AAATATCTAG	AAGTCCCCTT	AAACAGAAGT	240
AATTAATTCG	TTTGCAGAAA	TTGGCAAAAT	TTGGGGTTCC	CTTCTTAAAA	GTTTCCTTCT	300
GTCACTTGGA	AAAAATTTAA	AATATGTGCA	TTAGGTTGAC	AAAGATCAAA	AAAGTTAAAA	360
AAAAACCCTT	TTTGGAATGC	TGTGGAGAAA	GTAGCACTCG	AG		402

- (2) INFORMATION FOR SEQ ID NO:1028:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 320 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

AAAATAGATT CTGAGGCAGG CATCTCTACT CTACATGGGA	TTCATGGCCT AAGGGGCTGA AATT ATTTGGCTGG ATGTGGTGGC TCAC CAGATCACCT GAGGTAAGGA GTTC AAAAATACAA AAAATTAGCC AGGT GGCTGAGGCA GGAGACTCAC TTGA	GCCTGT AATCCTAGCA AAGACA AGCATGTCCT GTGGTG GCAGGTTCCT	TTTTGGGAGG GGTGAAACCC GTAGTCCCAG	60 120 180 240 300
GAATTCAATT	AGGCCATGAA			320
(2) INFORMA	TION FOR SEQ ID NO:1029:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 252 base pai  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		,	
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:1029:		
CCTGCATTTT TCAACTAGTT	GCTCTCATCC CATATCTATT GAGA ATTAAAATCC CTCCAGGTGA TTCT TTCATAAAGA AAACCTCTGG AGGG TTGAGATCTA GGTTATCTGC CAAG AG	GATGCA GGCTAGTTCA CCCATA GTGCCTGCAC	GTAAACAATA TCCAGGTCTC	60 120 180 240 252
(2) INFORMA	TION FOR SEQ ID NO:1030:			
(i) <i>i</i>	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 280 base pai  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:1030:		
TTGTTTTTAA CATATTTTAT TATCCTCTTA	TTCATGGCCT ACCTTATGGC CTAA ATGATTTCTT GTAATAGACT ATTG GTCATGTTAA TGATAAATTT TCTG GGTGGCCTTG GGGGACTTGC AGGT GAACTACAGA GTCAGATGCA GCAT	GGTCAG CTAATACTTT ACTTTG ATTTGTATGT CTGAGT AGCTTGGGTT	TTTGCATCTT TTTTGCCCTT	60 120 180 240 280
(2) INFORMA	TION FOR SEQ ID NO:1031:			
(i) [*]	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 291 base pai  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:1031:		
GACCATTATT	TTCATGGCCT AGAGCAAGTG GTTT TTTTAATGAC AGAACCTCCA CTCA TGTTTGAATC ATTTAACGTA CCAG	ATACAC CAGAAAACAG	AGAGTATCTT	60 120 180
			~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	

CTGGCCTTGG CGGCATCTTG GACATCTCGA CAAGTGGGTG AACGTACGTT AACGGGGATA GTCATTGACA GCGGAGATGG AGTCACCCAT GTTATCCCAG TGGCTCTCGA G	240 291
(2) INFORMATION FOR SEQ ID NO:1032:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 277 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:	
TAAAATAATT TAACTTTTT ATTACATTAA AAAACAGGAC TCTGGGAATT GTCACTTTAT GATCAGCCTT ATATTTTTC CAGACTGTGT CATTGTGTAT GCCTGTGCCA CCCAACGGAT GAGACCACTG ATCATGTTTA GCTCAAATTT ATGTTGGATA GAGGTTATAG GATGGTCCTT ATCTGAATGC AGAAAGGAAT GTTTATTTTG CTGTTATGTT TTATATGGGA TAATACTTTA TAATTGTGTG ACTATCCTAT TCCCCCAACAA ACTCGAG	60 120 180 240 277
(2) INFORMATION FOR SEQ ID NO:1033:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 298 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:	
GAATTCGGCC TTCATGGCCT AGGTTACATG TATAAAATAA TCGTAGCTGT TAATCAAACT GATCATTTGC TATTTGTTGT TTCACATGTT TTCATTTATT TGTTCATTCA GCAAACACTT AGTTGTTGC CAGGAATTAA AATCCAGTGT TGTTCTTTTC TTATTTTTT TTTGGCTAGT GGAAAATGAA AACCACTGTG ACTTTGTAAA GCTGCGGGAA ATGCTCATTT GTACAAATAT GGAGGACCTG CGAGAGCAGA CCCATACCAG GCACTATGAG CTTTACAGGC ATCTCGAG	60 120 180 240 298
(2) INFORMATION FOR SEQ ID NO:1034:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 339 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:	
GAATTCTGGA AGACACTGAC TGACTGGAAG ACCTGGATTT CTTTCTGGAA GACACTGATT GACTGGAAGA CCTGGATTC TTTCTGGAAG ACACTGATTG ACTGGAAGAT CTAGATTTT CTGGAAGAAC TAGATTTACT GGAAGACTTG GATTTGGTGG AAGACGTAGA TTTTTCTGGA AGACACTGAC TGACTGGAAGA ACCTGGATTT CTTTCTGGAA GACACTGATT GACTGGAAGA CCTGGATTTC TTTCTGGAAG ACACTGATTG ACTGGAAGAT CTAGATTTTT CTGGAAGAAC TAGATTTACT GGAAGACTTG GTAGGCCATG AAGGTCGAG  (2) INFORMATION FOR SEQ ID NO:1035:	60 120 180 240 300 339

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 263 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:	
GAATTCGGCC AAAGAGGCCT AGCACTGTAA AGATGAAGCT GGCTAACTGG TACTGGCTGA GCTCAGCTGT TCTTGCCACT TACGGTTTTT TGGTTGTGGC AAACAATGAA ACAGAGGAAA TTAAAGATGA AAGAGCAAAG GATGTCTGCC CAGTGAGACT AGAAAGCAGA GGGAAATGCG AAGAGCAGG GGAGTGCCCC TACCAGGTAA GCCTGCCCCC CTTGACTATT CAGCTCCCGA AGCAATTCAG CAGAGATCTC GAG	60 120 180 240 263
(2) INFORMATION FOR SEQ ID NO:1036:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:	
GAATTCGGCC AAAGAGGCCT AAAGCACCCG CTTCCTCACC ACCCCCACTG TTGGGCCTAT AGTAGCAGGT TAGTGAGTAC CTAGGGCGGC TCAACTCCTC CCACAGCACC AACCCAGCAT GGTCCCACTG AAGTCCTACT ACGCCCTCCC CTCCCCAGCC TTTTCCAGAA ACCATACTGG GCTCAGATCA GAGCTCCGAA GCGGTCAAAG TGAGCTGAGC	120 180
(2) INFORMATION FOR SEQ ID NO:1037:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 285 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:	
GAATTCGGCC AAAGAGGCCT ACGGAGCTGT CAGCCAGGGG AGTGGGGTCA GCCGTCAGCC AGCCCTCCCG TTTCCCGCCC GTGGGCCCTG ACCACACTCC CTTTTCTAGA AGTCAATCCT AAGGTTTCTC TGCTCTGGCT AAGAGGATGT AAATTTGGAT TCTTAGAGGG CATGGCACCC CCAGTCCCTG CCCAGATAAA GTAGCACAGT GGCATGCAC ACCTCTGTCT GTTGCTGACG TTGGGGGGCT TACACACCCA CCTCATCTCC GTGCACAGAC TCGAG	60 120 180 240 285
(2) INFORMATION FOR SEQ ID NO:1038:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 291 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

GAATTCGGCC TTCATGGCCT	AGCTCTGCAA	GGAAGAGAGC	TTCACGTCTC	TGGTCAGCCA	60
AGCGAGGCTG TCTCTCCAGC	TCTCAGAGAG	CTCTCGGGGC	TCTCCTGCAG	GAGACCAGGC	120
CAATGCTCCT GTGCTTCCTG	GGGCCAGTAG	CAGCACCCTG	AGCTCCCTGC	CACCAGGCAG	180
CTGAAAGGCA TAGCGTGAGG	TGCTTCTCTC	AGTCCCAATT	ATGACAGTGG	CCACCGGAGA	240
CCCAGCAGAC GAGGCTGCTG	CCCTCCCTGG	GCACCCACAG	GACGCCTCGA	G	291

- (2) INFORMATION FOR SEQ ID NO:1039:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

GAATTCGGCC	TTCATGGCCT	AACTCTACAG	CAGTGCTTAT	TTTTACATTT	CCAAGCGAAT	60
ACCAAAACCT	TCAGCAAAGA	TTGGGTTGGT	ATTAACGGGT	TTTTGTCTCA	GAACTGTATT	120
GTGGATCCCG	GAGTTTCCCC	CAAATCCATC	TACATCAAAT	TTGTAGAAGT	AGAGAGGGAT	180
TTTCTTTCCG	CAGGCTCTTT	AGTTGAGTGC	CTGGAAAAAG	CCATTGGATA	CCCCTTAAAA	240
TTTAACAACT	GAATGTCATC	CTTCATAAGG	ATTTGGGCTC	TTAGCTCCTT	CTTCTCTACT	300
CACTTCCCAT	TACCCGGACC	ACCCCTCATC	CAGATGCCGC	CGTCAGACTC	TTCATGGAAA	360
CCCTTTCTTC	AATTGGGCCA	GTACGATCTC	GAG			393

- (2) INFORMATION FOR SEQ ID NO:1040:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 603 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

GAATTCGGCC AAAGAGGCCT	ACCCTACTGT	GACACACCTA	CCATGCGGAC	ACTCTTCAAC	60
CTCCTCTGGC TTGCCCTGGG	CTGCAGCCCT	GTTCACACTA	CCCTGTCAAA	GTCAGATGCC	120
AAAAAAGCCG CCTCAAAGAG	GCTGCTGGAG	AAGAGTCAGT	TTTCAGATAA	GCCGGTGCAA	180
GACCGGGGTT TGGTGGTGA	GGACCTCAAA	GCTGAGAGTG	TGGTTCTTGA	GCATCGCAGC	240
TACTGCTCGG CAAAGGCCCC	GGACAGACAC	TTTGCTGGGG	ATGTACTGGG	CTATGTCACT	300
CCATGGAACA GCCATGGCT	CGATGTCACC	AAGGTCTTTG	GGAGCAAGTT	CACACAGATC	360
TCACCCGTCT GGCTGCAGCT	GAAGAGACGT	GGCCGTGAGA	TGTTTGAGGT	CACGGGCCTC	420
CACGACGTGG ACCAAGGGT	GATGCGAGCT	GTCAGGAAGC	ATGCCAAGGG	CCTGCACATA	480
GTGCCTCGGC TCCTGTTTG	GGACTGGACT	TACGATGATT	TCCGGAACGT	CTTAGACAGT	540
GAGGATGAGA TAGAGGAGC	GAGCAAGACC	GTGGTCCAGG	TGGCAAAGAA	CCAGCATCTC	600
GAG					603

- (2) INFORMATION FOR SEQ ID NO:1041:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 292 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

GAATTCGGCC	TTCATGGCCT	ATAGAAACAT	CAGTGGGCAC	ATTTACAACC	AGAATGTATC	60
CCAGAAGGAC	TGCAACTGCC	TGCACGTGGT	GGAGCCCATG	CCAGTGCCTG	GCCATGACGT	120
GGAGGCCTAC	TGCCTGCTGT	GCGAGTGCAG	GTACGAGGAG	CGCAGCACCA	CCACCATCAA	180
GGTCATCATT	GTCATCTACC	TGTCCGTGGT	GGGTGCCCTG	TTGCTCTACA	TGGCCTTCCT	240
GATGCTGGTG	GACCCTCTGA	TCCGAAAGCC	GGATGCACAC	ACTGAGCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:1042:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 331 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

GAAGAAAAGC	AGAAAGAACT	GGCAGAAACA	GAACCCAAAT	TCAACAGTGT	GAAAGAGAAA	60
GAAGAACGAG	GAATTGCTAG	ATTGGCTCAA	GCTACCCAGG	AAAGAACGGA	TCTTTATGCA	120
AAGCAGGGTC	GAGGAAGCCA	GTTTACATCA	AAAGAAGAAA	GGGATAAGTG	GATTAAAAAG	180
GAACTCAAGT	CTTTAGATCA	GGCTATTAAT	GACAAGAAAA	GACAGATTGC	TGCTATACAT	240
AAGGATTTGG	AAGACACTGA	AGCAAATAAA	GAGAAAAATC	TGGAGCAGTA	TAATAAACTG	300
GACCAGGATC	TTAATGAAGT	CAAAGCTCGA	G			331

- (2) INFORMATION FOR SEQ ID NO:1043:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 268 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

GATGGCCACT	TCCCAGGCTG	ACATAGAGAC	CGACCCAGGT	ATCTCTGAAC	CTGACGGTGC	60
AACTGCACAG	ACATCAGCAG	ATGGTTCCCA	GGCTCAGAAT	CTGGAGTCCC	GGACAATAAT	120
TCGGGGCAAG	AGGACCCGCA	AGATTAATAA	CTTGAATGTT	GAAGAGAACA	GCAGTGGGGA	180
TCAGAGGCGG	GCCCCACTGG	CTGCAGGGAC	CTGGAGGTCT	GCACCAGTTC	CAGTGACCAC	240
TCAGAACCCA	CCTGACGCAC	CCCTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:1044:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 391 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

GTCATTGCAT	CCAAGATAAT	GAAATATCTA	TAACCCCAAA	AGTTTCCTGT	GTECCCTTGT	60
TATTCATTGC	CCTGCCCAGT	ATTCAGGCAA	CACGGATCTG	TTTTCTGTTT	TAGGTTAGTT	120
					TCATGGGCCG	180
					ACAGCGTTGC	240
		ATTTGATTGT				300
				TCTTCCAGTT	TGGGGCCATT	360
ACAAATAGAG	GTACTATGAA	CTTTTCTCGA	G			391

- (2) INFORMATION FOR SEQ ID NO:1045:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 288 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

GAATTCGGCC	TTCATGGCCT	AATGTGAGCC	ACCGCACCCA	GCCGAATATT	TGTACTTTGT	60
ATAAATTCAT	TGTCTGTTTT	ACAGTTTGAA	TGGCTCTTTT	ACCCTGGCAT	AATTTTGTAA	120
CGTGTGGAGC	ATTTGGAAAA	TTTTTTTTGG	ATTATGCAGA	TATTTTCAAT	GCTGGTATTT	180
CATTATATGA	TAGTAAAAA	TCACTTTTTG	TTTTGTTTTG	TTTTGTTTAT	TTTTCTTTTT	240
TTTTTGAGGC	AGAGTTTCGT	GCTTGTCGCC	CAGCCGAAGG	CGCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:1046:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 279 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

GAATTCGGCC	TTCATGGCCT	AGTAACTTCA	TAACATTGCT	GGTGTTGAGG	TGAATCTTAG	60
TGGTCATCCA	${\tt GTCCCAAGGC}$	ATCCTTGCCA	GCCCCTACA	ATACCTGGAT	GGGCGCTTAT	120
CTTCAGGTAG	GCCTGAGCCT	TTCTGGTAAA	GAGGAGCTCA	CTATTTCTAA	AGGAAACCTG	180
TGCCATTGGG	TTAAAAAAGT	ATTAATTTT	AAACATTGGT	AGTTGTTAAG	CAGTTGTTGA	240
ATATTTTGAG	CCAAAATTTG	TTACCTCCCA	TACCTCGAG			279

- (2) INFORMATION FOR SEQ ID NO:1047:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 350 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

GAATTCGGCC TTCATGGCCT AGCAGCATTC AAGGAATTAA TATTAGTCAC TGAGAACAAA

AAGCGAAATT AGAAAATTTC AAGTCACTTC TAGGCTTGTA GGGGAGAAGA CGTGTAGTGA

60

120

60

120

CAGGCGCCTC ATTATTATTT	CATTTATGAA GTACCCACTG GATCCCACAC ACTGTGCAAG ACCTTTAGAT CCTCGGTTTT CTTCACCCTG TGCAGCAGGT GCTGTTATTT CCTTTTTAA ATTATTATTA TTTTTTGAGA CAGGATCTCC CTTTGTCACT CAGGCTGGAA TGATCACTGC TCACTGCAGC TTCGACCACC CGATCTCGAG	180 240 300 350
(2) INFORM	ATION FOR SEQ ID NO:1048:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 298 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1048:	
TCAACTTAAA TTTTATAGAG CGATCCTCCC	TTCATGGCCT AAAGCTTTTC AGTACTGTTT ACAAATTTGG TTTTATTGTG AGCATGAGTC TAAATCTATT AGTCATACCA AATTGTTTCA TTTTATTTTA	60 120 180 240 298
(2) INFORMA	ATION FOR SEQ ID NO:1049:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 367 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1049:	
AAAAAGTAAC ACATGAGATG TGTGCCAAAA AATAAAGTTT	TTCATGGCCT AGAGCTTTGG TGCTTTTCAC ATAAGGAACT TACTTGGGCT CTCAGAGAAA CAGTGCTCCC ATTTGGTGGA TAAGGAAACT GAGGTTCCAA AGATAAGCATG CCCCAAATCT AGCCAGTGAG CAAGAGAGGTA GACTTTTGCC CAGTAATCAC CATCCACAAG TGGCTATTTA AATTTTAATT ATTACAATTA AAAATCCAGT TCCCCAGTCC CACTGGCAAC TTAACAGCTA CCAGTGACTG AACAGCATAT ATAGACATAC AGCATATACA ACACATACAT AGGGATTCCC	60 120 180 240 300 360 367
(2) INFORMA	ATION FOR SEQ ID NO:1050:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 367 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1050:	

GAATTCGGCC TTCATGGCCT ACAATTTTAA AATTAAAATT TTTTCTATTT TTTTGCAATT

ATCAACCTAA CACATTGAAG AAACTTGGGA AATATAGAAA AAACACACCA AAAAGTATCA

GAGTTACACT	AAAATGTTCA	TAGTCAGTAA	TATAGTCTTT	CAGATTTTTT	TTTCTGTGTC	180
TGTCTGCTGT	CTATGTCCAT	GCCTACCTTA	CTTTCTTCCC	TCTCTCTTCC	CTCCCCACCC	240
TCCCTTCCTT	CCTTCCCTCC	TTCCCACCTT	CCCTGCTTCC	TTCTTGCCTG	CCTCCCTTCC	300
TGCCTGCCTC	CCTTCCTGCC	ACTTACATTC	TGTTAACAAT	GAGAAAAAA	TTCCCCCATC	360
ACTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:1051:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 340 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

GAATTCGGCC	AAAGAGGCCT	AAGAAGACCT	CAGCCTTCGC	CTGAAAAAGC	TGACTCACGC	60
					GTTTCAGCAA	120
					ATATCTTCTC	180
					ATCCTCAGCT	240
					AAGCATCAGA	300
		CCAAAGCACC		12.00.100100	resourceon	340
			~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~			340

- (2) INFORMATION FOR SEQ ID NO:1052:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 444 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

GAATTCGGCC TTCATGGCCT	ACTATGGACA	GCCACAGNTC	TTCCCAGGAC	AAGACCCTGA	60
CTCACCCCAG CATGGAAACT	ACCAGGGAGG	GAGGGTCCCC	CATCCTACTA	TGACAACCAG	120
GACTTCCCTG CCACCAACTG	GGATGACAAG	AGCATCCGAC	AGGCCTTCAT	CCGCAAGGTG	180
TTCCTAGTGC TGACCTTGCA	GCTGTCGGTG	ACCCTGTCCA	CGGTGTCTGT	GTTCACTTTT	240
GTTGCGGAGG TGAAGGGCTT	TGTCCGGGAG	AATGTCTGGA	CCTACTATGT	CTCCTATGCT	300
GTCTTCTTCA TCTCTCTCAT	CGTCCTCAGC	TGTTGTGGGG	ACTTCCGGCG	AAAGCACCCC	360
TGGAACCTTG TTGCACTGTC	GGTCCTGACC	GCCAGCCTGT	CGTACATGGT	GGGGATGATC	420
GCCAGCTTCA ACAACACACT	CGAG				444

- (2) INFORMATION FOR SEQ ID NO:1053:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 358 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

GAATTCGGCC AAAGAGGCCT AGATATTCAT TTCCATTGGA GCTGGTATTT TTAAGGTCTC

GTGACGTCAG TGACCTCATT TTACTTGATC TATTAGCAGC ATTTCATACA GTTGTTGACT	120
CTTCTCCATT AAAACATTTA CTTTATTTGG CTTCTAGGAA ACATATTTTC CTGCTTTTTC	180
TTCCTATTTC TCTGACTCTT TTCTCAGTTT CCTTTGCTGT TTCCTTTTCT ATCCTCTAAA	240
CATTGAAATA TCCTAAGCCT AGTTTGGGAT TCCCTTGATG GTCTTCATTT CTTTAATGGG	300
AACTGTGCTG GTGACTCAAA TTTATATCTC CAGCCAGAAC CTTTCTCCTG AATTCCAG	358
Therefore districts IIIIIII or Engerhand Cilicided Anticend	220
(2) INFORMATION FOR SEQ ID NO:1054:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 386 base pairs  (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:	
CCTTCATGGC CTACTTCTGG TATTACATCA CACTGATCAT GCTGCTGGTG GCCGTGCTGG	60
CCGGAGCTCT CCAGCTGACG CAGAGCAGGG TTCTGTGCTG TCTTCCATGC AAAGTGGAAT	120
TTGACAATCA CTGTGCCGTG CCTTGGGACA TCCTGAAAGC CAGCATGAAC ACATCCTCTA	180
ATCCTGGGAC ACCGCTTCCG CTCCCCCTCC GAATTCAGAA TGACCTCCAC CGACAGCAGT	240
ACTCCTATAT TGATGCCGTC TGTTACGAGA AACAGCTCCA TTGGTTTGCA AAGTTTTTCC	300
CCTATCTGGT GCTCTTGCAC ACGCTCATCT TTGCAGCCTG CAGCAACTTT TGGCTTCACT	360
ACCCCAGTAC CAGTTCCAGG CTCGAG	386
(2) INFORMATION FOR SEQ ID NO:1055:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 104 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:	
CGATTGAATT CTAGACCTGC CTGTGCTCCT CGATGGTGTC TCTCCCTCCA GAAAACGCAT GCTTATTGAC CTTGGTTTTG ATCTGCTTGG CCGTGTCGCT CGAG	60 104
(2) INFORMATION FOR SEQ ID NO:1056:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 650 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:	
GAATTCGGCC AAAGAGGCCT ACACAAGGCT AAGGGTATTG GATATAACGG AAAGTGGAAG	60
CTATACCTGA CTTCCAGAGA ATGTGGACCG GATATAAGAT CTTAATCTTC TCTTATCTTA	120
CTACAGAAAT CTGGATGGAG AAGCAGTATT TATCTCAAAG AGAAGTGGAC CTAGAGGCTT	180
ATTTCACTAG GAATCACACC GTTTTGCAAG GTACTCGATT CAAAAGAGCC ATTTTCCAAG	240
ACCOLUMN COM MICHIAN COCCOMMINATOR SINCE COLORS CONTROL CONTRO	200

360

TCTATGCGGC GAATGCGTTG TGCTACTGTG ATAAATTCTG TGACAGAGAA AATTCTGATT

CTTGGTATCC AAGAAAACTG GCCTTGTTCG	CTACAAGTCC TTTTGCCGTG AAGAGAAAGA ATGGCCTCCT CACACACAGC AGAAGGTTGC TTCAAAGATG GTCAACATTA TGAAGAGGGA TCAGTAATTA CAACTCCTGC ACATGCTCAG GACAGCAATG GAAATGTTCC CAGCATGTAT TCCAGAATTA ATTGAACAGG TCAATAAAGG AGACTATGGA TGGACAGCAC CCAATTTTGG GGAATGACTT TAGAAGATGG ACTCCTCGAG	420 480 540 600 650
(2) INFORM	ATION FOR SEQ ID NO:1057:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 378 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(11)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1057:	
GATCCGCCGG CTGAGAATAG TGTTCTGGAC GCGGGGGATA	AAAGAGGCCT ACACGTATTG GCCAGGATGG TCTTGATCTC CTGACCTCAT CCTTGGCCTC CCAAAGTGCT AGGATTACAG GCGTGAGCCA TCGCGCCCAG TTTTAAGAAT TGGTTGAGAG GCAGTTGCTT TTTCTTTGAA TATCTAGAAC TAACGTCAAA GAAACACCAT GGCAACATTA AAGGGAAGAT TATTTGAGAG GTATGGCTTA GGACTTGGGC TGCTACCTTT GACTTTGTAA TTCAAAAGAT CATATTTTCA ATCTGATCAT TAAAAATATC TGTGTTACAT GCAAAAAAAA AACTCGAG	60 120 180 240 300 360 378
(2) INFORMA	ATION FOR SEQ ID NO:1058:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 259 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1058:	
CTCCTAGTTA TTGTCATATC	TTCATGGCCT AATTTTAACA TTTACATAGA CAATTCATTT GGTGTTTTGT TTTGGCCCAA TCTCTGATGA TTTCCACTCT GTCTTGGCCA CTCACTCCGT TTGGCCATTA TCATCACCTC AAATTGCTCC ATCTTCAAAA TACTTGCATC ACCATATTCC TTCCACTTGG TTTATTGAAC TATTCCCTCT ATCATTCTCT CAGCCAATG	60 120 180 240 259
(2) INFORMA	TION FOR SEQ ID NO:1059:	
(i)·	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 246 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1059:	
TTTTTGAAA	ACTAACCACT GCAAGCTCTT GTCAAATTTT AGTTTAATTG GCATTGCTTG CTGAAATTAC ATGAGTTTCA TTTTTTCTTT GAATTTATAG GGTTTAGATT GCATGAATAT ATCACCTAAC ATCCTGACAA TAAATTCCAT CCGTTGTTTT	60 120 180

TTTTGTTTGT TTGTTTTTC TTTTCCTTTA AGTAAGCTCT TTATTCATCT TATGGTGCAG	240 246
(2) INFORMATION FOR SEQ ID NO:1060:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 103 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:	
GAATTCGGCC TTCATGGCCT ACGAGAGTAT ATTGGTAGGG CTGGAATTTC TGGTTCATAT GGTAACTAAC TCTATGTTGA ACATTTTGAG GAGCCCTCTC GAG	60 103
(2) INFORMATION FOR SEQ ID NO:1061:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 361 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:	
GAATTCGGCC TTCATGGCCT AAAAGGTTAG GCAATCACTG GGACCCGCAT GGTGTTCCTC CAAAGAATAG GGTAAAGGAG AGCTGGGAGG GAGCCCTCTC CGTTGGGTGA CTCTTGTGTG CCCTTTAGAC AGGCTGGCCT GCCGGTTCCA CAGGGTACAG TTAGGACTTG AGTCTTTCTT TTTCTGTTTT GAGTTGGTA GTGAGTGATA GGGTAACATG GGCCTTCAGG ATGACCCCTT GGAACTGTGC CGAGTTCCTT AAATCTCAGC TGGGATCCTG GACCTGGGAG GCCCCTGTGA GGGCCAGCTC TGGAAAAACC TGGGAGTTGA TGCCGGAGGC TGTGGAAGAA CTCTGCTCGA G	60 120 180 240 300 360 361
(2) INFORMATION FOR SEQ ID NO:1062:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:	
GAATTCGGCC TTCATGGCCT AAGAAAAATT GGGAACAAGC TAAGTGCCCA CATAGTTACA AAAATTACGT TAAATAGATA CACGGTTGCT TTTAAGCTCC ACATACAGCA CCATAGAGCT TTTTATATATT TTGTAGGCAT TAAAGCAATT CCAGGAAGGA TCTAAACCAA ACACTTGACC CAGGTTGTCT CTCTGGGGAG TGGAGCCACA TGGGATTTCA CTGTTTCTGT ATTCTTATTA CTTATATTAA AACACACATG AACAGAAGAA AAAATAGCCC CAGTATCTCG AG	60 120 180 240 292
(2) INFORMATION FOR SEQ ID NO:1063:	
(i) SEQUENCE CHARACTERISTICS:	

<ul><li>(A) LENGTH: 331 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:	
GAATTCGGCC TTCATGGCCT ACCGTTGTTA CACTTCTGGA CACAAGTTGG GCCGAAGTAA GCCAAGCCCA GTCCTTCTG TTTCCTTTCT CAGGAAATGT GACCACGTGC ACTGGGAAGC TTTGTTGTAAA GTAGATAGGG GTATGAGCCA ATTGCCCAGC ATTGGTGTTT TGTTTTTTTT TGTTTTGTTT	60 120 180 240 300 331
(2) INFORMATION FOR SEQ ID NO:1064:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 136 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:	
CGAGTGTTAC ATTCGTTCTT CCGCTCAAAT CCTGATCTGG TCCATTAAAG AGTGTTCGCA GACAAAGTTT CTGAAAGATT AGAGAAGAAT CCCCCAAGAA TCAATTACAA CCAAAATGGA AAGGGACAAC CTCGAG	60 120 136
(2) INFORMATION FOR SEQ ID NO:1065:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 255 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:	
GAATTCGGCC TTCATGGCCT AGAATAAAGG AAAATTCAGG TCATAGATTG AGTGCTATAT TTGAAGTAAA TACAGACCTT CAAAAAAATA TAATATCAAA AATCACTGCT GAGCTCTCCT GGCCTTCCAT ACTTAGCTCA CCCCGGCACT TGAAATTTCC ACTTACTAAT ACAAACTGCT CCTCAGAAGA AGAGATTACT TTAGAAAAATC CTGCAGATGT TCCTGTCTAT GTTCAGTTTA TTCCTCTGGC TCGAG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:1066:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 379 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
446	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

GAATTCGGCC	TTCATGGCCT	ACAACCTGCT	TTCCACCTTC	TGTAATCTCC	CATCAGTGAT	60
AAATTACCCA	TCAGCTTTCC	AGATTCCAGA	ATTTTGCTGA	CATCTCCTGT	TGGCTATGTT	120
CTTATTTCCT	TTTCTGTTTA	TTCCTGTGAC	CTTGTGCCCT	TTAATTCTTT	CCCATAATTT	180
GTTGGGACTT	CAGAAGGAAG	TGGAGCTAAA	GGCATGTGTC	TGCCTGCCCC	ATCTTGGCTG	240
					TGATGGATGC	300
TCAGCAAATG	TCTGTGGGTC	TTCTTTTTAC	TAAACAGGCA	GTTGATTTCA	CCAGAAGTAG	360
TGACCACCTA	AGTCTCGAG					379

- (2) INFORMATION FOR SEQ ID NO:1067:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

GAATTCGGCC	TTCATGGCCT	AACACAGCTC	ACATCAGAAT	ATAATAGTGG	AACTAGGGTG	60
ACTTCACTCC	CTTTCACCTG	ATGTCTATCT	TGGCCTTTTA	GCACCTTGAC	TATCCCTGAA	120
AAGACTGGGT	CTTTGTTTTC	CCAGGGAAAA	AACGAAGTGA	TGTAGATCTA	AGAAATAGTG	180
CCTCTTTAAT	ATTTAATTCT	TACATGACAA	CTAACACACA	GGGAAAAGGC	TATGTTAAGT	240
TGATTATAGC	TCCTCTTAAA	ATGTCCTATG	CTGTCAGTTG	GTCTTAGAGA	CATGGGAATA	300
ACCAAGCAAT	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1068:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 299 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

GCGATTGAAT TCTAG	ACCTC ACCTCTGATC	TATCTCTTTT	ACCTCAGCAA	TTTATTTCCC	60
AATTATTATA TCTAC	TTTAT TGTTCTTATG	AGACAATAGA	CTATGATAAT	TTTCCAGAAA	120
TAATTTTGTT TTCTT	CCTCC CATCTTCTAA	TGTTGAGACC	GTTTCTCTGT	TTTCTTTCAT	180
CTCTACCCCT CAGTO	TCATA GGTTTATTTC	TCATTTCCAA	TCCAGCGATT	TCAAAACCTG	240
TACAACAAAC CAACT	CAGCA GCCCTTGGCA	ACTTGAGGAG	ATTTCACAAA	CCACTCGAG	299

- (2) INFORMATION FOR SEQ ID NO: 1069:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 256 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

ACGTAGGGAT CTGCGTCTGT	TTCATGGCCT ACCATTTCCA CAACC TCCTCGTCTC ATCTTGGAAA CATTC CACGTGACAC CGTCTGAGCC TGTGG GTGGGGATGA CGGCAGTGGG CCTGG CTCGAG	GCCAGC AGTGGTTCTG	ATTTGGAAGC CCGGCAGTGC TTTTCCGTCT	60 120 180 240 256
(2) INFORMA	ATION FOR SEQ ID NO:1070:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 321 base pai:  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	rs		
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:1070:		
TCTAGACAGA AAGTGCTCAC CCCCTCCTCC TTTCTCTTTA	TTCATGGCCT AGCCATCATG TTTAT TACAGAATAA ATACCTGCGC CTTGA TACAGGAAGT TGCTGTGTCA AAATC CTGCTGACCT CAACAAGGGC TGTGC TTATTATTAA TATTATTATT ATTTC TTTCCCTCGA G	AGAACA GGAAGTCCAC CCAGGC AAGGACCCAA CTATTG TTTTTTATTT	GATTCATACA CTCCGGGCAG TATTATTTTA CTATCATTGG	60 120 180 240 300 321
(2) INFORMA	ATION FOR SEQ ID NO:1071:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 261 base pai:  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	rs		
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:1071:		
CATAGTCAAC AGAATCCAAA AAAATTCCAC	TTCATGGCCT AGGGAGGTAT TTGTC TTAACTAAAA AGAAGCTAAT ACAGC TTGCTCCAAA ATCTGAAACT TTCTC ATACAAGTAC TTAACACAAA CTTTC TTAACCTCGA G	STTGAG CATTCCTAAT	CCAAAAATCC CTACAAGTAG ACTAAAAATA	60 120 180 240 261
(2) INFORMA	ATION FOR SEQ ID NO:1072:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 304 base pai  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:1072:		
GGTGGCCATG GGCCGAATTT	TTCATGGCCT ACTTGGGCTC ATTTGGCCTATGAGG AGCAGAATCA GGCCCAGCAGATGC TCGAACAGCT TAAAAATCAGCTGCTT CAAGAGAATTT CAGTG	ACCTTG GAAGAAGCAG AAGCAA CAGGAAGAAG	AACAAAAAGA CTCAGGCAGT	60 120 180 240

GGAAAGTTCT CGAG	TCAGAAGCAT CAAAGTTGAG TTCCAAAAGT GCTAAAGAAT GGAGGTCCCT	300 304
(2) INFORM	MATION FOR SEQ ID NO:1073:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 397 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1073:	
TTATAAGTTG TTTCAGTGGA GGTAAGAAAA ATCTTCATCC CCCTCAGGTT	TTCATGGCCT AAAAAAGCTA ATGTCATAGG TCTTTATATG TGGGCAGGGT TCT7 AAGGGC CATCAGGTAG AGTTGGCCTT TTCTGTTGAG GTCCCCTAAA GGTCTTCTCT TTGGGGCAG TTTCTCTAGA AAACTGGGTC CTGATAGTAG GACAGCTGAG GACCCCAAGA TTTGTATGAT GACTTTTACT TAATCCCTCT TCTCTCATGC CCATCCGGCC CCACCCCCCA AATCCTCCTC TGGCTGCTGA CAGTTTTTCC TGTCAGTGGA GGTTGAGGGT GGGGCGTAGG CTGGCTGTGG AGAGGACCTG GGTTCCAGTA GCTCGAG	60 120 180 240 300 360 397
(2) INFORM	ATION FOR SEQ ID NO:1074:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 309 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1074:	
AGAAGCATGA CTTCAATCTA CCTGGCCCAG	TCTAGACCTG CACCACTGCG ATCCCTACGC CTGAGGAAAT GACAAGATTG ACAGACAACT CCAGATAAAT GTTGACTGTA CACTGAAAGA AGTTGACCTC GAGGAAACTT TGATCCAAAA GCCATGAATA ATTTTTATGA CAACATAGAA TTGTACCACC CAAGCCATCT AAAAAAGACT CCTCAGACCC CTGCACAATT CCCGAAGAAT TAGCGTGACC TCCAAAGTAC AGGCAGACAT CCATGACACC	60 120 180 240 300 309
(2) INFORMA	ATION FOR SEQ ID NO:1075:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 243 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1075:	
ATAAATCTTT TTGACTATTG	TTCATGGCCT AGAAAACTAA ACATTTGCCT TTTATAAAGA CTGACAAAAT ATTCTAACCC TATCCCCAAA ACTAGCCAGG CCACACCCCA GATGTTCTTA GGAAGATAGA AAAGGCGTTG TGTTTTTTGT TTTTTTGTTG TTGTTGTCAT TCAGAAGACC AGTGTCTCAG TTCTGTCTTA GTAGTACCAC ACCACGACTC	60 120 180 240 243

- (2) INFORMATION FOR SEQ ID NO:1076:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 598 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

CTCGAGCTGG	GGGCCACTTT	GGCACCTAAC	AAAACCAGAG	AAAACAAGTG	CAACTAAGCA	60
AGCAACTATG	CACATTCCAG	ACATAAAGAT	CATTAATAAA	CGCCTTAATC	TAAGGATCTG	120
TTGGTTCTAA	CGCCAGAAAA	AGAAGTTAAA	TTTTAAAAAA	TATCTAAAAG	AGATTTTAAG	180
TGGGCAAGCA	ATAGAGAAGA	TACCCAACAC	TGAGAAACGG	AAAGGAAAAA	AGACCACCCT	240
AATAACTACT	GCTCATCAAT	ATACATCTAT	AATTCTACCA	GAACAGTATT	AAGAAATGAG	300
AAACGCCAAT	ATTACATAAA	ATAAGGTAAA	AATAACTAAG	CATAGGTTAG	TGTCAGGGGA	360
CCTAGGGTTC	AGACACCCAG	AGTTTTATAT	AAGGATAATT	TGTCCTGAAT	CAAGACCACA	420
CTGTCCTCTC	CTTAAACCTA	ACTGCTACAA	GCAGACACCA	CCTCTTCTGA	CTGGGCTGAA	480
GTGTGGGAAA	CAGTCCAAAA	ATTAGGTATC	ACACCATAAA	CCCTCCACAA	GAGCAACCTT	540
TGCTCTCAAT	TAAGTTGTTG	ACAAAATAAT	TCTCAACTTG	CCTAGGCCTG	CCGAATTC	598

- (2) INFORMATION FOR SEQ ID NO:1077:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 346 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

GAATTCGGCC	AAAGAGGCCT	AGGTGGGTAT	TTGAATGGTT	TTGCTCCAAA	ATTGAACTCA	60
CATTGTTGAT	ATGACATGAA	ACTAGCTGCA	GCAAAAAATC	CAGATACAGT	AGATGAAAAG	120
ACTTGCTTTT	CAGGAGGCAG	CTGGTTGCCA	TTTAAAAAGA	AGATCATTTG	CTTTTCATTC	180
AAGTCTAACA	${\tt GAAATCCTAC}$	TGTATCTCCT	TCTTTCCAGC	ATGGGTGTAT	GTGAGGCTTA	240
CTTCTGGCAT	TGTACCAAAT	CAGCTGCCGG	CAGCCATCAT	ACGCACAGGA	GTATTCATCA	300
TCCCCAATGC	CGTAGCCTTC	ATGATTGAGG	AATTTGCTGT	CTCGAG		346

- (2) INFORMATION FOR SEQ ID NO:1078:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 419 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

GAATTCGGCC	AAAGAGCCTA	GCTCCTGTTA	CCATTATTAT	TATTCATACT	CATATTCATT	60
ACTTCTAACT	TCAAGTGGGC	CATTAGCACT	AACTGGCATA	CCACACTTCT	CTAGTCTATT	120
TATTCTCCTT	GATGACTATT	TCATACCCTT	CCCTCTTTCC	CCAAACTTCC	AACACCTCCT	180
CTTCCCATCA	TTCTCAGCTG	ACGGCCTTGC	TTTCTCCCAT	GATTGGGACT	AGAGAAGCAA	240
TTTGTAGGGA	ATTTCCACAA	GCTCCATCAC	ATGTGGCCAC	TCATCTACAT	CTGGATCCAT	300

CTATTTGGCC TTCCCTATTG TTCTTATACA CTCTCCCTGT CTTACTTTAT CTAAGGTCAA

CATCTCCACT CCACTTATGC ACTAGATCCT GGCATTACAC CAGCAATCCT CACCTCGAG

360

419

(2) INFORMATION FOR SEQ ID NO:1079:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 261 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:	
GAATTCGGCC TTCATGGCCT AGCTTATTCT TTTTTCTTTT TCTTTTTTTT TTTTTTTTC	60
GAGACAGGGT CTTTCTTTGT CACCACAGGC TGCAGTGCAG	120
GCAGCCCTCA ACTCCAGGCC TCAAATGATC CTTCTGACTC AGCCTGCTGA ATGACTGACA	180
TTACACGTGC ATGCCGCTGT GCCCAGCTAA TTTTTAAATT TTTTGTAGAG ATGAGGTCTT GCTTTGTTGC CCAGACTCGA G	240
	261
(2) INFORMATION FOR SEQ ID NO:1080:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 208 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:	
GAATTCGGCC TTCATGGCCT ACATTAACAG ATTAATCCAT CTGTATAGGG CTTTTGCTGT TGGATAGAAT TTAAATTGTC TACATAAATA TTTGTTTTAG GACCCTTAGA TTTTATCTGA	60
ATACACAGAT TAGACTTAA AAACAGATAT ATATGTCATT TTTGGCTTAA GGAGTTTGGC	120 180
TAAGTTAGCT TTTCAACTGG TTCTCGAG	208
(2) INFORMATION FOR SEQ ID NO:1081:	
(4) OROUPNOR CHARACTER TOTAL	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 425 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:	
GAATTCGGCC TTCATGACTC CTGATTCAGG GGTCAGTTTA CTTCATAAAA AATCATTAGA	60
AAAGGAAGAA TTATGCCAAA GACTTAAAGA ACAGTTAGAT GCTCTTGAAA AAGAAACTGC	120
ATCTAAGCTG TCAGAAATGG ATTCTTTTAA CAATCAACTA AAGGAACTGA GAGAAACCTA	180
CAACACACA CAGTTAGCCC TTGAACAGCT TTATAAGATC AAACGTGACA AGTTGAAGGA	240
AATTGAAAGG AAAAGATTAG AACTAATGCA GAAAAAGAAA CTAGAAGATG AGGCTGCAAG	300
GAAAGCAAAG CAAGGAAAAG AAAACTTATG GAAAGAAAAT CTTAGAANGG AGGAAGAAGA AAAACAAAAG CGACTCCAGG AAGCCAAGAC ACCAGNAAAA ATTCCAAGAA GAGGAACGTC	360 420
TCGAG	425
. 451	

- (2) INFORMATION FOR SEQ ID NO:1082:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 299 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

GAATTCGGCC	TTCATGGCCT	AAGACTTCTT	GCAGGAAAAA	TGAGTGCATT	GAGGATAGTA	60
					CTCTCCCAGG	120
					AGCTGCCCAG	180
					TGGATGTGTT	240
GATATCCAGC	AAGGACCTGG	CACTGTCTAG	TGAGGACGAG	GCCTGCACAG	GATCTCGAG	299

- (2) INFORMATION FOR SEQ ID NO:1083:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 444 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

		AAGTCACTTG				60
ATTAACCTTC	AACAGCTATT	AAAGTGGAAT	GTAAGTTAAA	TTTTGAAGGA	AAGGAAATAA	120
ATGTTTTCCA	TATTTCGTCT	TGATTTACTT	TCTGTATGAG	AACAGCTGTG	TTTTTGATAG	180
		CATATTTAAA				240
TAAATCTTGA	TGTTTATTTC	TGCCTTGTAA	AGTTCTATCA	CGGCCTACCT	GGAATTTAAA	300
ATTCAGTAGA	CAAATTAATT	GGTCCTCTGC	ACAACTTTTT	TAATAAGTAG	ATTATTTTAC	360
AAAGAAATTT	GAACAAATTT	AATTGAATCT	TTTGTTTAGC	TTGCCTCTAA	GAACTTTTCT	420
TAATAAAGCT	CCCAAACACT	CGAG				444

- (2) INFORMATION FOR SEQ ID NO:1084:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 268 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

GAGTGAGACT CCCTCTCAAA					60
TTGTTTCAGA ACTCATGATA	TGAGTCATGA	CTACAACCCA	CCATATTCAG	TAAAACCTCA	120
CCTTGTCCTG TTGTCTGACA	TTAAGTGTTC	TACGAGATCC	ATACCTGTGA	AATCAGCTCC	180
TCTGGAATGA CAGATGCTGG	AATAACTGGC	TGGGGCTGAC	TGCCCAAAAG	CCCAGACCCT	240
CGATCCCGTC CTGTCCGAAT	AACTCGAG				268

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) TOPOLOGI: TIMEAR	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:	
GAATTCGGCC TTCATGGCCT ACTTTAAGTG AACAACANCA ACAAAAAAGT TAAGGGTAAG	60
ATGAGGCAGC TTTTCAGTGG AAAATACTTG TCTTGGGGAC AGTATGTCAT GTCCCTATAC	120
CTGGTGCCAT TGATAAGGTT ATTCATTCAA CAATATTTAC TGATCACTGG CATATGCCAA	180
GCACTCTGCC AAGTACTAGG GATATAAACA TTAGAAAGAC AAGTTCCTCC CTTTTCAGTC	240
ACGATCTCGA G	251
(2) INFORMATION FOR SEQ ID NO:1086:	
(i) CHOURNON CUADACTER CO	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 258 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(D) TOPOBOGI: TIMEAT	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:	
GAATTCGGCC TTCATGGCCT AGAGCTTCAC GGAGGCAAGA GGGTAATGGA GTGCCTAAAA	60
AAAGCTCTAA AAATAGCAAA TCAGTGCATG GACCCCTCTC TACAAGTGCA GCTTTTTATA	120
GAAATTCTGA ACAGATATAT CTATTTTTAT GAAAAGGAAA ATGATGCGGT AACAATTCAG	180
GTTTTAAACC AGCTTATCCA AAAGATTCGA GAAGACCTCC CGAATCTTGA ATCCAGTGAA GAAACAGAGC AACTCGAG	240
GAMACADAGC MACICOMG	258
(2) INFORMATION FOR SEQ ID NO:1087:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 391 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:	
(MAY OBSOLUTE PERSENTITION, SEQ ID NO. 1001;	
•	
GAATTCGGCC TTCATGGCCT AATAAAAAGA ATTATCAAAG AATTGCAGGG GAAACCCCAT	60
AGAGAAGACT CATTCTTAGA TGAGTATACA ATCCATGGGG GTCTTTAGGA TATTTAACTG	120
ATTTGGGAGA GGTCGGATAA AGAAAAAGGA GCATTAACCT TGACTATGCC TTTAGCTCCA	180
GCCGCCTCTT TAAGAGGAAA TTGTTGGGCA GGTGGGGGAA GGCTAGTCAT GGAACGAAAC	240
TGTAAGCCAG ATCGGGTGTG AGGAGGGGAG GTGATAAAAG GATTATAGGG TGGGAGAGCA	300
CAGGCTGAGG AAGAATTGGG ACCTGGCTCA GCCTGGCAAG GCACAGCCTG GGGAGGAGGG	360
GAGAGGTCCT GTAGAAAAGG AGGATCTCGA G	391
(2) INFORMATION FOR SEC ID NO. 1000	
(2) INFORMATION FOR SEQ ID NO:1088:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 368 base pairs	
(B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

GAATTCGGCC	TTCATGGCCT	AGCCTTCNAA	GTTTGAATGG	CCCTTAGGTT	TTAAGTTATC	60
TATGCAAAGA	TGAANAAGGC	CTTCACATTC	TCAAAGGTGA	CAACTCATAC	CCAGCCATTT	120
GCTTATTTTT	GCCTGCAGAC	CTCCAATGGA	AGTCCGGGCA	CATGGCGGAG	AGCCTCACCA	180
ACATGCCACG	GCACTCCCTC	TACATCATCA	TTGGAGCCCT	CTGCGTGGCC	TTCATCCTTA	240
TGCTGATCAT	CCTGATCGTG	GGGATTTGCC	GCATCAGCCG	CATTGAATAC	CAGGGTTCTT	300
CCAGGCCAGC	CTATGAGGAG	TTCTACAACT	GCCGCAGCAT	CGACAGCGAG	TTCAGCAATG	360
CACTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:1089:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 409 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

GAATTCGGCC	TTATGGCCTA	GTTCATTTAA	CTAATACTTG	TATTAAATCA	CTTCTAAATG	60
CTTATTATAC	CCTGTATTAT	AGTATTATAT	TCTGAGTCTT	AAAGGTGCTT	AATGTGAAGA	120
TTCTCTCTCT	ACATATTCAA	CTCTTACTAA	CTTTTGGCTT	TAGGTAGAAA	TCAGTTAGTG	180
TATTATATGA	TAAAATAGGA	AACTATTTCC	CTAGGGGTAT	AGGTATTCAG	TAGGGAGCTT	240
TGGAGTCTCA	ATGAGCTTCT	TAAAGAAGCA	TTTTTAATGG	TAGGTTTTAG	GGAGAGTTTT	300
TGTAGTAAGA	TAAAGTAGAT	GAGAAAGTGT	TGCCTCTAAA	CAATCAACAA	GCTGGGAATG	360
GGGTGCAGAA	TGAGGAGAAC	CCTAAGCAAT	AGGCAATAAG	AAGCTCGAG		409

- (2) INFORMATION FOR SEQ ID NO:1090:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 359 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

GAATTCGGCC	TTGGCCTAGT	GAGAGAGCGT	CAAAAAAACT	TCCATCTCAG	CCAACCACTG	60
ATACTAGTAC	TGACAAAGAA	AGAACTTCAG	AGGACATGGC	TGATAAAGAA	AAATCTACAG	120
CTGACTCTGG	AGGTGAAGGA	CTGGAAACAG	CCCCAAAGTC	TGAAGAGTTC	AGCGACCTCC	180
CCTGTCCAGT	CGAAGAAATT	AAAAATTACA	CAAAAGAGCA	TAATAATTTA	ATTCTGCTAA	240
ATAAGGATGT	TCAACAGGAA	AGCAGTGAGC	АААААААТАА	ATCAACAGAC	AAAGGTGAAA	300
AGAAGCCAGA	CAGCAATGAG	AAAGGAGAAA	GAAAGAAAGA	AAAGAAGGAA	AAGCTCGAG	359

- (2) INFORMATION FOR SEQ ID NO:1091:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 280 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

(	GAATTCGGCC	TTCATGGCCT	ACATGTTCAT	TCTAAGAAAC	TTAACTCCAT	TTTTAAGCTT	60
7	TAAGATTCCC	CCGATCCCAA	ATAACCTAAC	ACACCAAAAG	CCTTGCCATT	TCACACATGC	120
7	TGTTCCTTTG	CTTAGAACCT	TTTCAATGTC	TAGCTCACTC	TGTTTGGGAC	TTCTTTTTC	180
7	TTTTCTTTTT	TTTGAGACAG	GGTCTGGCTC	TGTCATCCAG	GCTGGAGTGC	AATGGGGCAA	240
7	TTTCGGCTCA	CTGCAACCTC	CGCCCTTCCA	GGCTCAAGCG			280

- (2) INFORMATION FOR SEQ ID NO:1092:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 443 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

GGAAAATTGA	GAAAACCATG	AAAGAAAAAG	AAGAACTGTT	AAAGTTAATT	GCCGTTCTGG	60
AAAAAGAAAC	AGCACAACTT	CGAGAACAAG	TTGGGAGAAT	GGAAAGAGAA	CTTAACCATG	120
AGAAAGAAAG	ATGTGACCAA	CTGCAAGCAG	AACAAAAGGG	TCTTACTGAA	GTAACACAAA	180
GCTTAAAAAT	GGAAAATGAA	GAGTTTAAGA	AGAGGTTCAG	TGATGCTACA	TCCAAAGCCC	240
ATCAGCTTGA	GGAAGATATT	GTGTCAGTAA	CACATAAAGC	AATTGAAAAA	GAAACCGAAT	300
TAGACAGTTT	AAAGGACAAA	CTCAAGAAGG	CACAACATGA	AAGAGAACAA	CTTGAATGTC	360
AGTTGAAGAC	AGAGAAGGAT	GAAAAGGAAC	TTTATAAGGT	ACATTTGAAG	AATACAGAAA	420
TAGAAAATAC	CAAGCTTCTC	GAG				443

- (2) INFORMATION FOR SEQ ID NO:1093:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 256 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

GAATTCGGCC	TTCATGGCCT	ACCTCCATTG	TATATTAACA	TTTATCATAA	TTATTATTTG	60
CTCATTCAAA	AAATATTGCT	CTGATATGGT	ATTGAATATT	CCTCACATAG	GAAAATATGA	120
ACAGTTTATT	TGCCACCCAG	ATGGTTTGGA	AGCCTATACC	CTCCAAGACA	TTGAGAAAAG	180
AAAAATCTTT	CTCTCAGGAG	AGAGAATGAG	TGCCAAGCAA	TGGĠAGAAGC	CCCTTAAAAA	240
ACCATCAGAT	CTCGAG					256

- (2) INFORMATION FOR SEQ ID NO:1094:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 454 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

GAATTCGGCC	TTCATGGCCT	AAGCTGTTAG	TGATTCTGAC	ACCCTTGGAC	CTCCAGGAGT	60
AGCTCCTCCT	GCCACGAGAG	GACTCTGGCT	TTTCTAATAA	GGAAGGTTCT	GGCCAATCAG	120
TCCAAGAAAG	GCCCGGATTC	TCTTCCAAGG	TGTTGTCTCT	GCAGAAATGT	TCCTCAGGGT	180
GGAAGGTGCT	GCTGCAGCAA	GGGATGTCCC	CTGAGTTTTC	AGGTATGTAG	TCTGTGGCTG	240
CAGCAGGTGA	ACACTCCTCA	CACTCCCATT	TCTTACTGTT	AGATCTAAGA	GAGGAGCAGT	300
CCCTGTGGGT	TCCGTGGGAT	CCGCATGTAG	CACACAGAAT	GAGGCACCAC	CTCCCTTCAT	360
CCTCAAAGCT	GTCTCTGCCT	TGTTCATACA	GACAGATGGG	GGCATCACAG	TGCTGATAGC	420
GCTGATATAA	GTCTGAGAAA	GCCCCTGGCT	CGAG			454

- (2) INFORMATION FOR SEQ ID NO:1095:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 449 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

${\tt GAATTCGGCC}$	TTCATGGCCT	AGTGATCTCA	TCTCTCCGTC	CATGGGCGAA	AAAACAGCCA	60
TCACCAGGCC	ATTCACGCTT	TGTGCTTTTG	TTAGCAGAGC	CCAGGCAGCC	CTGCAGCCCA	120
CATCTAGGGT	ACAAACGGAA	CGGCGGCGTT	TTCCTTGTAT	CATTTAGAGG	AAATTTTTGA	180
GCTGAACAGT	ATTTTTTTC	TCCCTCTCTC	TCTCTCTGAA	ATATTGCTGA	GATTTAAAGG	240
AGGACGAAGA	CAACAGATTC	ATAGCTGGGT	CTTGCTGTTT	TCCTGACGCT	GACCACAGCG	300
GATCTAGTTT	CTCTGCAGAA	GACAGCAAGA	TGCCCCAGGG	AATGTTTGTG	AAAAAGGATG	360
ACTGGATGGG	AAGCAAGCTG	AAGAAAAAGA	AGGAAAGAAA	GAGAGAAATC	AGTAAATCAC	420
CACACAAGAG	GTGGAGAAGA	GGACTCGAG				449

- (2) INFORMATION FOR SEQ ID NO:1096:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 166 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

GACTGGCCGC	AAGGGACGGG	TTGTGAGCAA	TGATGATGGA	AGCATATCTT	ATGAGTCAAG	60
ATCTGAACTT	GATGTGCCTG	TGGAAATACT	AAACATCACA	GAAAAACAAC	GATTTATGGA	120
TGGAGATAAG	AATATTGCTA	TCATCTCAGA	AGCTGCCATG	CTCGAG		166

- (2) INFORMATION FOR SEQ ID NO:1097:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 501 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

GAATTCGGCC	TTCATGGCCT	ACATTATTTA	CACCTGTCCC	AGACTTTGAT	TCAGGAACTA	60
ATGCTGCAAA	GCAAGGACTA	TGATGGAAAA	TGCTCACTGC	AAGAATGGTA	GCTGCAGCAA	120
GATCAAGATC	CCAGAAAGCA	GTGGCCAAGG	CACTCACTGT	AGACTTTAGT	GCCTGCAGCA	180
		CTACGCCCAG				240
ATTCTGTGTA	AGATTTGATG	CGCTGTCCCT	GGCTGCAGTG	CCTGCAGACA	TCTCTCTCTA	300
GCCCTTCTAA	CAATTTCACA	GCAACTCAAC	ATCTTTAAAA	ATTTATTAGC	CAACCAAAAT	360
CAGCTTCTGT	GGCATGCAAG	TAAAAACCCA	GGCTGATATG	TCTGAATACA	GAAGATTTAT	420
ATTAGTTCCT	TAGAGTCAAT	AATCCATACA	GACTCTATTC	TAGCTTCTTT	GTGAAGTGGG	480
TAAGAATTCC	${\tt TCTGCCTCGA}$	G				501

- (2) INFORMATION FOR SEQ ID NO:1098:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 282 base pairs
    - (3) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

GAATTCGGCC	TTCATGGCCT	ACTTCAAAAA	CATATATTAA	TATTTTTGTA	CCACGTAAGT	60
TCATCAGAAG	CCTGACTTTA	ATCTCTGATT	TATTATATTT	GAACACTGTG	AAGAAGCAGT	120
TTAACACTGA	ACGAAAGTGT	CGTAATGCAG	CTTTCAAAGT	GGCCATTAAA	GACAGATCTC	180
TGCTTTTCTA	TTAGTACATT	TTCTAAGATG	ACTATCATTG	CCATTGTAGT	CAGCTTTGTG	240
TACCTTTATA	GAGATTCCAG	TATAAACCCA	GAAACGCTCG	AG		282

- (2) INFORMATION FOR SEQ ID NO:1099:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 266 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

GAATTCGGCC T	TCATGGCCT	AGGAAACTTT	TCAAAGAAGT	AGTCCACGAG	AACTACCTTG	60
AAAGAGCAAA A	CCAGCCAGG	TGCAGTGGCT	CACGCCCATA	ATCCCAGCAC	TCTGGGAGGC	120
CCAGGTGGGT G	GATCTCGTG	AGGTCAGGAG	TTCAAGACCA	GCTTGGCCAA	CATGGTGAAA	180
CCCCATCTCT G	CTGAAAATA	CAAAAGTTAG	CTGAAAATAC	AAAAGTGGCA	CATGCCTGTA	240
ATGCCAGCTA CO	CGGGAAAGG	CTCGAG				266

- (2) INFORMATION FOR SEQ ID NO:1100:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 310 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

CTCGAGCGTA	TCCCAGAACT	TAAAGTATAA	TAATAATAAT	AATAATAATA	ATAATAATAA	60
TAATAAAACC	TTCCAACAAG	CTTCCTTTCC	ACCACAGGAA	ATCCTGTTGG	GAGTTCCCCC	120
TGAACCAAAA	AAAAAAAAG	ATAGAGTATA	AAACATACAC	TTTTCAGGAA	TGCTTATTGG	180
GTAATGTAAG	ATAACACCTC	AAAATGAAAC	TCAGAATTTT	ATTTTATTTT	ATTTTTTGAG	240
ATGGAGTCTC	ACCTAGGCTG	GAGTTCAGTG	TGGTAATCTT	GGCTCACTGT	AGGCCATGAA	300
GGCCGAATTC						310

- (2) INFORMATION FOR SEQ ID NO:1101:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 367 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

GCGATTGAAT	TCTAGACCTG	CCTCGAGTGT	ACCTCATTCT	GCCATCTCTG	ATATTATGTC	60
ATCTGATCAA	GAAACTTACT	CTTGTAAACC	TCATGGACGG	ACTCCACTTA	CCTCAGCTGA	120
TGAGCATGTA	CATTCCAAAC	TGGAAGGAAG	TAAAGTAACG	AAATCTAAGA	CTTCTCCGGT	180
GGTATCTGGT	TCATCTAGTA	AATCAACCAC	CCTTCCAAGG	CCACGACCTA	CCAGGACTTC	240
CCTCTTGCGC	AGAGCACGAC	TTGGTGAAGC	TTCAGACAGT	GAACTTGCTG	ATGCTGACAA	300
AGCATCTGTT	GCTTCTGAAG	TATCCACAAC	AAGTTCTACA	TCAAAACCTC	CCACAGGAAG	360
GCTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:1102:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 368 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

${\tt GAATTCGGCC}$	TTCATGGCCT	AAGAAAGCAA	GAAAGCACGA	AAGCAATCAA	GCAAGAAAGC	60
AAGCAGGAAA	GAAACAAAAG	AAAGAAAGAA	NGCGAGAAAA	CAAGAAAGCA	CGAAAGCAAG	120
CAAGCAAGAA	AGCAAGCAAG	AAAGAAACAA	AAGAAAGAAA	GAAAGAAAGN	AAACAGGAAA	180
GCAAGAAAGC	ACGAAAGCAA	GCNAGCAAGC	AAGAAAGCAA	GCAAGAAAGA	AACAAAAGAA	240
AGAAAGAAAG	AAAGAAAGAA	AAAGAAAACA	GGAAAGCAAG	AAAGCACGAA	AGCAAGCAAG	300
CAAGCAAGAA	AGCAAGCATG	AAAGAAACGA	AAGAAAGAAA	GAAAGCAAGA	AAACGGGAAA	360
GACTCGAG .						368

- (2) INFORMATION FOR SEQ ID NO:1103:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 328 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GAATTCGGCC TTCTGGCCTA GAAACCCGTG ACACACACA ACACACTGC ATAGATTTTT CCCAAGCACA CGATATGCAC GTGGATACAC AGACTTACAA GCACAGGGCC ACGTGCAGAC AGACACAGAC CCTGTCTGCA CCACAAACAT ACCACACACA GCCACACACA CAGAAGCCAA ACATCCTCGC ATAGGTGGAT ACAAGCACAG ACTCACATAC ACATATGCGA TACACATATG GATACATACA CAGAGTACCC CCACAAACAC ACAGACACAC ACGGGCAGAG ACAGACAG	60 120 180 240 300 328
(2) INFORMATION FOR SEQ ID NO:1104:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 246 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:	
GAAAAAAACT GAGTTAATGG CCATGACTAG ATGGGAGGTC AGATTCGCCG TTATATCCTC TCTGTTTTGC AGTTTAGACA CAACTGACCA GCATTGTTAA AATGGAGATC ATACGGCTGG TAGAACAGAC TCTTTGTGGC CCAAAATTAG CAAATTATAA ATAGAATCTA AAGCCATCCC AGGCAAGGGT TAAGTTATGC ACCCCTACAC TTAAAGAATA AACTATGTTG GCCGGGCCAA CTCGAG	60 120 180 240 246
(2) INFORMATION FOR SEQ ID NO:1105:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 298 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:	
GAATTCGGCC TTCATGGCCT ACGATCAGAA AGAAAACACA GATCTCGAAG TCGGGATCGA AGAAGATCAA AAAGCCGGGA TCGAAAGTCA TATAAGCACA GGAGCAAAAG TCGGGACAGA GAACAAGATA GAAAATCCAA GGAGAAAGAA AAGAGGGGAT CTGATGATAA AAAAAGTAGA GAAAGAAGAC GGAGCAGAAG TAGAGATCGA CGAAGAAGCA GAAGCCATGA TCGATCAGAA AGAAAAACACA GATCTCGAAG TCGGGATCGA AGAAGATCAA AAAGCCGGGA AGCTCGAG	60 120 180 240 298
(2) INFORMATION FOR SEQ ID NO:1106:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 211 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:	
GAATTCGGCC AAAGAGGCCT AGGGATGGAT GGTTCAGCTG CTAGAATTTC GATGCAGGAC TTCTTCAAAA TTGAGTGGAT GATGCCTTGC AGAGCCTGAA AGCCGTCATT CACGGGAAAC ACATGATCCT TACTGTCCGC AATCCGGGCC AGCTGTGTCT CATTGAAATC TTTCACACCA ACACAGTAAA CAATTGCACC AAGATCTCGA G	60 120 180 211

(2) INFORMATION FOR SEQ ID NO:1107:

460	
(ii) MOLECULE TYPE: cDNA	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 240 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(2) INFORMATION FOR SEQ ID NO:1110:	
GAATTCGGCC AAAGAGGCCT AGCTTTTCT AATCATAAAT TATATGACCT TTACAGAAAA TTTAGAAAAT ACAGAAAAAC TGAAAAGTTA CACATGGTAC AACTCACAAC CACAATCCTC GAG	60 120 123
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:	
(ii) MOLECULE TYPE: cDNA	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 123 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(2) INFORMATION FOR SEQ ID NO:1109:	
GAATTCGGCC AAAGAGGCCT ATGAAAATTG ACTGCAATTA GTAAAGTTGG TATAACGTAC GTTCCCAGTT GTGCTATTTA GAATTATGAT AGTATTATGC TCCTACTTTT CTTTGATATT GAGTAGTCTC GAG	60 120 133
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:	
(ii) MOLECULE TYPE: GDNA	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 133 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(2) INFORMATION FOR SEQ ID NO:1108:	
GAATTCGGCC AAAGAGGCCT ACCTGCTTGA ATTGGGGCCC CTTGTGAAGC TGCTGCCGCA TCTCTTCCAT TCGCTGCTTC CGGTACTGCT GCAGAAACTC TTCATCATCT TGGTCCTCAT TCATTATGGC AAACTCCTTC AGAGTCATCT TCCCACTGAT CTTCTCCTGG AGGTCTTTCT GTTTCTGTTG CTCCTCCTCT TCATCCAGAT GGGACCTGCA AGTCATTGAC AGCTTCTTGA TCAGCCTTTC CATCTCCGG CAACTCGAG	120 180 240 269
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:	
(ii) MOLECULE TYPE: cDNA	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 269 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

GAATTCGGCC	AAAGAGGCCT	AGTGTTCCAG	ATCCTACGGC	TTATGAGGAT	TTTCCGAATT	60
CTAAAGCTTG	CCCGGCACTC	GGTAGGACTT	CGGTCTCTAG	GTGCCACACT	GAGACACAGC	120
TACCATGAAG	TTGGGCTTCT	$\tt GCTTCTCTTC$	CTCTCTGTGG	GCATTTCCAT	TTTCTCTGTG	180
CTTATCTACT	CCGTGGAGAA	AGATGACCAC	ACATCCAGCC	TCACCAGCAT	CCCCCTCGAG	240

- (2) INFORMATION FOR SEQ ID NO:1111:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 264 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

GAATTCGGCC	AAAGAGGCCT	AGGTGGGGAG	GGGAGGGGAC	AGGAGAAATG	AAATACCTTC	60
ACCGAGAACT	CAGCAGCTGC	CACCGCAGCT	GCCTCCTCAG	GATCCGGTCG	TCGGGGATAG	120
GGAAGGGAGG	GGAAAGGGGA	ACGGAAAACA	AAAAAAGGG	GGAGGGAAGG	GGGAGGAAGG	180
AGTCGGGGAC	GGCCTCAAAC	TCAGCTCAGA	GGAGTCGCTG	CTGCAGCCGC	CACTCGGTAC	240
CCGCTGCTAG	GCCTCTTTGC	CGAG				264
	ACCGAGAACT GGAAGGGAGG AGTCGGGGAC	ACCGAGAACT CAGCAGCTGC GGAAGGGAGG GGAAAGGGGA AGTCGGGGAC GGCCTCAAAC	ACCGAGAACT CAGCAGCTGC CACCGCAGCT GGAAGGGAGG GGAAAGGGGA ACGGAAAACA	ACCGAGAACT CAGCAGCTGC CACCGCAGCT GCCTCCTCAG GGAAGGGAGG GGAAAGGGGA ACGGAAAACA AAAAAAAGGG AGTCGGGGAC GGCCTCAAAC TCAGCTCAGA GGAGTCGCTG	ACCGAGAACT CAGCAGCTGC CACCGCAGCT GCCTCCTCAG GATCCGGTCG GGAAGGGAGG GGAAAGGGGA ACGGAAAACA AAAAAAAGGG GGAGGGAAGG AGTCGGGGAC GGCCTCAAAC TCAGCTCAGA GGAGTCGCTG CTGCAGCCGC	GAATTCGGCC AAAGAGGCCT AGGTGGGGAG GGGAGGGGAC AGGAGAAATG AAATACCTTC ACCGAGAACT CAGCAGCTGC CACCGCAGCT GCCTCCTCAG GATCCGGTCG TCGGGGATAG GGAAGGGAGG GGAAAGGGGA ACGGAAAACA AAAAAAAGGG GGAGGGAAGG GGGAGGAAGG AGTCGGGGAC GGCCTCAAAC TCAGCTCAGA GGAGTCGCTG CTGCAGCCGC CACTCGGTAC CCGCTGCTAG GCCTCTTTGC CGAG

- (2) INFORMATION FOR SEQ ID NO:1112:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 519 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

GAATTCGGCC AAAGAGGCCT AAATATTAGA AAATGTATAT TATAGAACAT GATATATATT	60
TACATTCATC TCTGTATTCT CTCAGCTGTT GTTAGAAGGA CAGAATGTTA AACTTTATCT	120
TAATTAGTAT ACTAGAAAGG GCAGTATAAT ACTGTTTTAA AGTGAAGGCA TGACTGAAAC	180
TAAAATATTT CATAAGGCTT AGCTAGAGGC AGAGTAACGT GTTTTTGTTC ATTGGGCTTC	240
CTTGTACTTA GTTTTTCAT TTAATAATTC AAACCAACAC TTTTAAAAAA ATAATTCAGA	300
TGAGACTGAG CCATATCTGC AGTAAGAGAA ATATTTCTTA ATGTTTTGGT TACTTATGAT	360
AGAGTACTTT TCTTGATACT GTTAACTTTG TGCTTTTTAA AAAAAGTGAT TCTCTAACAG	420
ACCTCTTAAA TTGTGACATG AAGGTATGTA ATTAGATTTC AGAAATTGGT TTATTAGTGA	480
GGAATTTTTA TCAATAAATG TCATGGGGCG GCGCTCGAG	519

- (2) INFORMATION FOR SEQ ID NO:1113:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 562 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

GGCCCACCTA	GTTGGTATCC	CAAATTCACA	CATTCAAAAG	CAAAGCCATT	TCTCACCTTC	60
CTCCAAAATA	CTTGTAATTC	CTAATATCCT	GACTCCAATC	CATTCTTTAT	TTTCTATTCC	120
				TACATGGTGT		180
				CATTCCTCTT		240
GCTCTGATGG	CTTCCAGTCT	ATACAAGATA	TATTAAGGCT	CAACTTACAG	TTCCAGTCTC	300
ACCTGCCCCA	CCTCCACCTT	CCCAAACCCT	CTGTATTCTA	GCCAGAGCAT	ACCTGCATTC	360
CCTTAGCTCA	ACATGTGTCC	TTGCTCACAC	TGTCCCTTTG	GTTGACCTAG	CTTCAATTCC	420
TTCCTCATGT	GCAGTTATGT	${\tt GTCTACTAAG}$	CAGCAATGTG	AAATGTCTTT	ATTGTAGGTC	480
TGTCAAAAGC	TAAAGTCATG	GCCCGGTGCA	GTGGCTTGGG	CCTGTAATCC	CAGCACTTTG	540
GTAGGCCTCT	TTGGCCGAAT	TC				562

- (2) INFORMATION FOR SEQ ID NO:1114:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 435 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

GAATTCGGCC AAAGAGGCC					60
CAAGCAGCTG GTCAGTCTT	T GCTCAGTGTC	CAGCTTCCAA	AGCCTAGACA	ACCTTTCTGT	120
AGCCTAAAAC GAATGGTCT					180
TGAAGTAGGT GGCTTGAGC	T AGAGATAAAA	CAGAATCTTC	TGGGTAGTCC	CCTGTTGATT	240
ATCTTCAGCC CAGGCTTTT	G CTAGATGGAA	TGGAAAAGCA	ACTTCATTTG	ACACAAAGCT	300
TCTAAAGCAG GTAAATTGT	C GGGGGAGAGA	GTTAGCATGT	ATGAATGTAA	GGATGAGGGA	360
AGCGAAGCAA GAGGAACCT	C TCGCCATGAT	CAGACATACA	GCTGCCTACC	TAATGAGGAC	420
TTCAAGCCCC CTCAG					435

- (2) INFORMATION FOR SEQ ID NO:1115:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 477 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

GAATTCGGCC	AAAGAGGCCT	AGTGCCTAGA	TTGATCGGTA	TAAGGCTCAC	TCTCCCGCCC	60
CCCAAAGTGG	TTGATCGTTG	GAACGAGAAA	AGGGCCATGT	TCGGAGTGTA	TGACAACATC	120
GGGATCCTGG	GAAACTTTGA	AAAGCACCCC	AAAGAACTGA	TCAGGGGGCC	CATATGGCTT	180
CGAGGTTGGA	AAGGGAATGA	ATTGCAACGT	TGTATCCGAA	AGAGGAAAAT	GGTTGGAAGT	240
AGAATGTTCG	CTGATGACCT	GCACAACCTT	AATAAACGCA	TCCGCTATCT	CTACAAACAC	300
TTTAACCGAC	${\tt ATGGGAAGTT}$	TCGATAGAAG	AGAAAGCTGA	GAACTTCGGA	AAAGGCTCAT	360
CTGTCACCCT	GGAGAAGGGA	AACTGTACTT	TTCCCTGTGA	GGAAACGGCT	TTGTATTTC	420
TCTGTAATAA	AATGGGGCTT	CTTTGGAATT	TGATAAGCCT	AGGCCTCTTT	GGCCGAA	477

- (2) INFORMATION FOR SEQ ID NO:1116:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 620 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

${\tt GAATTCGGCC}$	AAAGAGGCCT	AAGATGAAGC	CCAACATCAT	CTTTGTACTT	TCCCTGCTCC	60
TCATCTTGGA	GAAGCAAGCA	GCTGTGATGG	GACAAAAAGG	TGGATCAAAA	GGCCGATTAC	120
			AAAAGGGCCA			180
			${\tt TTTCTATTCA}$			240
			AGCAATATGA			300
			GTCAACAACT			360
GCAGAGACCA	TGATAAATCA	AAAGGTCATT	${\tt TTCACAGGGT}$	AGTTATACAC	CATAAAGGAG	420
			${\tt CTCAAGATCA}$			480
AGGGAATATC	CAGTCAATAT	TCAAACACAG	AAGAAAGGCT	GTGGGTTCAT	GGACTAAGTA	540
AAGAACAAAC	TTCCGTCTCT	GGTGCACAAA	AAGGTAGAAA	ACAAGGCGGA	TCCCAAAGCA	600
GTTATGTTCT	CCAAACTGAA					620

- (2) INFORMATION FOR SEQ ID NO:1117:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 158 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

GAATTCGGCC	AAAGAGGCCT	AGACCTGCCA	CATTTGTTAA	CATTTTTCCA	TTTCTAAACC	60
ATCCTTAAAG	AAAATCATAT	ATGGGGTCAC	ACCATCCTCA	CGGTAGTCCA	ATAGAGCAAC	120
CATGCCATCT	GGATTCATGT	TTTCACCAAA	CCCTCGAG			158

- (2) INFORMATION FOR SEQ ID NO:1118:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 410 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

GCACTGCTTC TGTTAAAGTC	ACTGACCTTA	ACAGTTTAGA	ACTAGATAAA	GGAAATTTTG	60
TGGTTGACCA AATGTGTGAA	ATAGGTAAGC	CAGAACCATT	GAATGAGGAG	GAAGCAAGGG	120
GTGTGGTTGA GAATTATAAT	GATGAAGAAG	TGTCAATTAG	AGTTGGTGGA	AATACACAGC	180
CAAGTAAAGT TTTGAACAAA					240
GCAAAGCAGA TTATGAGCTA					300
CGTTTGCTGA AAATAGAAAT				GAATCTGATA	360
GAAACAAGGA ATCCAGTGAC	CAAACAGGCA	TTAATATTAG	TGGACTCGAG		410

- (2) INFORMATION FOR SEQ ID NO:1119:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 452 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

GAATTCGGCC	TTCATGGCCT	AGTTGCCCTA	ATTTGCAGCC	GAACTTGGAA	GCCACTGTAT	60
CCAATGGACC	TTTTCTGCAG	CTTTCTTCCC	AGTCTCTTAG	CCATAATGTT	TTTATGTCCA	120
CCAGTCCTGC	ACTTCATGGG	TTATCATGTA	CAGCAGCAAC	TCCGAAGATA	GCAAAATTGA	180
ATAGAAAACG	ATCCAGATCA	GAGAGTGACA	GTGAGAAAGT	TCAGCCACTT	CCAATTTCTA	240
CCATTATCCG						300
AAATTTCTCT	TCAACCTATA	GCAACTGTTC	CCAATGGAGG	CACAACACCT	AAAATCAGCA	360
AAACTGTACT	TTTATCTACT	AAAAGCATGA	AAAAGAGTCA	TGAACATGGA	TCCAAGAAAT	420
CTCACTCTAA	AACCAAGCCA	GGTTATCTCG	AG			452

- (2) INFORMATION FOR SEQ ID NO:1120:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 592 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

GAATTCGGCC TTCATGGCCT	ACATGAATCT	ACTTCTGATC	CTTACCTTTG	TTGCAGCTGC	60
TGTTGCTGCC CCCTTTGATG	ATGATGACAA	GATCGTTGGG	GGCTACATCT	GTGAGGAGAA	120
TTCTGTCCCC TACCAGGTGT	CCTTGAATTC	TGGCTACCAC	TTCTGCGGTG	GCTCCCTCAT	180
CAGCGAACAG TGGGTGGTGT	CAGCAGGTCA	CTGCTACAAG	TCCCGCATCC	AGGTGAGACT	240
GGGAGAGCAC AACATCGAAG					300
CATCCGCCAC CCCAAATACA					360
CTCCTCACCT GCCGTCATCA					420
AGCTGCTGGC ACCGAGTCCC					480
CTACCCAGAC GAGCTGCAGT					540
CTCCTACCCT GGAAAGATTA	CCAACAACAT	GTTCTGTGTG	GGCTTCCTCG	AG	592

- (2) INFORMATION FOR SEQ ID NO:1121:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

GAATTCGGCT	TCATGGCCTA	AATAATTTTT	ATTCAGAATA	ATAAATCACT	CTTTATCATA	60
GTATCTTCTC	TTCCCTCTTC	CCCTTTAGTT	TGGATAGCCT	AACTCTGAGA	AGTTAACCCT	120
TAAACAGTTT	TCTGGAAGAG	ACTGAATTTC	TGGGTCCTTG	CAGCTGTGAT	GGTTTCAGAG	180
CTCAGACTGA	TCAGGCATCA	AGCTACCCTC	AAGAGTTTCT	GGGCTGGATG	TTTCAGAACA	240
ACATCTACAC	CAGTAAAGTG	TAATAGGTCA	GTTTCAAAAC	GACCAAAAGA	CCCCACCACT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:1122:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 388 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

	TTCATGGCCT					60
	ATTTGGAATA					120
	GGATTTACTA					180
	TACAGAGTAG					240
	CCAGATGTCT					300
	TTGGTGTCTC		AATGATAGTT	TATTGGGTGC	TTATGTCAAA	360
TTTTCTTTTT	AATACTGGTA	ACCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:1123:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 478 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

AGCAATTCCA	TAAACACATC	CTGGTGTCAT	CACAGCCAAG	GTTTTTAGGT	TGCTATACCA	60
ATGGCTTATT	AAATGAAAAT	GGCACTAAAA	GTTTCTTGAG	ATTCTTTATA	CTCTCTGCCT	120
TCAGCAATCA	ATTCCATTCA	TACATCAGCA	CTCTGCTGGT	TCTGTTTGAA	ATATGTTCTG	180
				TGACCAATGA		240
GTTGATGGTT	GACAAAGCTT	GCTTCACTCC	ATCAGAGAAT	GACTATCAAT	TTTTTTTAA	300
CTGTCCTATC	ACGTCCTCTC	CTGTCACCCA	TTTTGAAGAG	TGGCAGAACT	TGAAGTTCAA	360
				TAGAATAACC		420
				GCCTCTTTGG		478

- (2) INFORMATION FOR SEQ ID NO:1124:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 450 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

GAATTCGGCC	AAAGAGGCCT	AGGAATTCAG	TGCAAACACT	ACTTTGAACT	GTGGTTCCTA	60
ATTTCCACGA	AAGTTTTTCT	CTGTTCTTCT	ATTATGGCAC	TTTTCAGGGT	CTCCCTTGTA	120
CATTTTAGTT	TTTGTGTTTT	TCAGTAAGTG	CCTTGAGATC	AGGGACCGGT	TCTACTGGTC	180
				ATTGGGTGAA		240
TTTATAGGAA	GCTCCTTAAC	CTGGGGTCCT	CAGACCTCTA	TGGGGTCCAT	GGACAGAATT	300
TGAAGTGGGA	AGGATATATG	AACTTGGATG	GAGGAAAATT	ACTTATTTGT	TTTTTACCAA	360
CCTCTCCTTT	GTAATTTAGC	CATTTGTTCA	ATTATAATGT	AGGCAAATAA	AAATAAAAT	420
	TAAAGGCAGC					450

(2) INFORMATION FOR SEQ ID NO:1125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 550 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

		ATCCTTAGTG				60
		TTTCTGGGGT				120
CCGGCGTTCG	GTTCATCCCG	CAGCGCCAGT	TCTGCTTACC	AAAAGTGGCC	CACTAGGCAC	180
		CACGCCAGCG				240
GAATAGGTTG	AGATCGTTTC	GGCCCCAAGA	CCTCTAATCA	TTCGCTTTAC	CGGATAAAAC	300
TGCGTGGCGG	GGGTGCGTCG	GGTCTGCGAG	AGCGCCAGCT	ATCCTGAGGG	AAACTTCGGA	360
		TTCGATTAGT				420
GATTTGCACG	TCAGGACCGC	TACGGACCTC	CACCAGAGTT	TCCTCTGGCT	TCGCCCTGCC	480
CAGGCATAGT	TCACCATCTT	TCGGGTCCTA	ACACGTGCGC	TCGTGCTCCA	CCTCCCCGGC	540
GCGGCGGGCG						550

- (2) INFORMATION FOR SEQ ID NO:1126:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 381 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

GAATTCGGCC	AAAGAGGCCT	AGTTTGCAGG	AAGAAGGCAT	GGGATAGTCT	GAGAACAAAC	60
				GGAGCTGGGA		120
GACTCCCAAG	GCCTTGCTGC	TGTTGGTCTG	CAGGCAGCTC	TGTAGGGCAG	GCTGTTGTCA	180
TTTTGCAAGT	GAGCAAGCAG	AAGCCCAGGC	AGGTGAGTCA	TTCACTCCAC	AGTTCATAAC	240
TTGGATTGTG	GGTTAGTTAC	ACCTGACTCC	AAAACTTGAC	TTTTTACTAC	TCAGCTATAC	300
TGGCCTCTCA	AGAAAGGCTA	GGCCCTAATT	TCTAGACTCT	CTTTTACCAA	TAATACCTGT	360
TGCCACGAAG	TAGGCCTCTT	T				381

- (2) INFORMATION FOR SEQ ID NO:1127:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 361 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

GAATTCGGCC	AAAGAGGCCT	ACTCTCAAGG	TGGGCATATG	CAAAACATAA	TCTCTAAATT	60
CTTCAATACT	AAGAAATACC	TTTGTTTTAC	CCCTAAAATC	AAATGCCATT	TTGGCTGGAT	120
ATAGGATTCT	AGGATTAAAG	CCTTTTTCCA	GCAGAACTTT	GAAGACATTG	CTCCATTTAC	180
TTCTAGCATC	CAGTGTGTCC	AGTGATAAGT	CTGCTGTCAA	CCTGATTCTT	GTTCCTTGGT	240
AGGTAATTTC	TCTTCTCTCT	CTAGAAGCCC	TTATTATTTT	CTCTTTATCA	CTAGAATTCC	300
		CTAGGAGTCA				360

G	361
(2) INFORMATION FOR SEQ ID NO:1128:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 359 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:	
GCAGCCAATG GCGGCGCCAG AGGGGAAACN GAGCCTTGCT NACGGGCCCA ACGCTGGGGA GCAGCCAGGC CAGGTGGCGG GCGCAGACTT CGAGAGCGAG GACGAGGGCG AGGAATTTGA TGACTGGGAG GACGACTACG ACTATCCCGA AGAGGAGCAG CTCAGTGGTG CCGGCTACAG AGTATCAGCC GCTCTTGAAG AAGCCGACAA GATGTTTCTG AGAACAAGAG AACCAGCCCT GGATGGCGGG TTTCAGATGC ATTATGAGAA GACCCCGTTT GATCAGTTAG CTTTTATCGA AGAGCTTTTT TCACTGATGG TTGTCAATCG TCTGACCGAA GAACCCGGCT GCTCTCGAG	60 120 180 240 300 359
(2) INFORMATION FOR SEQ ID NO:1129:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 274 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:	
GATGGCACCC TCCTCAGAAA GCAGCGTCCC CTCTCACAGT ATGTCCTCCC GACGGGACAC AGACTCGGAT ACCCAGGATG CCAATGACTC AAGCTGTAAG TCATCTGAGA GGAGCCTCCC GGACTGTACC CCTCACCCCA ACTCCATCAG CATCGATGCC GGTCCCCGGC AGGCCCCCAA GATTGCCCAG ATCAAGCGCA ACCTCTCCTA TGGAGACAAC AGCGACCCTG CCCTAGAGGC GTCCTCGCTG CCCCCACCCG ACCCCTGGCT CGAG	60 120 180 240 274
(2) INFORMATION FOR SEQ ID NO:1130:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:	
GGCTTTCCAC CTTCCCTGCG GAGATGAGGG TGGTGGCCTC CCTTTTTGTC ACCCTTCCAA GGGTCATGCT CGTCTGCTGG CTTTTCTCCA AGATGCTGCC AAAAATGATC TTAA1AAGAC ACAAGCCTGG TTGTGATATT TTCCTGATTC AAGTGTCTCT GTGGTTCTTG GTTGCCTTCA GGAGAGAGTT CAAGCCTCTT ATGGTGGTTT GTGAGGCCAG GCCTGAACTA GCCCCATCGT CTGTTCATTC ACCACCCCAG TATCCCTGCT GCAGGTTTTT AAAGATCTCA TGTCCCTGAT TGCCTGTCAC TGTGTCTGAC TCGAG	60 120 180 240 300 325

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 639 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

CTCGAGGATC	CCCGGGGACG	GGACGGGCCG	GGGCTTGGAG	GGGGGTCGGC	TGCCACAGGC	60
TCACATCACG	GCCTCCATAT	GCAGGATCCT	CAGGGCCTCG	GAGATCTGCG	CGCTGGGGTC	120
CATCTGGCCG	TACATGCCCA	CCAGGAAGGC	CCGGTGGAGC	AGCACAGCCG	CGTGCTCTTG	180
GCACAGGAGA	GCGTACTCAG	GCAGGTTCCG	GAGGGCCGTC	TGCACCACCT	CAAAGTCCTG	240
GCTGCCCAGG	CAGTACATGA	ACGTNGGGCA	GGAAAGCGGC	TGCAATGCNG	GGGGCTGTCT	300
GCATGGAGCG	CAGGGCCAGG	CTGAAGGCGA	GGTTGCGGCA	ACACTCCTCG	GCCGAGCTCA	360
TCAGCCGCTG	CAGGTTGGTC	GAGAAGAAGC	TCAGGATCTC	GGGTCTCCGC	CGGGACATCT	420
CGTCTATGTC	ACTCAGAACC	TCCAGCAGAT	CCTCCACCGT	TTGGCCCCGG	GAAAGCCGTT	480
TCATGTAGGG	GGCCATCTCG	GCCGCGGTCA	GAGGGGTGAA	CAGGGAGACG	CTGACCAGGG	540
			CCTCTTCGTC	CAGGCCTCGG	TCGGTCCTGT	600
CGTCCCTGCT	GGGCAGGCTG	AGCCCTGCAA	GGAGGGATC			639

- (2) INFORMATION FOR SEQ ID NO:1132:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 448 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GGTCTGTGGT	CTTGGAGGCT	TAAATTGTAA	AATACATCCC	TTATGGAATC	CTAAATTCCT	60
CTAGGTGTTT	TTGGAAGGCG	CATTTGAGCC	TTGTGAGCTA	AAATGGAATG	GATTTAATAT	120
TTCCTATCTG	GCATTTCCAT	CTTGCCCCTG	GTACACAAGT	CACTGGCCTG	GAACTCAGCC	180
TTGATTCACT	GTCCGTCTTC	ACGGATTAGC	TGTGCTGTTA	TGTTGTCTGT	GCTGCAGATT	240
GGCCCATGTG	${\tt GGAAGTCGGG}$	GGGGACCTGA	TTTCCTGCTT	GGAAGACTTG	GGGGACTGCC	300
GAGCATATCA	AAGTGTTTAT	AGTCACCAAG	TGAACTGCAG	CACAACCATC	TCCTCTCCAG	360
CAAGCCCTGA	AGTCAGTAGT	GCCTGCAGGT	GAAACCAACC	AGCCCTGTGT	TAGAGGAGGA	420
AAAGCGGAGA	${\tt TGACGTGGAA}$	GTCTCGAG				448
GGCCCATGTG GAGCATATCA CAAGCCCTGA	GGAAGTCGGG AAGTGTTTAT AGTCAGTAGT	GGGGACCTGA AGTCACCAAG GCCTGCAGGT	TTTCCTGCTT TGAACTGCAG	GGAAGACTTG CACAACCATC	GGGGACTGCC TCCTCTCCAG	300 360 420

- (2) INFORMATION FOR SEQ ID NO:1133:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 372 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

GAATTCGGCC	TTCATGGCCT	AGGGCTATGG	CCGGAGCTTG	AGATACGCCG	CTCTGAATCT	60
TGCCGCCCTG	CACTGCCGCT	TCGGTCACTA	TCAACAGGCA	GAGCTCGCCC	TGCAGGAGGC	120
AATTAGGATT	GCCCAGGAGT	CCAACGATCA	CGTGTGTCTC	CAGCACTGTT	TGAGCTGGCT	180
TTATGTGCTG	GGGCAGAAGA	GATCCGATAG	CTATGTTCTG	CTGGAGCATT	СТСТСААСАА	240

CAACATCTCG AG

GGCAGTACAT TTTGGGTTAC CGAGAGCTTT TGCTGGGAAG ACGGCAAACA AGCTGATGGA

TGCCCTAAAG GACTCCGACC TCCTGCACTG GAAACACAGC CTGTCAGAGC TCATCGATAT

300

360

(2) INFORMA	TION FOR SEQ ID NO:1134:	
(i) :	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 452 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1134:	
TTTTTAGTGC CCCATTTACA CATAGAAAAC AAGAAGGAAC TTTTATTCTG TATAACACAG	TTCATGGCCT AGCTGGTTCT TTTATTTTGG TGTCTCAGGG ATGTAAAAGA ATAATATTAA ATGGCAAAAT CAAATTTCCC AACAATATAC AAAATAAAAT	60 120 180 240 300 360 420 452
(2) INFORMA	ATION FOR SEQ ID NO:1135:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 283 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1135:	
AGAGGAGGTA CTTATTTAAC GGTAGCCGTC	TTCATGGCCT AGGAGGAGGG AAGGATTGGG AGCAGTGGGG TGTGAGTGGG GGGAACCAGA TGGGGAGAAT CGAGCCAAGT TCTGGGTTGG AGGAAACTTT TGAGCTGGTG GGTTACATAT CTAATGTTGC AGGTGATGAA TACAGGCTGG TAAATCCACC GAAAGAAGTA AATGAAAGTG GTTTCTTGTA GGTCGAAAGG TGGCTGGTTT TTAGGAAACA ACTGATCCTC GAG	60 120 180 240 283
(2) INFORMA	ATION FOR SEQ ID NO:1136:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 264 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1136:	
TGGATGAAAT CATACTGCAC	TTCATGGCCT ACTGGAGACT TGTAATTAGT CTAAGCATAA TATGATTAGG ATTTTGGAGT TTGGTTTTGT TTTAAATGTA AATACTCATG AAAAGTAAAA TGTGTCCCTG GGAATATTTT TGTTATCTTT AAAATACTCA GTATTATAGG CACAGCCTTA CATTTGCCCG GTTTGACCTG GAGGCCGAAA TGAATTGTGA	60 120 180 240
	469	

(i) SEQUENCE CHARACTERISTICS:

CTTATGTCCC AGCTGGGTCT CGAG

(2) INFORMATION FOR SEQ ID NO:1137:

PCT/US98/06956

(A) LENGTH: 653 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:	
GAATTCGGCC TTCATGGCCT ACCACGTTTC CTCACCTGTA AAATGGACAC TGCAGCTATG TCTGCTGTTC CACATTGTTG ATAGAACTGG ATGCTGTGGT GACATTTGGG ACACTATCAT GGTGCCTGGG GTGGTGGGT GCCCAGGCCT GTGGGCTTCT GTCTTTCATC AAAGAACTTC AGATCCCAGA AAATTAAGAT TCTCAAAACA TAACTGTCGG AAAGGGCTTT TGAATCCACC TTGGTGGCCT CTTCCTGCCT CCAGGGCTCA TGAGATAGGC TGACTTCATA TGAAAGTTTT GAGGATGAGG AAGTCTCTCT CCTCTTCAGA TACTGACCCT CTCTCTCATA TGAAAGTTTT GAGCACACCTA AGGCCTCTT TGGGTTCTGC TCAGCTTGAG GGCATCACCT AAAGGCCACT GGCTGCATTT TCCAGGAGGT GTTTTCTAAG CTGTATCTAT ATAGGAATGG GGAGGAAAGC TAAGTCATTG TAGACTGAGA GAAAGGGAAT AAGAGTCTGT TCCAGACCAG CTAGGGCTGA CAAGCTTAGG CAGCTGGGGG CAGAGGGCAC TGAGAATGAG GCCCTAGCTC GAG  (2) INFORMATION FOR SEQ ID NO:1138:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid	6 12 18 24 30 36 42 48 54 60 65
(C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:	
GAATTCGGCC TTCATGGCCT ACAAAAGGTT CTTGATGACC ACCACAATCC TCGCTTAATC AAAGATCTTC TGCAAGACCT AAGCTCTACC CTCTGCATTC TTATTAGAGG AGTAGGGAAG TCTGTATTAG TGGGAAACAT CAATATTTGG ATTTGCCGAT TAGAAACTAT TCTCGCCTGG CAACAACAGC TACAGGATCT TCAGATGACT AAGCAAGTGA ACAATGGCCT CACCCTCAGT GACCTTCCTC TGCACATGCT GAACAACATC CTATACCGGT TCTCAGACGG ATGGGACATC ATCACCATTC TCGAG	60 120 180 240 300 319
(2) INFORMATION FOR SEQ ID NO:1139:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 304 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:	
GAATTCGGCC AAAGAGGCCT AGTTAATACT TATTTTATTT	6( 12(
470	

TGACTTGATG	CTTTCTGTAT CTGGTGCACA GCTGTTACCT TGGAATCTTC CCTTCATCAT GTTTCTGTAG TTTTCTCTT GCATTGGATT TTGTGCTTCC TGAATCCTCT	180 240 300 304
(2) INFORM	ATION FOR SEQ ID NO:1140:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 303 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1140:	
TTAAGATTTT TTTTAGGAAA TATTCCTTTA	AAAGAGGCCT AGGGTTTTGT TTGGTTTGGT TTTAGTTTTT TGTGGGAGAA TTAAAGAGATA TTTTCAGATT TTTCTGTTGT CAGTTTTGGT AATTTCTGTC ATTCATTTC ATCCAAGTTG TTGGATTAT TGGCATAAAA TTTTTCAGAA ATATCCTTCT AATGTCTGTA GAATCTAATC TGTATTGCAG TCTCTTCATA GTGTTTTTTC TATTTTTCC TGGATCAGTC AGTCTAGCTG GGGAGAACTC	60 120 180 240 300 303
(2) INFORM	ATION FOR SEQ ID NO:1141:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1141:	
TACTCTCTCC ATGGAAGTAT CTCTGCTCCA GCTTCATTTC	AAAGAGGCCT AGTAGCTTAG TTATTGTTTA CTTTGAAGCC CTTTTGCCTC CATATATCTT CTCCTGACAG GGTGAAGTCA CCTATAGCAT TTCCTAGTGT TAATTTCTTT CTTTACTGGA AGAGCTACTA GCTTTTCTTC ATACAGTTTC GTTTCATAAG TTTCTTTTTG GCTTGTATCT GTTTAGGATC AGGTGATATG TCATGACTGA AGCCCGGCAA CATAACACTG AAATTCGAAT GGCAGTCAGC ATAAAACGGA TCATCTCGAG	60 120 180 240 300 330
(2) INFORMA	ATION FOR SEQ ID NO:1142:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 294 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1142:	
TTCTGGGGAT AGAGAGCTTT	AAAGAGGCCT AGAGGGGAGC CTGGCCTCTG GCATATTCAT CAAGTATGAG GAGTCACTGT AATGATGTGA GCAGGGAGCC TTCCTCCCTG GGCCACCTGC CCCACCAACT TTGTACCTTG ATTGCCTTAC AAAGTTATTT GTTTACAAAC TAAAAAGCCTC CTGCCCCAAA GCTTGTGGGC ACATGGGCAC ATACAGACTC	60 120 180 240

ACATACAGAC ACACACATAT ATGTACAGAC ATGTACTCTC ACACTCCAGT CGAG

(2) INFORMATION FOR SEQ ID NO:1143:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 331 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:	
GAATTCGGCC AAAGAGGCCT AGTTTTAGTT CAGAATAACA TTAATTTTGA GAGATTGAGG TAAAGAACCT TAACTAATGC TAAGGAGTTT ATTTTGATTA ACATAGGTTA TTCTGACCAC CACCTCTTCC TTCCTTAATC TCCTTAGAAT CTGACAGTCT CAAAGCTGTC ACACAAATTA GACTAATTTT GACACTTTGA AATGAAAACT TCAAGGAAGA AGTAGCCACG GACAGTTATG TTTATAATCA GTAGGTGGCA CTCTTTCCTC AGGTAGCCCC CCATTTTCAC ATGATGTGTT TGAAGGTTAA ATGCCACCAA AAGTGCTCGA G  (2) INFORMATION FOR SEQ ID NO:1144:	60 120 180 240 300 331
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 508 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:	
GAATTCGGCC AAAGAGGCCT ACTTCAGCAT GACTACTCAG TTGCCAGCTT ACGTGGCAAT TTTGCTTTTC TATGTCTCAA GAGCCAGCTG CCAGGACACT TTCACTGCAG CTGTTTATGA GCATGCAGCG ATATTGCCCA ATGCCACCCT AACACCAGTG TCTCGTGAGG AGGCTTTGGC ATTAATGAAT CGGAATCTGG ACATTTTGGA AGGAGCGATC ACATCAGCAG CAGATCAGGG TGCGCATATT ATTGTGACTC CAGAAGATGC TATTTATGGC TGGAACTTCA ACAGGGACTC TCTCTACCCA TATTTGGAGG ACATCCCAGA CCCTGAAGTA AACTGGATCC CCTGTAATAA TCGTAACAGA TTTGGCCAGA CCCCAGTACA AGAAAGACTC AGCTGCCTGG CCAAGAACAA CTCTATCTAT GTTGTGGCAA ATATTGGGGA CAAGAAGCCA TGCGATACCA GTGATCCTCA GTGTCCCCCT GATGGCCGTT CGCTCGAG	60 120 180 240 300 360 420 480 508
(2) INFORMATION FOR SEQ ID NO:1145:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 461 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:	
GAATTCGGCC AAAGAGGCCT AAATTGCTGG CGGATTTAGA CCCGGGAAA ACCCGGGATG GTTTATTTTG ATTGAGCCCC CTCTGGGTGG CAGAGAGGAG GCTTGGGCTC TGGGCCCTTT ACGTTTGGAG AAATGGCTTT ATCAGCTCAG TTGAAAGGTT TTTCCCTCTA GCTAGTGAAA GATAAACTTG GAAATGCAGG TTTCTCCAGC GGTTGGTGGT GGGGGACAGGG GTCGCCTAGG	60 120 180 240
470	

(2) INFORMATION FOR SEQ ID NO:1146:  (i) SEQUENCE CHARACTERISTICS: (ii) LENGTH: 291 base pairs (iii) MOLECULE TYPE: cduela caid (iii) MOLECULE TYPE: cDNA (iiii) MOLECULE TYPE: cDNA (iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	TTTTCTAGAG TCATGGTCCT	GGGCCGCGGC CTCTGTTGTG CTCTTCTGGA GAGTGCACTG TTTGTGGAAC TGGCAAAAAC GATCTCCACT GTCGGTGAAA GGGCAGTTCC TGAAGTCAGC GGCTCCCCTT CTCCCCAGCA GTGAACTGGG GGTGACTTCC TGATCTGCCC AGCCCCGCAA AGCGCCTGGG AGGCCCTCGA G	300 360 420 461
(A) LENGTH: 291 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:  GAATTCGGCC TTCATGGCCT ACCATTTGG ATTGATTTTT GTGTATAGTG TAAGATGAAC CCCAATTCCT TCTTTAGCAT GTGGGAATTC TGTTTTTCTG TCACCCTTT TTTTTGAGAT 120 GGGGTCTCAC TATGTGCCC AGGTTGGCCA TGAACTCCTG AGGTCATGT ATCCTCTCC CTCAGCCCC TGAGTAGCTA GGACTACAGG CATGTGCCAC TGTGCCTGG TCCAGCACAC GTGTTGTAGAA GAACTCTCT TTATTTACTT ATTGTATCCT CTGTGCTCGA G  (2) INFORMATION FOR SEQ ID NO:1147:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 338 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:  GAATTCGGCC TTCATGGCCT ACCCACCTGC CCAGCCGCA TTGGGAGGAT GGTGGCCTGC AGCGGCCAAG AAGCCAATAAA AAAAAATTTT TTTTTTTCA GATACTGTGC TTGATTTTG 120 GAGAGGGGAAA AACCCCTTTTC CCTGAATGGC CTAATGCACT GTTCCCTCCA GCCCGAATGC CTCCTGCCAA ACCCCTTTTC CCTGAATGGC CTAATGCACT GTTCCCTCCA GCCCGAATGC CTCCTGCCAA ACCCCTTTTC CCTGAATGGC CCACCTGAG GATCTTCTT TCCCTGGGT CTCCTGCCAA ACCCCTTTTC CCTGAATGGC CTCAATGCAC GTCCTTGTT TCCCTGGGT CTCCTGCCAA ACCCCTTTTC CCTGAATGGC CAATGCAC TCCTTGTTC TCCCTGGGT CTCCTGCCAA ACCCCTTTTC CCTGAATGGC CAATGCACTTTA GGTTTCCAA CTCTTGCTTT GGTGTTTTGCC GCAGCATGGA AAACAGGCAC CCCTCGAG  (2) INFORMATION FOR SEQ ID NO:1148:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDENNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCCCTG AAGGGGAGA CATGAGCAAG GCAGAGCTGA GCCACTGCGC CCGCCTGAA GAGTTTTTGC TAATTGCAT TTAGGGAAAA 120 CCACAGGAACCA GATTAACACTCA TTAGTAAGCC GCACTCCCTGC AAGGGGAGA CATGAGCAAG GATTATCTCT CTCTGCTGCTTTTTTCTCAC TTTTCTGTGC AAGCTCTTTT TGTTGGTTTG TTTATTCTCAC TTTTCTGTGC AAGCTCTATCC ACCTCTTTTT TGTTGTTGTTTG 240	(2) INFORM	ATION FOR SEQ ID NO:1146:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:  GAATTCGGCC TTCATGGCCT ACCATTTTGG ATTGATTTTT GTGTATAGTG TAAGATGAAC CCAATTTCCT TCTTTAGCAT GTGGGAATTC TGTTTTTCTG TCACCCTTTT TTTTTGAGAT 120 GGGGTCTCAC TATGTTGCCC AGGTTGGCCA TGACCTCCTG AGGTCATGTG ATCCTCCTC CTCAGCCTCC TAGATGACTA GGACTACAGG CATGTGCCAC TGTGCCTGGC TCCAGCACAC GTTGTTGAAG AGACTGTTCT TTATTTACTT ATTGTATCCT CTGTGCTGGA GCCACACAC GTTGTTGAAG AGACTGTTCT TTATTTACTT ATTGTATCCT CTGTGCTGGA GCCACACAC GTTGTTGAAG AGACTGTTCT TTATTTACTT ATTGTATCCT CTGTGCTGGA GCCACACAC  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 338 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:  GAATTCGGCC TTCATGGCCT ACCCACCTGC CCACGCCGAC TTGGGAGGAT GGTGGCCTGC AGCGGCCAAG AAGCCAAAAA AAAAAATTTT TTTTTTTTCA GATACTGTGC TTGATTTTTG 120 GAGAGGGGA AGGTGGAAAT TCTAAATGG CTAAACAGGA GATCCTTGTTC TCCCCTGGGT 240 CCCGAAACATT TTTTCCGAGG ATGAACAGGG GACACTTTTA GGTTCCTCAA CTCTTGCTTT GGTGTTTGCC GCAGCATGGA AAACAGGGCA CCCTCGAG  (2) INFORMATION FOR SEQ ID NO:1148:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 395 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGAG CATGAGCAAG GCAGACGTGA GCCACTGCGC CGGGCCTGAA GGTTATGTCT TAGGGAAAA  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:	(i)	(A) LENGTH: 291 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
GAATTCGGCC TTCATGGCCT ACCATTTTGG ATTGATTTTT GTGTATAGTG TAAGATGAAC CCAATTTCCT TCTTTAGCAT GTGGGAATTC TGTTTTTCTG TCACCCTTTT TTTTTGAGAT GGGGGTCTCAC TATGTTGCCC AGGTTGGCCA TGAACTCCTG AGGTCATGGT ATCTCTCTTC 180 CTCAGCCTCC TGAGTAGCTA GGACTACAGG CATGTGCCAC TGTGCCTGG TCCAGCAACA GTTGTTGAAG AGACTGTTCT TTATTTACTT ATTGTATCCT CTGTGCTCGA G 291  (2) INFORMATION FOR SEQ ID NO:1147:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 338 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:  GAATTCGGCC TTCATGGCCT ACCCACCTGC CCACGCCGAC TTGGGAGGAT GGTGGCCTGC AGCGGCCAAAA AAAAAATTTT TTTTTTTTCA GATACTGTC TTGATTTTTG GAGAGGGAA AGGCCAAAAA AAAAAATTTT TTTTTTTCA GATACTGTC TTCCCTCCAG GCCGAATGC CTCCTGCCAA ACCCCTTTC CCTGGTGCCC TGTCCCCCC ATCCTTGTCT TCCCCTGAGT 240 CCGAAACATT TTTTCGGAG ATGAACAGGG GACATCTTTA GGTTTCCTCCA GCCGAATGC CCCAAACAAT TTTTCCGAGG ATGAACAGGG GACATCTTTA GGTTTCTCAA CTCTTGCTTT GGTGTTTTGCC GCAGCATGGA AAACAGGCAC CCCTCGAG  (2) INFORMATION FOR SEQ ID NO:1148:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGG CATGAGCAAG GCAGGAGTGA GCCACTCCCC CCGGCCTGAA GAGTTTTTCC TAATTGGATA TTAGGGAAAA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGG CATGAGCAAG GCAGGAGTGA GCCACTGCCC CCGGCCTGAA GAGTTTTTCC TAATTGGATA TTAGGGAAAA 120 CCCACAGGGAT GATTAAGACA AAGAGGGGAA GGTAAGGTTT TGAATCACAGG GATTATGTCT GTTAGTTGGT TTTATTGTCAC TTTTCTTGCC AAGCCTTTACC TTCTCTTTT TTTTTTTTTT	(ii)	MOLECULE TYPE: cDNA	
CCAATTCCT TCTTTAGCAT GTGGGAATTC TGTTTTCTCT TCACCCCTTT TTTTTAGAT 120 GGGGGTCTCAC TATGTTGCCC AGGTTGGCCA TGAACTCCTG AGGTCATGTA ATCCTCCTTC 180 CTCAGCCTCC TGAGTAGCTA GGACTACAGG CATGTACCCAC TGTGCCTGGC TCCAGCAACA 240 GTTGTTGAAG AGACTGTTCT TTATTTACTT ATTGTATCCT CTGTGCTGGA G 291  (2) INFORMATION FOR SEQ ID NO:1147:  (i) SEQUENCE CHARACTERISTICS:	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1146:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 338 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:  GAATTCGGCC TTCATGGCCT ACCCACCTGC CCACGCCGAC TTGGGAGGAT GGTGGCCTGC AGCGGCCAAG AAGCCAAAAA AAAAAATTTT TTTTTTTCA GATACTGTGC TTGATTTTG 120 GAGAGGGGAA AGCCCATTTC CCTGCTGCCT CTGTCCCCGC ATCCTTGTC TCCCCTGGGT 240 CCGGAAACATT TTTTCGAGG ATGAACAGGG GACATCTTTA GGTTTCTCAA CTCTTGCTTT 300 GGTGTTTGCC GCAGCATGGA AAACAGGCAC CCCTCGAG 338  (2) INFORMATION FOR SEQ ID NO:1148:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGG CATGAGCAAG GCAGACGTG GCCACTGCGC CCGCCTGAA GAGTTTTTGC TAATTGGATAA TTAGGGAAAA 120 CCACAGGATG GATTAAGACA AGAGAGGGAA GGTTAAGGTTC TAGACAGCAG GATTATGTCT 180 GTTAGTTGGT TTTATGTCAC TTTTCTAGCC AAGCTGTAC ATCCTGTTTT TGTTGGTTGG 240	CCAATTTCCT GGGGTCTCAC CTCAGCCTCC	TCTTTAGCAT GTGGGAATTC TGTTTTTCTG TCACCCTTTT TTTTTGAGAT TATGTTGCCC AGGTTGGCCA TGAACTCCTG AGGTCATGTG ATCCTCCTTC TGAGTAGCTA GGACTACAGG CATGTGCCAC TGTGCCTGC TCCAGCAACA	120 180 240
(A) LENGTH: 338 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:  GAATTCGGCC TTCATGGCCT ACCCACCTGC CCACGCCGAC TTGGGAGGAT GGTGGCCTGC AGCGGCCAAG AAGCCAAAAA AAAAAATTTT TTTTTTTTCA GATACTGTGC TTGATTTTTG GACAGGGGAG AGGCGAAAA AAAAAATTTT TTTTTTTTCA GATACTGTGC TTGATTTTTG GACAGGGGAG AGGCGAAAA AAAAAATTTT TTTTTTTCA GATACTGTGC TTGATTTTTG GACAGGGGAG AGGCGAAAA AAAAAATTTT TTTTTTTCA GATACTGTGC TCCCCCGGATGC GCCCAAAACATT TTTTCCGAGG ATCAACAGGG GACACTCTTA GGTTTCCTCAA CTCCTGGGT 300 GGTGTTTGCC GCAGCATGGA AAACAGGCAC CCCTCGAG  (2) INFORMATION FOR SEQ ID NO:1148:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGG CATGAGCAAG GCAGACGTGA GCCACTGCGC CCGGCCTGAA GAGTTTTTGC TAATTGGATAA TTAGGGAAAA 120 CCACAGGATG GATTAAGACA AGAGAGGGAA GGTTAAGGTT TGATTGGCTTT TGTTGGTTGG TTTAGTTGGT TTTATGTCAC TTTCTAGCC AAGCTGTACC ATCCTGTTT TGTTGGTTGG 240	(2) INFORM	ATION FOR SEQ ID NO:1147:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:1147:  GAATTCGGCC TTCATGGCCT ACCCACCTGC CCACGCCGAC TTGGGAGGAT GGTGGCCTGC AGCGGCCAAG AAGCCAAAAA AAAAAATTT TTTTTTTTCA GATACTGTGC TTGATTTTTG 120 GAGAGGGGAG AGGTGGAAAT TCCTAAATGG CTAATGCACT GTTCCCTCCA GCCCGAATGC 180 CTCCTGCCAA ACCCCTTTTC CCTGGTGCCT CTGTCCCGGC ATCCTTGTC TCCCCTGGGT 240 CCGAAACATT TTTTCCGAGG ATGAACAGGG GACATCTTTA GGTTTCTCAA CTCTTGCTTT 300 GGTGTTTGCC GCAGCATGGA AAACAGGCAC CCCTCGAG 338  (2) INFORMATION FOR SEQ ID NO:1148:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGAG CATGAGCAAG 60 GCAGGACGTGA GCCACTGCGC CCGGCCTGAA GAGTTTTTGC TAATTGGATA TTAGGGAAAA 120 CCACAGGATG GATTAAGACA AGAGAGGGAA GGTAAGGTTC TAGACAGCAG GATTATGTCT 180 GTTAGTTGGT TTTATGTCAC TTTTCTAGCC AAGCTGTACC ATCCTGTTTT TGTTGGTTGG 240	(i)	<ul><li>(A) LENGTH: 338 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
GAATTCGGCC TTCATGGCCT ACCCACCTGC CCACGCCGAC TTGGGAGGAT GGTGGCCTGC AGCGGCCAAG AAGCCAAAAA AAAAAATTTT TTTTTTTTCA GATACTGTGC TTGATTTTTG 120 GAGAGGGGAG AGGTGGAAAT TCCTAAATGG CTAATGCACT GTTCCCTCCA GCCCGAATGC 180 CTCCTGCCAA ACCCCTTTC CCTGCTGCCT CTGTCCCCGC ATCCTTGTTC TCCCCTGGGT 240 CCGAAACATT TTTTCCGAGG ATGAACAGGG GACATCTTTA GGTTTCTCAA CTCTTGCTTT 300 GGTGTTTGCC GCAGCATGGA AAACAGGCAC CCCTCGAG 338  (2) INFORMATION FOR SEQ ID NO:1148:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 385 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGAG CATGAGCAAG GCAGACGTGA GCCACTGCGC CCGGCCTGAA GAGTTTTTGC TAATTGGATA TTAGGGAAAA 120 CCACAGGATG GATTAAGACA AGAGAGGGAA GGTAAGGTTC TAGACCAGCAG GATTATGTCT 180 GTTAGTTGGT TTTATGTCAC TTTTCTAGCC AAGCTGTACC ATCCTGTTTT TGTTGGTTGG 240	(ii)	MOLECULE TYPE: cDNA	
AGCGGCCAAG AAGCCAAAAA AAAAAATTTT TTTTTTTCA GATACTGTGC TTGATTTTTG GAGAGGGGAA AGGTGAAAT TCCTAAATGG CTAATGCACT GTTCCCTCCA GCCCGAATGC CTCCTGCCAA ACCCCTTTC CCTGCTGCCT CTGTCCCCGC ATCCTTGTTC TCCCCTGGGT CCGAAACCATT TTTTCCGAGG ATGAACAGGG GACATCTTTA GGTTTCTCAA CTCTTGCTTT GGTGTTTGCC GCAGCATGGA AAACAGGCAC CCCTCGAG  (2) INFORMATION FOR SEQ ID NO:1148:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 385 base pairs  (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: CDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGAG CATGAGCAAG GCAGACGTGA GCCACTGCGC CCGGCCTGAA GAGTTTTTGC TAATTGGATA TTAGGGAAAA 120 CCACAGGATG GATTAAGACA AGAGAGGGAA GGTAAGGTTC TAGACAGCAG GATTATGTCT 180 GTTAGTTGGT TTTATGTCAC TTTTCTAGCC AAGCTGTACC ATCCTGTTTT TGTTGGTTGG	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1147:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 385 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGAG CATGAGCAAG GCAGACGTGA GCCACTGCGC CCGGCCTGAA GAGTTTTTGC TAATTGGATA TTAGGGAAAA 120 CCACAGGATG GATTAAGACA AGAGAGGGAA GGTAAGGTTC TAGACAGCAG GATTATGTCT 180 GTTAGTTGGT TTTATGTCAC TTTTCTAGCC AAGCTGTACC ATCCTGTTTT TGTTGGTTGG 240	AGCGGCCAAG GAGAGGGGAG CTCCTGCCAA CCGAAACATT	AAGCCAAAAA AAAAAATTTT TTTTTTTTCA GATACTGTGC TTGATTTTTG AGGTGGAAAT TCCTAAATGG CTAATGCACT GTTCCCTCCA GCCCGAATGC ACCCCTTTTC CCTGCTGCCT CTGTCCCCGC ATCCTTGTTC TCCCCTGGGT TTTTCCGAGG ATGAACAGGG GACATCTTTA GGTTTCTCAA CTCTTGCTTT	120 180 240 300
(A) LENGTH: 385 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGAG CATGAGCAAG  GCAGACGTGA GCCACTGCGC CCGGCCTGAA GAGTTTTTGC TAATTGGATA TTAGGGAAAA 120  CCACAGGATG GATTAAGACA AGAGAGGGAA GGTAAGGTTC TAGACAGCAG GATTATGTCT 180  GTTAGTTGGT TTTATGTCAC TTTTCTAGCC AAGCTGTACC ATCCTGTTTT TGTTGGTTGG 240	(2) INFORM	ATION FOR SEQ ID NO:1148:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:  GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGAG CATGAGCAAG GCAGACGTGA GCCACTGCGC CCGGCCTGAA GAGTTTTTGC TAATTGGATA TTAGGGAAAA 120 CCACAGGATG GATTAAGACA AGAGAGGGAA GGTAAGGTTC TAGACAGCAG GATTATGTCT 180 GTTAGTTGGT TTTATGTCAC TTTTCTAGCC AAGCTGTACC ATCCTGTTTT TGTTGGTTGG 240	(i)	<ul><li>(A) LENGTH: 385 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
GCAGGAATCA GATTCACTCA TTAGTAAGCC GCACTCGCTG AAGGGGAGAG CATGAGCAAG GCAGACGTGA GCCACTGCGC CCGGCCTGAA GAGTTTTTGC TAATTGGATA TTAGGGAAAA 120 CCACAGGATG GATTAAGACA AGAGAGGGAA GGTAAGGTTC TAGACAGCAG GATTATGTCT 180 GTTAGTTGGT TTTATGTCAC TTTTCTAGCC AAGCTGTACC ATCCTGTTTT TGTTGGTTGG 240	(ii)	MOLECULE TYPE: cDNA	
GCAGACGTGA GCCACTGCGC CCGGCCTGAA GAGTTTTTGC TAATTGGATA TTAGGGAAAA 120 CCACAGGATG GATTAAGACA AGAGAGGGAA GGTAAGGTTC TAGACAGCAG GATTATGTCT 180 GTTAGTTGGT TTTATGTCAC TTTTCTAGCC AAGCTGTACC ATCCTGTTTT TGTTGGTTGG 240	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1148:	
	GCAGACGTGA CCACAGGATG GTTAGTTGGT	GCCACTGCGC CCGGCCTGAA GAGTTTTTGC TAATTGGATA TTAGGGAAAA GATTAAGACA AGAGAGGGAA GGTAAGGTTC TAGACAGCAG GATTATGTCT TTTATGTCAC TTTTCTAGCC AAGCTGTACC ATCCTGTTTT TGTTGGTTGG	120 180 240

GCTCTTTGCA GGCGGCTTAC TCGAG

ATCTAGCTAG GGTGATGAGT AGGAATAGCA ATAAGTGACA GGGAAGTTGA AGGCTGCAGG

GCTCTTTGCA GGCGGCTTAC TCGAG	385
(2) INFORMATION FOR SEQ ID NO:1149:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 303 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:	
GAATTCGGCC TTCATGGCCT AGTCACATGA ATGAGAGAAT TCTAAATGCA AGAAATGTGC AAAGGCACAG AAACACAGAA GAGCATGTTG TACAACCTGG CTATAGTTTA GATTTTGTGT GTGTGCTATG AGAGTGTGCG TGTGCTGTGA GTGTGTGTGT GGGCGCACGC ACGCATTTGT AGGAGGTAGG GAGAAGAGTG CCGGCATAAC ATGAAATGAT ATTGGACCTC AAATGGTATG CTAAGATGTT TGACAATTTT ATTCTAAGCA GTGAGTTTTT AAATTTAGAC ATGCAATCTC GAG	60 120 180 240 300 303
(2) INFORMATION FOR SEQ ID NO:1150:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 419 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:	
GAATTCGGCC AAAGAGGCCT AATTGAATTG TATTGGTCTT TTTCTCTTTA ATATTTTAGG TGCTTTATTA TATATTAGGA TTATTAGTCC TTAGTTTGTG AAATAAGCTG CAAATATTTT TTCCCCAATT TTTCTTTTGT CTCTTTGCTT TATTTCTGGT GTTTATTTTT CCCCAGGTGT ACTGTTTTCT ATAGCCAAAT TATTGATCTT TTCTTTAATT GCTTTTTTTT TCACTCAAAG GAAGGTTTTC ACCACTGAGA GGTTATAAAA TAATTCACTC ATATTTTTAC TCTTTTTTTT	60 120 180 240 300 360 419
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 394 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:	
GAATTCGGCC AAAGAGGCCT AGCGGATGGA GTCTTTGACA GTGTTTTTGA TCTCCTGCAG ACGGCTGCTC AGGAAGCTGT TGACCCGATC CAGTTCCCGG TCGGGCCACT CCAAGAGCCT CTCCCTGGCA GGCCTTGGCT CCCGGCTTCC AGAAACACGA TTTGCCTGCT TTAGAGCTTC TGCTGCCAAC TGGGCCTTCT CCTTTTCCTT CTTTTTCAGC TTGTGCCGGG CCCGCTTGGC GGCCCTGGCG CTGTTGGGGA CTTTGGGCTC CGTGCTGTTG ATGAATTCCA GCAGCTCATC	60 120 180 240 300
474	

CACATCTCGG TGGTCCACGG CGGGCTCCCC AGGGATCCCG CCCAGGGTGC CCCCCTTCAT

GGGCAGCTCC	TCTTTCCGCC TGGTCAGCCT CGAG	394
(2) INFORMA	TION FOR SEQ ID NO:1152:	
(i)·S	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 426 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1152:	
AGCTGTTCCG G GTCTGCAGCC A TTCCTGAATC A GCGCTCCTGA A TACGGCCGGG G	AAAGAGCCTA CTGTGAATCA CGAACTGGCT GAGGGCGGCT GACCGCTTGT GCCATGCACC ATAAGAACCG GCCAAGATGC TTAAATTGAG TGATGGAGAA AACGAAGCCT GTTTCCTTC CTTTCCTTCC ACTCCCACGC CGCAGTCAGA ATGCTGACGT CATTGCCTCC GTCCCCTACT GCACAGGTGA GCTTGCCCGT AGCAGGCGCA CGATCTGGGC CTTCTGGGTG GGGGCACATC NGCAGCAGAC CACTGGCAGG CCAGCTCCAT GAACTCGTAC TCATAGTACT TGAGGCAAAC ICTCCCCGAGA TGACCAGGGC ACAATCATGC TTCCTGCGGA AGGCGTTCAG	60 120 180 240 300 360 420 426
(2) INFORMAT	TION FOR SEQ ID NO:1153:	
(i) S	EQUENCE CHARACTERISTICS:  (A) LENGTH: 270 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1153:	
CGGCTTGGAT TAGGTGCTGTG A	AAAGAGGCCT AAGCTGATAT TTATTGGACA TTTGCACCAT GCCAAGCATT IATCCCATTT GTTTCTCACA GCCGGTATTT ATTGTCTGCT CCTCTGTGCC CTCTGGGCAG GGGCACTGCA TGGGCTGCCT GCCCTGGTGG AGCTTGTGGT AGGCTGACCC AAGCCCACCC CATTGCCAAC AGGGCCAGGG CAAGAGTACA ICATACCATA TGTCCTCGAG	60 120 180 240 270
(2) INFORMAT	FION FOR SEQ ID NO:1154:	
(i) S	EQUENCE CHARACTERISTICS:  (A) LENGTH: 582 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1154:	
ACACAAGGAA A GTTCCAAGAA 1 ACAGGCAGCA 1	AAAGAGGCCT AGCTGAAATC ATTCTGAAAA CTCAAACAGT AGACTTCAGC AGCCAAAGCC ATTTGAGGGG GAATAAAGCC AAAAGCCTTT CACCTTATTC ICTCACCGCC CCCTCCTTAT CCCCCTCCAA AAATAAGCCA TTGCACACAG IGGCTAGCAA ACGAAAATCT ACAACTCCAT GCATGGTTCG GACATCACAA AAGATGTGCC CGAGGAAGTA GACAGGGCCA AAGAGAAAGG AATCGGCACA	60 120 180 240 300

CCACAGCCTG ACGTGGCCAA GGACAGTTGG GCAGCAGAAC TTGAAAAACTC TTCCAAAGAA AACGAAGTGA TAGAGGTGAA ATCTATGGGG GAAAGCCAGT CCAAAAAACT CCAAGGTGGT IATGAGTGCA AATACTGCCC CTACTCCACG CAAAACCTGA ACGAGTTCAC GGAGCATGTC GACATGCAGC ATCCCAACGT GATTCTCAAC CCCCTCTACG TGTGTGCAGA ATGTAACTTC ACAACCAAAA AGTACGACTC CCTATCCGAC CACAGACTCG AG	360 420 480 540 582
(2) INFORMATION FOR SEQ ID NO:1155:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 279 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:	
GAATTCGGCC TTCATGGCCT AGGATCCGTG AGGGAGACCG CATCATCCAG ATTAACGGTG CAGCACCA GAACCGGGAA GAGGCGGTGG CCATCCTGAG CCAGGAAGAG AACACCAACA CCTCCCTGCT GGTGGCCCGA CCTGAGAGTC AGCTGGCGAA AAGGTGGAAG GACACCGACC GGGATGACTT CCTGGATGAC TTTGGCTCTG AGAATGAGGG GGAGCTGCGT GCTCGTAAAC CCCTGCCCAG CAGCCCGGAA ACACTCGAG	60 120 180 240 279
(2) INFORMATION FOR SEQ ID NO:1156:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 353 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:	
SAATTCGGCC AAAGAGGCCT ACATTGTTAA TATAATTTAA CAGAAGTTGT GAAACTAAAA FTTTCTAAGA TTAACTGGTA GTTCATTGTA AATGAACATA ATGAACAGAA TTTATGACTC CACTGTGGAA AATGCTATCA AATAACTAAG GAATATATAT GGAATAAGTG TACATATGTA AAATATTGTT ACTAGAGTTA GATATGTGCC AAAGTCCATT TATCCCAAAT CCTGTCTGAA AAGGAGGGGT ACATTGGTAA ACATTTTGGA GTGCTTAAAA ATGCCAAAAA CAAAATGGTA ATTCTACTT TGATAAAGTA AAAAAGTTAA ATGTGTGTAA AAAAGTGCTC GAG	60 120 180 240 300 353
(2) INFORMATION FOR SEQ ID NO:1157:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 331 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:	
SAATTCGGCC TTCATGGCCT ACGGTGGCCT TTGGGGCCGA AGTGGGCGTG CGGCTCGCGC PGTTCGCGGC CTTCCTGGTG ACGGAGCTGC TCCCCCCGTT CCAGAGACTC ATCCAGCCGG AGGAGATGTG GCTCTACCGG AACCCCTACG TGGAGGCGGA GTATTTCCCC ACCAAGCCGA PGTTTGTGCG TGGAGAAAGA TCGTCTTTCC TCCCTCCCCA TGACCGGGCT TCCCGCGGGC	60 120 180 240

ACCTGTGCGT TTTCCACCCC GAGACGGCCT TTGTAGGGAC CCACTGCCCA CTCCGCTGCT GTGCGCTGGG TTCCGCCTCC TAGGGCTCGA G

(2) INFORM	ATION FOR SEQ ID NO:1158:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 178 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1158:	
GTTTTATTT TTGGTGAATT	TTCATGGCCT AAAAACTTAG ACTGACATCT AGCTTTGACA ATCATAGTAT CCTGAGGGGG AATAACTTAT AATGCTGTTT AGTTTTGTAC TATTGGTGTG TTTAAACTGT GTGCTAACTG CACGATTGAA TTCTAGACCT GCCTCGAG	60 120 178
(2) INFORM	ATION FOR SEQ ID NO:1159:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 401 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1159:	
CTGGAGTTCA CTTTACTGTT AATATTATCT CATGATCATC CATACCTTAT	TTCATGGCCT AAGCACTTTG GGATGTTGAA GTGAGGGGAT TGCTTGAGCC AGACCAGGCT GGGCAATATC GCCAGACCCC ATCTCTTAAA AAAAGTAGTT GCCTCTATTG ACTCTTGAAT GCAAGAAAGA ACATTTGCCC TTTGACTTCT TATATTCTCT CTTCTAAA AGATCAGAAG CACATGCTGT AAACATCAAT TTTGTCTCCC TTATCAGATT GTCAAAATTA TATCTTTTCC TATTTTCCTG CTTTTTCCTA AATTCTCAGT TCTCCAAGTT CTCAGAAATC ATAACTTCAG GATGACTCTG TCCCACCCC ATCGTCTCGA G	60 120 180 240 300 360 401
(2) INFORM	ATION FOR SEQ ID NO:1160:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 350 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1160:	
GTGCACTGGG CGGGTTAAAA TTCTGTTCTC CGTCCTCTGC	ACACGCNTGG GGTAAGAAGG GCCTGGTGGG AGGAGTTCAC AGAGCAGACG ACCAGGAGAG CAGAACACAG GCCATAACTA TAGGGCAGGT GGGGCAGGAA ACGAGATCCA AGCCAGCCAG ATCGCAGGAG GTGCGGGGGC GTCGTCCCCC CCCCCAAGGT CACAGTGCAT GCAATAAAAT ATATATACAG GAGCTAGATC AGGGGCTCTG AGGGTCCAGA GCTCCCTTCG GGTGGCGGGA AGCCAGTGGC GGCCAGGCCG GGCTGGAGCC ACATGCGTCG GGGTCTCGAG	60 120 180 240 300 350
(2) INFORM	ATION FOR SEQ ID NO:1161:	
	477	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 597 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

GCCCCGGAGC	ATCTTAAGAG	CTGAGCGCAG	CTGACAACTA	GGGGCCGGAC	CGTCGCAGGA	60
GGCGTCCGCT	GGATACCTTC	CCCCTTCCCT	GACCTAGAGC	TCTACAGCTG	CTGCCTCGGT	120
ACTGACCGAG	GGTTCCCAGA	GCTGTCTCAC	CATTGCAAAA	ACGTTATAGC	AACAGCCTCT	180
GATTACGACA	TGGCTGAGAT	CACCAATATC	CGACCTAGCT	TTGATGTGTC	ACCGGTGGTG	240
GCCGGCCTCA	TCGGGGCCTC	TGTGCTGGTG	GTGTGTGTCT	CGGTGACCGT	CTTTGTCTGG	300
TCATGCTGCC	ACCAGCAGGC	AGAGAAGAAG	CACAAGAACC	CACCATACAA	GTTTATTCAC	360
ATGCTCAAAG	GCATCAGCAT	ATACCCAGAG	ACCCTCAGCA	ACAAGAAGAA	AATCATCAAA	420
GTGCGGAGAG	ACAAAGATGG	TCCTGGGAGG	GAAGGTGGAC	GTAGGAACCT	GTTGGTGGAC	480
GCAGCAGAGG	CTGGCCTGCT	AAGCCGAGAC	AAAGATCCCA	GGGGGCCTAG	CTCTGGATCT	540
TGTATAGACC	AATTACCCAT	CAAAATGGAC	TATGGGGAAG	AACTAAGGAA	CCTCGAG	597

- (2) INFORMATION FOR SEQ ID NO:1162:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 476 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

GAATTCGGCC	TTCATGGCCT	AGAAATAACT	TAAAATCCTG	AATCAGATGT	TTCTCCGTAC	60
ATGGCCTATC	CAGATCACCG	${\tt TAGGGTGAAG}$	${\tt CTCAAAGTCA}$	GCAAGCCTCA	CCCACATACT	120
CAGAĞCTTCC	TTTCAGTGTT	GAGACCTTCT	TCCCTCTGAG	CAGATGACAA	AGGAGTTTGA	180
AACCAGCCTG	GCCAACATGG	TGAAGCCCCG	TCTCTACTAA	AAACACAAAA	ATTAGCTGAA	240
ATGGTGACTG	TAATCCCAGC	TACTCAGGAG	GCTGAGGCAG	GAGAATCGCT	TGAATCCGGG	300
AGGCGGAGGT	TGCAGTGAGC	TGAGATCGTG	CCATTTCATT	CCAGCCTGGG	CAACAGAGCA	360
AGCCATCACA	${\tt GATTTGGGAG}$	CAACCAAGAA	AGCCAGGGAC	AGGGTATGCT	TGGTAACCTG	420
GCAAGAGCTG	ACAAAGGGGA	AAAATAAAAC	CCCACAGAAA	GAGCAGGGAA	CTCGAG	476

- (2) INFORMATION FOR SEQ ID NO:1163;
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 482 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

GAATTCGGCC	AAAGAGGCCT	AGATGAACAT	GAACCTGCGG	GAGCTGTACC	TGGCGGACAA	60
CAAGCTCAAC	GGCCTGCAGG	ACTCGGCCCA	GCTGGGTAAC	CTGCTCAAGT	TCAACTGCTC	120
CCTGCAGATC	CTGGACCTCC	GGAACAACCA	CGTGCTAGAC	TCGGGTCTGG	CCTACATCTG	180
CGAGGGCCTC	AAGGAGCAGA	GGAAGGGGCT	GGTGACCCTG	GTGCTGTGGA	ACAACCAGCT	240
CACGCACACA	GGCATGGCCT	TCCTGGGCAT	GACACTGCCG	CACACTCAGA	GCCTGGAGAC	300

PCT/US98/06956 WO 98/45437

GCTGAACCTG GGCCACAACC CCATCGGGAA CGAGGGTGTG CGGCACCTCA AGAACGGGCT CATCAGCAAC CGCAGCGTGC TGCGCCTCGG GCTGGCCTCC ACCAAGCTCA CGTGCGAGGG CGCGGTGGCG GTGGCGGAGT TCATCGCTGA GAGCCCCCGC CTCCTGAGAC TGAACCCTCG AG	360 420 480 482
(2) INFORMATION FOR SEQ ID NO:1164:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 494 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:	
GAATTCNGCC AAAGAGGCCT AAGGAGCGCT GTTAAAGCTG ATACATTCCT GTGGGTCAAC TATGCAACTA ACTCAGATTT TGAGCAAACA AAGCTCTCAAA GTTGGTGATC CTCAGGAGTC TCTGCATTAG TTGGACAGCT CTTCTGGAAT TATCTTCTAA GTCAACTGTG GGTTGGGTAG GTGGCTCTGC TGATTTTTCG CTGGACTTCC ACATTTGGCA CCAGTTGGCT GTNATCAGCT CTAGAAAAGGG TGTGGCTGTT TTACATTGGC TGTTTTCCTC ACATTCCTCA AGCAGGTACT GTAATAAAGA ACTGGAGAAA TACAGTCAGA TGGGAAGTAG CCCCTGCTGT CAAGGAGCTT GCCATCTAAT GGGGGAGACA GGCAAGTAAA CCAAAGACTA CACAGTGCAG TATGGTAAGT GCCATGATTT TGATGTGACA GGGCACAGTG GACGACCTTC CAAATCAAAG CAAGTAACTA GGGGCAGACT CGAG	60 120 180 240 300 360 420 480 494
(2) INFORMATION FOR SEQ ID NO:1165:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 298 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:	
GAATTCGGCC TTCATGGCCT AACTCTTATC TGTGAACACA ACTTTTCAGC ACTACAAATG CAAGCAACTG CGCAGTCACA GTTGGGGCTG CTAATTTGGA AATCCAGTTT AGGCTGATTT GAAAAGACAA CAGCATTTT GCAATCACTG GTGTATCCTT TACGAGAGAG CTAGTCATGC CATTTTTTGT TTTCTGAAGA CGGCCTTTTT TTCTTTTTTA TTATTATTAT TTTTTTAAAT TTGGGATCTT GCCTAATTCT TTAGTACAAA GCCTGGCCCT AAAACCGTAG AGCTCGAG	60 120 180 240 298
(2) INFORMATION FOR SEQ ID NO:1166:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 266 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

AGTGGAGCCA	GATTCAGAGA	ACTTTNAGAA	GCAGGTAAAG	AAGTTTAGGA	TTAATGGACA	180
AGTCATTGGG	TCTCCAGGTT	TCTTTGAGGG	AGAGTGATAT	CTGAGCTCTG	TTTTAGAAAG	240
ATTAATCTGA	AAGGAGGTAA	CTCGAG				266

- (2) INFORMATION FOR SEQ ID NO:1167:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 499 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

GAATTCGGCC	TTCATGGCCT	AGGTAAATAA	TGCCAAGTTA	CTGGGGTCTA	GAAAGAAAGT	60
TTTCTCTTGG	ATCAAGAGAG	TGTGAGTTTC	CTAAGTTTCT	TCAGCAGGGA	TGTTGGTCCT	120
TTAGTTAGGA	GGTTTAAAAT	CACCAGGAAG	TAAGGGTGAG	GAAGAAAGTC	TGGGTCCATG	180
TTTGAGAAGG	TGACTGATGG	TGGTGGAAGT	CCTTCCTGTG	ATGAGTTAAT	GATGCGTATT	240
TCTGATAAAG	ATGGGAAGTT	ATTTACATCG	ACATTAACCA	AATCTACCCT	TCATGCAGAA	300
AGAAAGAGCT	CTTGGGCCAT	TCTCTATTAA	TGAAACCATA	CCAGGGTCAA	TATTACAGTG	360
TCTCTGAAAT	ACACTGAAAA	TACTTCCCTG	GCTCAGGTGG	TGGCCCATGC	TACCTCCAGG	420
CAGTTCTACT	TGATTAATGA	TGCAATGGAG	ATAATCCTAT	TGCATCCACC	ATCAAGGAGA	480
GTTGGGCAGT	CAACTCGAG					499

- (2) INFORMATION FOR SEQ ID NO:1168:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 425 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

GAATTCGGCC	TTCATGGCCT	ACACAAACAA	ACCCAGAATA	CTCTATTACT	GTATTTGTGG	60
GGTACAATCC	ACTCAACTCT	ATTATGAAGC	CCAAAAAATA	AATCTGTTAA	AAACAATAAT	120
AGCTACACCA	ACCTGTTAAG	AGATAGGTAA	TATAAAAATA	TATAGTTTGA	GACAACTAAA	180
TCAAAATGGA	GGAGGGGATA	GAGTTCAAGA	AGTAGAATTT	TTTTGCGTGT	GCTTTTCTTG	240
GCCTTTGTTT	GCTTCTATTC	TTTTATTTGG	AATCAAAGAT	AAGTTATCAA	CTCTTTAAAA	300
TAACTTGTTA	TATGTATAAG	ATGTTTTCTG	TAAGCCTCAT	GGTAACCACA	GTACAAAAAC	360
CTATAGTACA	ATTCCTAAAA	ATAAAATACA	AAAAAATTAA	AATATACTAC	CAGAGAGCTC	420
TCGAG				•		425

- (2) INFORMATION FOR SEQ ID NO:1169:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 318 base pairs
    - (B) .TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

TGGCCAGCCA GCCTTCAGAA TAGCTAAAGG CCTTCCTTCC TTCCAGTCAG CCTGAGAGAG	120
AACACCTGTC CCCTAAGCAC CTGGTGTCTC CATTGGAGGC AGACTGCTCT CAGGAGACTA	180
CTAGAAGCTT CAGCCCGGAA GACAGGCTGC TCTCTCATGC TGGTGGCCCA AATTGAGAAA	240
GTGGTGTCCC TTCCTGATTT TGCCACCAGC CCTACCGAAT AGTTGTAAAC CAGTATCAGG	300
AATTGGGATC CTCTCGAG	318
(2) INFORMATION FOR SEQ ID NO:1170:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 346 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(34) MOLECULE TARE. ADMA	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:	
GAATTCGGCC TTCATGGCCT ACATTGGTCG TTTTATTGCC ATGGCACTAT TTCATGGAAA	60
GTTTATCGAT ACTGGTTTCT CTTTACCATT CTACAAGCGT ATGTTAAGTA AAAAACTTAC	120
TATTAAGGAT TTGGAATCTA TTGATACTGA ATTTTATAAC TCCCTTATCT GGATAAGAGA	180
TAACAACATT GAAGAATGTG GCTTAGAAAT GTACTTTTCT GTTGACATGG AGATTTTGGG	240
AAAAGTTACT TCACATGACC TGAAGTTGGG AGGTTCCAAT ATTCTGGTGA CTGAGGAGAA	300
CAAAGATGAA TATATTGGTT TAATGACAGA ACGGCGTTCG CTCGAG	346
(2) INFORMATION FOR SEQ ID NO:1171:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 240 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:	
GAATTCGGCC TTCATGGCCT ACACTTTATT CCCTTTTAAG TCTGGTAAAG AATGAATACT	60
IGGACGTTTT GTTTCATGCA GATTTAGTTA GCAACTCGAT TATCAAATGG TAGAATATCT	120
GTATGCACTG AAGCCAAATT CTCAGTAACT CAGCTTTTGN TAGTCATATG AGGATGATGA	180
ATAATAGGAN TCCAGAGCAG TTAACAAATT GATACAAGTG GTAGGAAAAT TTGATATGAA	240
(2) INFORMATION FOR SEQ ID NO:1172:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 277 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:	
GAATTCGGCC TTCATGGCCT AGTTTCNTTT TTGTATCTCT ACTGATATCA CCAGGATAGT	60
NTACTCTCCT TCTAGCCTTC TGCTTACCGC ACACTGGATA ACACACACAT ACACACCCAC	60 120
AAAAATGCTC ATGAACCCAA TCCGGAGAAG GTTCCAGCAG GTCCCCCACC CTCCCCTCCT	180
CCTCCTACTT CTCCTCTTGA CAGCGAGGAC AGGAGGGGGA CAAGGGGACA CCTGGGCAGA	

277

CCCGCCGGCT CTCCCCCAC CCCACCCCCA TCTCGAG

(2) INFORMATION FOR SEQ ID NO:1173:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 258 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:	
GATTTGTTAG ACCAAGAGCA AGGGAGACCA TTTAATGCAG TTATTTAACA ATATTTAGTA CTTTCCTTTA CCTTGTCTGC TGTGCCATCA TTCATGCCTG TCAGTGTTAA AAATCCCCAA ATTTCCCAAAA CAGATTTTCA TTTCACTTCC GTCAACTTTT AAATTAAAGT TTTTAAATTC 2	60 20 80 40 58
(2) INFORMATION FOR SEQ ID NO:1174:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 334 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:	
GAGGCATCAG TTAGAAGAAT GTCTTGCTGG TAACAATCAG CTTTCTCTGG AAAAAAACAC 12 TATTGTGGAG ACTCTAAAAA TGGAAAAAGG AGAGATAGAG GCAGAATTGT GTTGGGCTAA 18 AAAGAGGCTG TTGGAAGAAG CAAACAAGTA TGAGAAAAACC ATTGAAGAAT GTCTTGCTGG 24 TAACAATCAG CTTTCTCTGG AAAAAAACCC TATTGTGGAG ACTCTAAAAA TGGAAAAAGG 36	60 20 80 40 00 34
AN ANIOMETER FOR BEG ID NO. 1175;	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 403 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:	
GCGATGGGC AGGGCCACG GAAAGAGTCT GAGGGCTGCT TGGTGTAGTC AGGTTGTGTC CAGGCATGCG GAGCTGTGAG TGCCTGCAGG AGAGACACCC AGGAGGAGTT TTTACATTTT 18 GGTCTAAAAA GCTCTTGGAT TCATCTCATC TCATGGAATG ATCCTGTCGG ATGACGCTGA 26 CGTGATTGCT TCAGACTTAG AGGTGAATAA ATTGAGGTCC AGAGAGGGTCA CAGTCACGAA 36 GCTCATGGTA GACTGAGGCC ACTAAACACC CGTCTCCTGA TTTTCAGTGG CGTCCTCATT 36	60 20 80 40 00 60

- (2) INFORMATION FOR SEQ ID NO:1176:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 590 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

				TAAATTAATC		60
TTGGTGGAGT	CTTCCTGATT	TATTGAAGAG	AATAATCACG	AAAATAATTT	TTGTTTGTTT	120
TTTGAGACGG	AGTCTCGCTC	TGTCAACCAG	${\tt GCTGGAGTGC}$	AGTGCCACGA	TCTCGGCTCA	180
				TGAGCCTCCT		240
				TTTTTAGTAG		300
				AGGTGATCTG		360
				CTGACATAAA		420
AATACCGTGT	AAGACTTTTC	CATTGGGTTT	TGAGAAACAC	GTTAATGAGA	GAAATTGCTT	480
AACATTGGAG	AGGATTGCAG	AGAATATTGA	CTAATATGGT	GGGGTGAGGA	GGAACAACAT	540
CAATTAAGAT	TCAGATTTAT	TATTTAAAAA	AACTAAAAGG	CGGCCTCGAG		590

- (2) INFORMATION FOR SEQ ID NO:1177:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 562 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

CTCGAGGTAG	CCACAGTCCT	GATCCTAGTG	ACAAATGGGG	GCATGTGTCT	ACATCCGGGT	60
CGGCGGAGGG	CTCATTTCAT	CTGGCCTGGG	GGGAAATGAG	TATTAATTTG	TTTACACAGA	120
CGTAAACACA	GCCCAAAACG	CATCAGCACG	TTGACTCAAA	CGCCCGCAAC	GCCAGGGCAA	180
AGGCAATTTG	GTTAACAGGG	GGAAGCGAAC	AGACGGAGAC	GCCTGGAGAC	CCAGGTGCCA	240
CAACCCGGTT	AATCGCGGTG	CAAATAAGGG	CAAGTCCCCT	CCCCTTGTCC	GTGTGGTCTT	300
GACAACGACA	CTAGTTCATT	CTACTAACAA	GGCGGGCGGG	GGGTCAGATG	GGCCACACAC	360
ACCCATTTTC	CTCAACGGGA	CCCCAACGCG	ATCTCAGCCT	TGCTGTGCTA	CTTTAGGGCA	420
AGACGCGTTC	CCCATTCGGA	AGCCGCAGGA	AAGCGCGGCG	AGAGCGGGTT	AGCCCTCGGA	480
GCGGCTAAGA	GCCTCGGAAT	AGCGCAGAGG	AAGTCCCCAC	CCCTCTCGGG	GCTGGGAGCC	540
CTAGGCCATG	AAGGCCGAAT	TC				562

- (2) INFORMATION FOR SEQ ID NO:1178:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 339 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

GTGATCTGAC TCTATCTGCA AGGTAGTGTT GGAAGTGAAC AGGGTTGGAG AATGCCCAGC TGGTGTCCAC CGCAGAATTG ATTCATGTT TGGTATGCAG GGACCCCCCA CTCCACACTT AGTCACAGAA ATCTGTGTTG ATTGTTGTGG CATGAAAGCA GGGAAAAAATA GTTTGTTTT TTCTCCACAC TTCCTTCCCA AGATCCCGGC TAACTCGAG	120 180 240 300 339
(2) INFORMATION FOR SEQ ID NO:1179:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 353 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:	
GAATTCGGCC TTCATGGCCT ACTCACCGGA GAAAAGAAGT TTCNGAAGAA AACCACAACC ATGCAATGA ACGAATGCTA TTTCATGGGT CTCTTTTGT GAATGCAATT ATCACACAAAG GCTTTGATGA AAGGCATGCG TACATAGGTG GTATGTTTGG AGCTGGCATT TATTTTGCTG AAAACCTCTTC CAAAAGCAAT CAATATGTAT ATGGAATTGG AGGAGGTACT GGGTGCCAG TTCACAAAGA CAGATCTTGT TACATTTGCC ACAGGCAGCT GCTCTTTTGC CGGGTAACCT TGGGAAAGTC TTTCCTGCAG TTCAGTGCAA TGAAAATGGC ACATCTCCTC GAG	60 120 180 240 300 353
(2) INFORMATION FOR SEQ ID NO:1180:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 296 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:	
GAATTCGGCC AAAGAGGCCT ACAGAGTGCT GTGCTTAAGT TTTACTTCTT TCCACCTTTA AATCTCTGAT AAGTTTCTTT TTATCTAAAG GTTCCACTTT GTTCATTACT TTTTTTTCC TTATTATTGA TTTGTTCGAG AACCTGAGTT TCTTGACCTG TGTGATTTTG TACCACCTGG ACTTTCTGAC TGTGTTTTGCC CAGGCTGGAG AGCAGTGGTG GGATCATAGC TTACTGGACT CAAGCCATCC TCCCGCCTCA GCCTCCCAAG TAACTGGGAC TATGGGCACA CTCGAG  (2) INFORMATION FOR SEQ ID NO:1181:	60 120 180 240 296
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 277 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:	
GAATTCGGCC TTCATGGCCT ACTTGAGTTG TACATTAGAT CTTTAAACTT GTTAGTCCTA CATATCTGCT ATTTTTATC CTTTGACCTA CATTTTCCCCA TTTCCTCCCA GTGTTCTCTC CCCAGGTAAT CATTGTTTA TTCCCTTTCT CTGTAAATTT GACTTTTTT TTTGGATTCC ACATATAAGT GAGATCATGA TCATGCGGTA TTTTTCTTTC TGTGTCTGGC TTATTTCACA	60 120 180 240

## PCT/US98/06956

TAGTATTATG TCCTCCAAGT CTACCCACGA ACTCGAG	277
(2) INFORMATION FOR SEQ ID NO:1182:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 192 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:	
GAATTCGGCC TTCATGGCCT AGAGATACTG GCTGGCAATT CTTGGCGTTC CTTGGCTTGT AGCTGTAAGA TGCGCTCTAA TATCAGTCTC TGTTGTCATT TGCCTTTTCT CTGTGTCTGT GTTCAAATGT CCTTTTTTT TTTTTTTTA GGGAGTCTTG CTCTGTTGCC CACTCAAACT GCTGGGCCCG AG	60 120 180 192
(2) INFORMATION FOR SEQ ID NO:1183:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 296 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:	
GAATTCNGCC AAAGAGGCCT AGTAAATAGT TGTTCTGTTA CATTGTTTAG AGAATAATGA CAAGAACAAA AATCTGTGTG TTCAGTATAG ACACAACCAT CCTTTTCTTT TTTTTTTTTT	60 120 180 240 296
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 234 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:	
GAATTCGGAC TACTACAGGT GATACTACAG TGACTACTAC AGTAATTCGG ACTACTACAG GTGGCTAATT CGGATTACTA CAGGTGGACA TAATTCGGAC TACTACAGGT AATTCGGACT ACTACAGGTG AGCTAATTCG GACTACTACA GGTGGACATA ATTCGGACTA CTACAGGTGC ACCTGTAGTG GAGAACATTT AGCAATGATA AAGCCGCTGC TGATCCTTCT CGAG  (2) INFORMATION FOR SEQ ID NO:1185:	60 120 180 234
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 300 base pairs (B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

GAATTCGGCC	AAAGAGGCCT	AGAACAGTTT	AGAAACAATT	TCCCTGCCTT	TGCTTTGGGT	60
TCCCTGTGAT	TGTTCTCCAC	ACTGTTTTCC	TGGCTCTATC	TGTCTCCCTT	GCCACGGCCA	120
CTCAAGCCTA	GCTGCCCAAC	AGCTCCTTCC	CTGAAGAACC	CCGGCCTTCA	GGCTTGACAG	180
GTGATCTCAT	CCCTCTTCTT	TTCCTCCAGG	TTGTTGTAGA	CTTCCACCTT	CCCTTCTTCT	240
CCTGGTCCTT	TCCCCTTTCT	AGTGCCAATG	TGGGCCACGC	TTTCATCCCA	CCTACTCGAG	300

- (2) INFORMATION FOR SEQ ID NO:1186:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 324 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

GAATTCGGCC	TTCATGGCCT	AGTGATGAGC	CCTCCTCTTC	AGCTAGGAAA	ATGACGGTGT	60
TCAGAAAGTT	AAAACTTCTT	CGCTGGAAGG	ATTTCATCTT	AAAGTTGGGA	GACTGGAAGA	120
AATTAAAGTG	${\tt TTCTAAATGG}$	AAGAGCATTC	ACCACATGTG	TTCTGTTTTG	GGTTGACATT	180
${\tt TAGCTTTTGT}$	${\tt TTTTATTTTA}$	GAAACGGAAG	ACTCTGGTAG	CAGTCCTTGA	AATCTTGATG	240
CCATTGCTAT	TTTCTGCATT	GTATTGTATC	TTCGTTTTAG	TAGTGCTCCA	ATAAAAAGAC	300
CTGCTACTAG	CTGCAAAACT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:1187:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 308 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

GAATTCGGCC	TTCATGGCCT	AGTACGTTGC	TGAAAAGAAG	TTTATTGCTA	TTTTCTTATT	60
TTATTATACA	AAACTAGATT	TGCTTAAAAC	ATTTCCCAGT	CTCTTTAAAG	GAATGCTAGT	120
TAGTGGGAGG	CCACAGCTAG	TAAATTACCC	TCAGTAGTGG	TTTCAAGTAG	TCCATAACTA	180
TAAAAATCGT	TACGGCCAGG	ATATGCCGGA	ACAGAACACT	CCCCACTGGG	GTCCTCAGCC	240
TTGGATGTCA	GCTCGGCCCC	TCAAGGGGTC	CCTACACCTG	GAAGCTGATT	CCACTCATCA	300
GTCTCGAG						308

- (2) INFORMATION FOR SEQ ID NO:1188:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 251 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

GAATTCGGCC	TTCATGGCCT	AGAATGAAGA	AGGTTCCCAA	GAAGTTAGAG	GAGATTCCCC	6
CAGCCTCTCC	GGAGATGGCA	CAGATGAGGA	AGCAGTGCCT	GGACTATCAT	TACCAGGAGA	120
TGCAGGCTCT	GAAGGAGGTC	TTCAAGGAGT	ATTTGATTGA	ACTGTTTTTC	TTGCAACACT	18
TTCAAGGGAA	CATGATGGAT	${\tt TTCTTAGCTT}$	TCAAGAAGAA	ACATTATGCC	CCATTACAAG	246
CACCACTCGA	G					25

- (2) INFORMATION FOR SEQ ID NO:1189:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 359 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

GAATTCGGCC	TTCATGGCCT	AAGGAGTTGG	AAATTGTGCA	CAAAGAAAGG	TGGTGAATAA	60
GTAAAGTCGT	AAATTCAAGA	CCACAACAGA	AAGCTTCACT	GCAGACACTG	GACTTGAACC	120
					TCTAGCTGTG	180
GAATTTATTG	TGGGCAAGCA	TAGGAATGAG	AAAGTACAAT	GAAAAAATGT	AAGTAGACCC	240
ACCAAGTTAG	AGAAGAAGGT	CCTGGTTAAG	AAAAATGAAA	GATTTTTTTG	AACAACAGAT	300
TAATGTGATG	AAATAGATGT	TCAAGAGTGA	AGATAAGTTG	AAGATAGGGA	CCCCTCGAG	359

- (2) INFORMATION FOR SEQ ID NO:1190:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 245 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

GTTGTTAGGC	TGGTGTTGTT	ATGTTGCTGT	TGTTATGCTG	GTCGTGCTGC	TCCATGTTCT	60
CCAGGTGTTC	TTCCCTTTTA	TCGTCACAGT	TACCCCGTAC	ACCTGACAAC	TGGACATCTG	120
CGCCTGGGGT	CTTCAGCCTA	AACACACCTA	AACCCTCCAC	CAAACCCCTC	TGCTTCCGCC	180
TCCCCGTGTC	TGTGAGCGCC	TCCACTGCCC	ATCCCTCTGC	TCAGGCCCCA	TTTCCAGGGC	240
TCGAG				·		245

- (2) INFORMATION FOR SEQ ID NO:1191:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 257 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

GAATTCGGCC TTCATGGCCT AGTCTCAAAA AAAAAAAAAA	ITTCTAT ACATCTACAA 12
(2) INFORMATION FOR SEQ ID NO:1192:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 748 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192	:
GAATTCGGCC TTCATGGCCT AAGGACATGG CAGAGTTCCT GCTT TTTAAGGAGG TTTGAGATTC AAGGCTTTT TTAATTTTAA AATT TGTGTGTTAA TATGCTGAGG GAAGTTGCCA ATAGTGAGAT GAAG TAGCAAGGTG ACTGCACCAG ATACCTGGAT CTGGGCAGGA ATAC TGTTGACCTT GAGTGACAGG GTATAATGTT TGGGAAGGTG CTTT AATACAAACA TGTAGTACAC CTTCTCTGAG ATCCGGGAAA GGAC GGGGCTGGTC ATAGGCCACT CTCCCCTACT GTTTCTCTAG AGTC AGTCTCAGAT GCCTCGACCT TCATGGCCTA GAGAGTTCTC ATCA ATGATCCATT GCATGGGCAG GATTGTTCTA CGAAGACGAA GATC GACCCGGAGG AAACTAACCT CAACCTCTGC CATCACAAGG CAAC GTTTGTGGCC CTCCTGAAGC GGTTTAAAGT TTCAGATGAG GTGC TGTGTCCCGC GAGCAGATCC GGGAAGTGGA AGAGGACTTG GATC GGAGATGTAC AACCCCAGTC GACTCGAG  (2) INFORMATION FOR SEQ ID NO:1193:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 227 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	TAACCAT GGTAGAAACC AGATCTA GGCAAGGGGA AACCTCA ACAGTGATCA CGTAAAC TATAAGGGGC CAACCTG AGCATAGGTT GTGTGTA GTCCCTAGCA AGAACAG GAAGGCAGTG TCCGGA AAGTGAAGAA STCCGA AGGTAAGAA CTCAGCA AGGTAAGAA GCCTTAGCA AGGAACAGAA GCCTTTG GGCTGGAGCA GCCTTTG GGCTGGAGCA 660
(ii) MOLECULE TYPE: cDNA	
(11, 11, 11, 11, 11, 11, 11, 11, 11, 11,	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193	:
GAATTGCGAA CATGGCAGCG CGTTGGCGGT TTTGGTGTGT CTCCCGCTGTGTCAT CGTTTGCGAC GTTCCCTCAG CCTCTGCCCA AAGAATCTGAAAA GGTTAGTCAG CTGATGGAAT GGACTAACAA AAGAATGGAGACAA GTTCCGTCGC CTTGTGAAAG CCCCACCTAA TCTCCCCCCCCCC	NAAGAAG GAGATGGTGT 120 NCCTGTA ATAAGAATGA 180
/s, minimized for PPA ID MO:II34:	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 258 base pairs
    (B) TYPE: nucleic acid

  - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

${\tt GAATTCGGCC}$	TTCATGGCCT	AGTATATATA	TAAAATACTG	AGGATTTAGG	GCTGATGTAT	6
ATAAATAAAA	TACTGATAAC	TTTTTTCCTT	TCTTTTTCTT	TTTTTTTTGA	GATAGTGTCA	120
TGCTCTGTTG	CCCAGGCTGG	AGTACAGTGG	CACCAAACCG	CTAACTGCAG	CCTTGCCCTC	180
CCAGGCTCAA	GCAATCCTCC	TGCCTCAGCA	CCCTCAATAA	CTGGGACCAC	AATTGCATGC	240
CACCAAACGC	ACCTCGAG					258

- (2) INFORMATION FOR SEQ ID NO:1195:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 314 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

GAATTCGGCC	TTCATGGCCT	AATGAATTCT	CATTTCCTGG	AGGCTGAAGA	TCTGTGCAGG	60
TGTCTGTGGC	CAATGTTAAG	CCTACGACTT	TAGATGAGCT	GGCATAAATC	TTGGGAGAGT	120
TTTCTTGTCT	GTGTTCCCTC	TGAATTTCTC	TGTGCTGTTA	GAGGCAGGGA	CAGAAGAGAA	180
CCAGCATGGC	AGTGCTGGGC	TCAGGGTGAT	GCCTGCCTGC	CAGCACAGCG	GTTCTTGTCC	240
CTGTCCCACA	TTGCTTCTTG	GAAGCCTTTT	TACAGCCTCA	ATCATCTTGC	TTTTTCTACC	300
GCAGCTATCT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:1196:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 385 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

GAATTCGGCC	TTCATGCGGG	GACTTCCACT	CTTTCTCGTT	TTCTCGGAGC	TCCGCCTCCA	60
GCTCCTCTAT	CTTCCTCTTC	AGCTGCGTGT	TCTTCTCCTC	TCTGTGGATC	TCACGGCCTC	120
TTCCTCTGCT	CCACGCTGGC	CACCGACTCC	TGCAGCGCCG	TGGGCAGCCG	GGCGTCGCTC	180
TCCCGCCGGG	TCTGCAGCTC	CATCTCCCAC	CTCTTCCCGT	GGGCAGCTCT	CTGCGTCGAG	240
GCCGCCTTCA	GCTTGTGGTT	CCCAGACTGC	AGGTGCGTGT	CAGCTGCAGC	GGCCTGAGAG	300
GCCTTTCATC	GTCCGTCCCG	TTGACACTGG	ATGCCGGAGT	AGAAGATGGG	GCTCCATGCC	360
CGGATTCTCG	GGATTATTAC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:1197:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 256 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

 $\frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right)$ 

CCATTTCAAA AAAAAATCTT AAAAATACGA AGTTTTTCAT TTTTCTTAAA TTTTCATTGT GACTACTTTA GTAGACTTGC CAGTAATAAG CCAGTTACCG CTTGAATCTC AGTTTCTTTA

TCTGGAAAGT GGTCATTATT TATCTGCTGT CCCCTTACCT AGAGGGAATC AAATGCGTTT GATACAGGTT CTCGAG	240 256
(2) INFORMATION FOR SEQ ID NO:1198:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 446 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:	
GAATTCGGCC TTCATGGCCT AGAGAGCCCA TCTCCATCTG CCAGCCTGGA AGCAGCCATG GCAAATGGGA TGTGTCCACC TGCCCCCGTT TGGTGCACAA GTTGGGTTTA TTCTCACAGC TGCAAACCCA CGTGCTGGGC TGCACAGCTG CCTGAACGAA GCTGGAGCGT GCAGAACAAA CTGCATGGAA TGTCACGTGG GGTTTTCCAC TCTCGCCCAC AGTGAGTTGG CAATGCCTGG CCACGTGTGC TCTGTGGTCT TTGAACTTGA TCTGGGAGGA CAGAANTTCA AAAGGAAGAT GAAGGCCCCA GCAAGGGAGG TATTCCTGTC TTGAGCAGAA GGTAAAGGTA GAAGGTCCAG ATTAGGTACT GGGAATAGTC ATGGTTTGGT TTGAATGGAG TAGAAGATTC CAGAGGAAGA GCAGTGGGGC ACAGTGGCTC CTCGAG  (2) INFORMATION FOR SEQ ID NO:1199:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 369 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	60 120 180 240 300 360 420 446
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:	
GAATTCGCCT TCATGGCCTA AATTGTAGCT AGGAAAATAA TATATGTCTT AGTTTAAGAA CTCATACTCT GGAATCAACT CATTGCACTT TCCTATATGT TTGGCCATGG GCAAAGCACA TAACCTCTTA ATCAATTGC TCGTCTCCAA GGTGAGGATA GTTATACTTA ATCCTCTTTA GGAGTGAGAA TAAAAATTAA ATATGTGTGT AGCATAGTGT CTACAATGTT AGAGGTATTT GAAAAGTGAT AGTTTATTTT TTGGAATTAT TTAGCATTAT TAAAAACAAG GGGGAGCACA CGGTGGCACG TTTCTGGTCC CAGCTACTTG GGAAGCTGAG GTAGTAGGAT CGCTTGAGAT CCGCTCGAG	60 120 180 240 300 360 369
(2) INFORMATION FOR SEQ ID NO:1200:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 483 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:	
GAATTCGGCC TTCATGGCCT AGACAGGTTG CTAGCTACAT GGGTCTCTGA AGAAGAGTTT	60

AGGACCACGG AGGGAGGCTC GTCATTGGAG GAGTAAGTTA AGACTATCCT	GGAGCAACTA GTGCAAAGCC CCTGAGACAC AACTGCACCT ATCCAGATTA AGGAAGCCAC TGTAGGAGCA CAAAAAAAGT AGGAGATGAA CAGAGAGGTG CGTAGGTCCT AGTATGCACT TTGGCATTTA TTTACTGATT GAGATGGCAG GATTCGGAGC AGAGGAAGGA TATAATCTGA CATTTTAGCA GGATCCCTTT GCTGCGTAGA CCTAAGATGA ACAAGGACAG CCACAGCAAG ACCTGTAAGG TGTAATCCAG GCAAGAGATG ATGCAGCTT GGACCAGGGT AGTAGCAGTG GAAGTGGTTG AAATCTGGAT ATATTTTGAA GATGGAGCCC ATGGGGTCTC	120 180 240 300 360 420 480 483
(2) INFORM	ATION FOR SEQ ID NO:1201:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 192 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1201:	
TATATTCATT	TTGCCACTTG AAGTGTACAA ATTCAGTGAC TTTTAGTAAA TTCACAGTTA AGGATATTCA GAGTTATATA TTCATCACCA CAGTCACTCT TAGAACATTT AAAAAGAAAC CATGCACTCC TTAGCCATCA CTCCTAACCC AACTCTCCCT AG	60 120 180 192
(2) INFORM	ATION FOR SEQ ID NO:1202:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 281 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1202:	٠
ACTCTTAATT TTAAGGGTAA TCAGAAGAAA	TTCATGGCCT ACTTTAAACA TGTGGTCTTA CTGCCTGCAA ACACATACAG TTTATTTACA TAGATGTAAA TATACACATA TATTACTCTA AAGATAAACC GAAAATTATA AAGTATGTGT GTTTNTGTGA ATATGAATTT GTACCTATAT AGAGCAATAT TGGCACAAAA CAAATCATCT TAATAAGGTA ACTAATTGGN GGCTCACGCC TGTAATCGCA TCACACTCGA G	60 120 180 240 281
(2) INFORM	ATION FOR SEQ ID NO:1203:	
(i) .	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 328 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1203:	
GAGCAAGACC	TTCATGGCCT AGTGATCTAC TTAGGTAGCT CCTGGAAAGC AAAGGAGAGA TGTACAGACT TTGTTTATGA GGAAAGCTAT ATAAGGATTA TAAGAACTGA TTTGTTTCCT TTTTGACAAA ATGGATTTC TTCAGTTTCT TAAGCAGATG	60 120 180

TATTATTTCT GGGACGTTTT AGCCATGTAG TTTCTTTTTA TTCCTCTTTG ATACCCTGAA

TAACTAGCCT TAGAAACACA AGTAAAGCTC CCAAAATTTC ATTTTCTACA TATTTTATTA CCAGATTGAA TTCTAGACCT GCCTCGAG	300 328
(2) INFORMATION FOR SEQ ID NO:1204:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 307 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:	
GAATTCGGCC TTCATGGCNT AGGTCCTAAA AAGAGTAAAA GGTGAAAACA CTAAGTGATA TTCNAAACAA AAGAAAAAGA TGAAAAATAA GAACCTTGGT TAAAGAGCAG TCGAAATAAG TAATGATTAT AGCTATGATT TATATAGCAC TTNTTACAAG AAGCCAGGCG CTGTTTTAAA CACTTGACAT ACTTATTTGC TCATTTCATA ATTGTAACAA CCCTATCAGA TAGGTACTAT TTTTATCCCA CTTTACAGAG GAGAAACTGA GGCACAGAAT TTTAAGTGAT TTGGCCGGGT GCTCGAG	60 120 180 240 300 307
(2) INFORMATION FOR SEQ ID NO:1205:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 425 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:	
GAATTCGGCC TTCATGGCCT AAAAAAAAT GTAGTCTAGA AAGAGACTAG GAATAGAACA CTGCTGACTT GTTCTTATAC CAAGAGCTGG AGGCATAAAC AGTTTTAATA AAAAAGAATA CTTTGTATCT TTTGATGTAA CTTCCCTTTA GAGATTCTGT TTCCCCTGTC TTAAATTGTC AGGCTATTTC TGATTGCTGT TTAAATAATT GGTAGTTACT ATTTGAGTCA NGCTTCTTAA AAAAAAAAAA ATTAAAAAAT TCGCCAGCTC AGCTTTCATT TAATTAGTAT CAAAGAAATG ATATCTGTGG CAGTGAACAT TAGTAGCTTG TTCCAGGGTT TATTGTAGGT TTGTTCAAGT CAGTACTGCC CATCTTGGCA CTTAGGTTCT TGGAATACAG AGGTGGATAA GGTTTGCCCC TCGAG	60 120 180 240 300 360 420 425
(2) INFORMATION FOR SEQ ID NO:1206:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 504 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:	
GAATTCGGCC TTCATGGCCT AAGACCAGCA CCATCGTGAG CAAGATTCCT GCTGCGCTGC	60 120 180
492	

GGTAGGTTGT GGATGTCTTT CTCTAGAGGG GTCCCACACC TGGAAAAGAG GACACCCAGC CCGNGGGATG AGGGAAGCTG GGCAAGGGAG AAAGTTGTTG AGTCACACTG GGGACCCCAG ATGTAGTGAG CTCAGCAAGA AAAGCCAGGT CCAGAGAGAG TCGCACAGAA TTCCTGACTC ACAGCGCCCC TCGGTCCACA GTGGAGAGGA GGAGGAGGAG GAGCAGAAGG AGGGGGAGGA GCTGCAGGAG GAGGAGGATT TGAAAGCGCT TTGGCCTTGT GTTATGTTTT GCTTCTTTTC TGTGCCCCCC TCTAGGCCAT GAAG	240 300 360 420 480 504
(2) INFORMATION FOR SEQ ID NO:1207:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 242 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:	
GAAATTTTTC AGTAACTCAG TGTCTTTAAC TAATAATTTA ATCATTCTAG TAAGAAAACA TGCTTTGTAT GATTTTAGTC TTTACATTTA TTAATTTATG TAAATTAATA TGTGGGTTTT ATGATCACCC ACGACATTGT CCTAACTTGT CGACTGTTCT GTGTGCTCTT TTAAAGAAGG TAGTCTGTTG GCCGGGTGCG GTGGCTTACG CCTATAATCC CAGCACTTCG GACAGGCTCG AG	60 120 180 240 242
(2) INFORMATION FOR SEQ ID NO:1208:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 152 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:	
GTAGAATTGT ACAGTGCTTA TGAGTTATGC ATGTGTTCCT GGTCTTTGTT CTAGGATTTT TTTTTTTTT TGATTGCTGC TCCAGTTGCC TTACTTACTT TGACATTGGA GTTGACCACA IGATGGTGTT CCACACTTCC CCTAGGCTCG AG  (2) INFORMATION FOR SEQ ID NO:1209:	60 120 152
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 317 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:	
GAATTCGGCC TTCATGGCCT ACTACCCCTT TATCATTCAC TAACGTGAAT GTGGTGCTAA PTTTTCCAGT CCATATCTTT GAACTTTTTG TAATATATGC ACATCAATAA GCAATCGAGT PTTTATCTATT CTAATTGTTT TAATGTACAA CTTTATGGGT ACATGTGCAA TTTTGTTTCT PGCATGGGG CCAAATCAGG GCTTTTAGAA CATCCAACAT GCGAATAATG TACATTGTAC CCATTAACTA ATTTCTCAAAT ACTTCTGAGT CTTCCTTGTC TATGATTCCA CTCCTACAT	60 120 180 240 300

- (2) INFORMATION FOR SEQ ID NO:1210:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 282 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

GACAGATTTC	ATTACCTTGA	AGTTCACTGC	ACTGAACAAT	TCTCACTCTG	GATGTATTCC	60
TGCTCTAGGA	TGTGAATTTA	GACTTTTGTA	ATAGAGTGGG	CTTTGAGAAA	TAGCTTTTCT	120
GCTCATTTTA	GTTTCATGAT	GACTGCATGG	AATGTTTTGC	TTCACGCTTA	TGCATTGAGT	180
TTTATCAAGC	ATTAAGCAGT	TGGCCGAAAC	AGGTAATACT	TGAACATTCA	GTCCAAGAAA	240
AACAAAATGG	ATTTGAACAT	ACGTAGAATC	AGTAAACTCG	AG		282

- (2) INFORMATION FOR SEQ ID NO:1211:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 482 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

GAATTCGGCC	TTCATGGCCT	AGTCAAACCC	TAGAGCAATG	CAGGCCTTGT	TACAGATTCA	60
GCAGGGTTTA	CAGACATTAG	CAACGGAAGC	CCCGGGCCTC	ATCCCAGGGT	TTACTCCTGG	120
CTTGGGGGCA	TTAGGAAGCA	CTGGAGGCTC	TTCGGGAACT	AATGGATCTA	ACGCCACACC	180
TAGTGAAAAC	ACAAGTCCCA	CAGCAGGAAC	CACTGAACCT	GGACATCAGC	AGTTTATTCA	240
GCAGATGCTT	CAGGCTCTTG	CTGGAGTAAA	TCCTCAGCTA	CAGAATCCAG	AAGTCAGATT	300
TCAGCAACAA	CTGGAACAAC	TCAGTGCAAT	GGGATTTTTG	AACCGTGAAG	CAAACTTGCA	360
AGCTCTAATA	GCAACAGGAG	GTGATATCAA	TGCAGCTATT	GAAAGGTTAC	TGGGCTCCCA	420
GCCATCATAG	CAGCATTTCT	GTATCTTGAA	AAAATGTAAT	TTATTTTTGA	TAACGGCTCG	480
AG						482

- (2) INFORMATION FOR SEQ ID NO:1212:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 343 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNÂ
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

GAATTCGGCC	TTCATGGCCT	AGGGTGATAT	TTAACTCGTT	GCCAATGGCT	AAGCTCCAGA	60
CTTTGCCTCT	CACACTTGGA	GGGATTCCCT	GCCACCATAA	ATCTCGAACT	TTTCTAGAGC	120
ACCACATTGT	TTCCCAGTTA	GGTAAGATCT	CATTATTCCA	GGTGAGCACA	GCGTTTCCAA	180
TGCTTTCCTC	GACTCTGCAT	CTTTCTTCCA	GCTGCTTCTT	CCTTCGCTGG	GCTTCTTTCA	240
GCTCTCGCTT	TTTGGCCTGA	ACCACCATTT	CTTCATACTG	CTGTCTGTGC	TTCTGAGCTT	300
CTTCAGCTGG	TTTTGCTGGG	AGATTTGCTG	GTCTGTCCTC	GAG		343

- (2) INFORMATION FOR SEQ ID NO:1213:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 285 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

GAATTCGGCC	TTCATGGCCT	AGAGAAACTA	AAACTCAGAG	AAGTTAATTA	CTGAACTCAA	60
GATCCCAAAG	TGCTGGGATT	GCAGGCGTGA	GCCACCGCGC	CTGGCTGAAA	GAGCTTTTTT	120
AATGTATTAT	TTATTTGTGT	CAGGATAGAC	TCATTGATGC	GTGTTTTATT	CAGTGGGTTA	180
TAATTCTTTA	TTATGTATTC	TGATGTTGGT	GTTTTCCCAG	TTTTAGCCAA	TGGCATCCCC	240
TTCCATCTGG	ATCCTGTGTT	CTTTTGACAT	GGCTCCAATC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:1214:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 320 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

GAATICGGCC	TICATGGCCI	AGAACCAGGC	CTTCCAGTAC	GAGTTTGGAG	CCATGTATGC	60
ATGGATGCTG	TGTGTCTTCA	CTGTCATCGT	GGCCTACAGC	ATCACTTGTC	CCATCATCGC	120
GCCATTTGGC	CTCATCTACA	TCCTGCTCAA	GCACATGGTG	GACCGGCACA	ACCTCTACTT	180
CGTCTACCTC	CCAGCCAAGC	TGGAGAAGGG	GATCCACTTT	GCCGCTGTGA	ACCAGGCCTT	240
GGCAGCCCCC	ATCCTGTGCC	TCTTCTGGCT	CTACTTCTTT	TCCTTCCTGC	GCCTGGGTAT	300
GAAGGCCCCC	GTCACTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:1215:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 446 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

GAATTCGGCC	TTCATTTTGA	AAGATATTTT	TGTAAAAATC	TGTTTGTTTT	CTTTTAATAC	60
TTTCCAGTGT	${\tt TATCTGGGTT}$	TCTTAATTTC	TGACTTAAGG	TCTGTAATAA	TTTCTGCTTT	120
${\tt CATTCCTCTT}$	AATATATTGT	GTCTTTCTTT	GTCTACATTT	AAGATTTTAT	CTTTATCACG	180
TGTTTTGAAA	AGTTTTATTT	TGATGTGCTC	TTTATGTTTT	TCTTTATTTG	TAGTGCTTGG	240
ACCTTGTGGT	GCTTTTCTTA	TTTATAATTT	TCATCAAATT	TGGGGGGTTT	GACCATTATT	300
GCTTCAAAAA	TAATCTCTGT	TCTCTTTCTT	CACTTTCTCC	AGTTACATAC	TGTAGAGTAA	360
ATGATAGCTA	CCGAAGACAG	AGTGATCCGT	GATAAATATC	ATTAATGCCT	CTGAAGAGGA	420
GAATGACTCC	AGTGGAACCA	CTCGAG				446

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 263 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:	
GGACTTTTTG GAGAAGCAGT ACTATTCATT AATTAAGTAT AGAGTGTCTT GTTAATCCTA AAAGAAAGAG AGCCTTAATG AGGATCATGA ATTTTTTTT TTTTTTTTTT	60 120 180 240 260
(2) INFORMATION FOR SEQ ID NO:1217:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:	
GAATTCGGCC TTCATGGCCT AAACAACAAC AATAACAACA ACAAAAACAT GTATAACTGG GAAAAAACTG AAAGAGAATG CAGGATCATA AAAATATAGC AAACAAAGTG AGTGGGATTT AAAATTAGTG GAATAAGAAA TAATGGGTAA CAATGAAGAA CATAATTTAG GTAATAGTAT AGTATCTTGG GAGCCCTCCT GGAAGTATCT AGTTATGGAC AGTGAGCAGC AGAAACAGGA TGTAACTCAA TTCAGCATAC TTGATGGTTG TGGTAACCCT AGAAAATGAC TCCAGGAAAT AGGTGAGAAT CCAATCTATC TCGAG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:121B:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 293 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:	
GAATTCGGCC TTCATGGCCT ACAGAGATAG GGTCCCATCC AGGTTCCTAA CTGGGTGGCA CATGCATGGG CTAGATCCAA ATAGCATTGC AAAGGCCTGG AAAACAGAAC TAGAATTGAA ACCACCGCGG AAGACTCATT CGAACTCGTG GGCTGAACTC AACCAGGTCA ATGCTTCAGA AAAATACCAG CATTCTCCAC AGGACATAAA CAAGATTGTC TCATAACATA CCATTCAAAA TATTAGGATA CAATCCAAAA TTGCTCATCA TAAGAAGACA GGAAAAACTC GAG	60 120 180 240 293
(2) INFORMATION FOR SEQ ID NO:1219:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 265 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
404	

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

GAATTCGGCC TTCATGGCCT	ACGAGGATTG	GGGTAGGTAT	GNGCTTTNGG	CTCATGTTTG	60
TGATGATAAC TGAAGTCTNT					120
GAAGAGAATG AAGGTGAGTC	CCCGCCGTTG	CAAACCTTCA	CCAAACCACG	CGGCCCAGTT	180
TTCGTGAGTA CCCCTGTGTC	CCAGAGAGGA	GGACCCAGCG	TCCTCGGCTC	TGCCGCAGGC	240
CTTCTTGGTC TGGTGGGTAC	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:1220:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 266 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

GAATTCGGCC	TTCATGGCCT	AAGGAATTGA	AACCCAGTAC	TTTGCAGAAC	TTCTTATGAC	60
TTCTGGAGTG	GTCCTCTGTG	AAGGGGTCAA	ATGGTTGTCA	TTTCATAGCG	GTTACGACTT	120
TGGCTACTTA	ATCAAAATCC	TAACCAACTC	TAACTTGCCT	GAAGAAGAAC	TTGACTTCTT	180
					TGAAGAGCTG	240
CAAAAATCTC	AAAGGGGGAT	CTCGAG				266

- (2) INFORMATION FOR SEQ ID NO:1221:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 312 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

${\tt GAATTCGGCC}$	TTCATGGCCT	AGCTCATTCT	GCTGGGGGTA	GAGATGAGGG	GAGGGAGTAA	60
		${\tt GTAGAAGCCT}$				120
		TGAAAACTGG				180
		GCAGGAAGCA				240
GTGCTTTGCC	CCTCCTCCCC	TTCCCTTCTG	GAAGTCTTGG	GGCCTCAGTG	CTTGCAACAG	300
CCACTCCTCG	AG			•		312

- (2) INFORMATION FOR SEQ ID NO:1222:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 512 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

GCGATTGAAT TCTAC	GACCTG CTGGCCTCAA	GTGAACCTCC	CGCCTCGGCC	TCCCAACGTG	60
	ATGAGT CATTGTGCCC				120
	AGGCCT TTGTTAAATG				180
CTCCTCTCTA CTCCA	AAATAC TGGCCCATCC	CTGCTTAAAT	ACTGCTCAAT	GAAGTTACTC	240
ATGCTAGTTC TTGAC	GGGAGT AACTCTAGAA	TGATTCCATC	TAGGAAGACA	TAAGATAAAA	300
TGGTAAGTAT TCTAA	AGTTCT ATAGGTAGTT	TAGTCATGCC	ATATTATAAA	CCTCCACTCC	360
AAAAATAGTG TGAGG	STCATT TCTGGCCAGA	GTGAAATAAA	AAATGTATAA	TGCCTGAACA	420
GTCTATTATT CTGAC	CAATGA AAAAGATTAA	TGCAGTTCCC	TTTATCACTT	GCATGAGTAA	480
AAAAATATAT ATATA	ATATTG GCTGGGCTCG	AG			512

- (2) INFORMATION FOR SEQ ID NO:1223:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 447 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

GGGTGTTTCA	TACAAAGAAT	ACAAGTAACT	GATGAATGAA	GGGGGCATCT	TGTGTCCCCA	60
CAATCCTGCT	GTGCGCACAC	CACAGGTGAG	CCGTTCTGCC	TAAGGGAACA	GCCCCGGCCC	120
CTCCCTCCGG	CTCCTCCCCA	GCACCGTCTC	CTCCACCCAG	TGGCCTGGCC	GTGGATGCTG	180
CCTGTGGCCC	AGCTTTGAGA	CACCGCCCTG	ACACGTGTCC	AGCCTTACGT	GGAAGGATTT	240
GTCTGTTTTG	TGGCATCCTA	GTAGATGCCA	CGTTAGTAGA	TGCCATGTTA	GTAGAAGGGA	300
TGTGGGCATT	TCTTTGTAAG	TTCCCAAAAG	CCTATGAGGG	TTTTTTCCAC	GATTCCGTTC	360
CCAGTTTGGC	TTTTGTTGTT	GTTGTGGCTG	TTCTTGGCCC	CCCTGGGCCC	TGCAGTGGAG	420
TGGGGGGCTG	CACCTGGGAG	CCTCGAG				447

- (2) INFORMATION FOR SEQ ID NO:1224:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 235 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

GAATTCGGCC	TTCATGGCCT	ACTTTGTTTT	ATATAATAAA	GTATGCCTGT	TATATTAAAT	60
AATAAGAATA	TGGCAATTAG	CGATATAGCA	TACCCAAACA	AAGATGTTCT	CGATACAGTC	120
TGGCAAAGAC	TATCCCAAGG	TTATTTTAAT	GAATTCAGAC	ATTTTTTCCT	GTGGATATTT	180
CTCCATCCTA	AAAAAAGTGG	CAACCAAGGA	משששתשמממ	ATGCAAATAC	TCGAG	235

- (2) INFORMATION FOR SEQ ID NO:1225:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 134 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

GCGATTGAAT TCTAGACCTG CCTCGAGACT GACGCCGCAC CATGACCCTC CTGCTGCTGC
CCCTTCTGCT GGCCTCTCTG CTCGCGTCCT GCTCCTGTAA CAAAGCCAAC AAGCACAAGC
120
CACCGCATCT CGAG
134

- (2) INFORMATION FOR SEQ ID NO:1226:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 556 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

GAATTCGGCC	TTCATGGCCT	ACACACATCT	GGTAAGCAGA	AGCACGGAAG	GCCTTTGTTT	60
		GTTTGTATAG				120
TCTCTCTTAT	GGTTTGAATG	TGTCTCCAAC	ACTTTATGTG	TTGAGACTTC	ATCCCCAGTG	180
		GCCTTTAAGA				240
		ATGTGGGAAC				300
		AGATTGTCTC				360
		CCCTCACCGG				420
		ATAAATTACC				480
AAATGGACAG	AGACACCCTC	AAATTAAAGG	ACAGTCTTGC	TGACTATGAA	TTAGAAAATA	540
TCTGGGTTAG	CTCGAG			•		556

- (2) INFORMATION FOR SEQ ID NO:1227:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 175 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

GAATTCGGCC	TTCATGGCCT	ACCTGCCTCG	AAATACTACC	GTATGGCCCA	CCATAATTAC	60
CCCCATACTC	CTTACACTAT	TCCTCATCAC	CCAACTAAAA	ATATTAAACA	CAAACTACCA	120
CCTACTTCCC	TCACCAAAGC	CCATAAAAAT	AAAAAATTAT	AACAAACCAC	TCGAG	175

- (2) INFORMATION FOR SEQ ID NO:1228:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 220 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

GAATTCGGCC TTCATGGCCT ACTGTTTCCT TGCCCTTTTC ACCGTCTGGT GGTTCCCTGC

AGCCCTTGGC TTGTGGCCCT CTCATCCATC TTCCGAGCCT AGCACTCCAG TCTCTGCTTC TGTCATCACA TCGCCTTCTC TTGAGAAAGA TCCCAGGCTG GTATTTAAAT TGCCTGTTGG CAGGAACTTT GCCTGTCTTC CCCTACCCCC ACAGCTCGAG	120 180 220
(2) INFORMATION FOR SEQ ID NO:1229:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 526 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:	
GAATTCGGCC TTCATGGCCT AAGTCTCTTG ACATCTCAAT TTACCCCAGA ACATCTCTAT TTAATTATTC CCTGAGGAGG GGAAGTTGGG TATGGCGGTT GGAGGTGGAC ACGCCCTG AGGCTTCGCC ACTTTCTAAT GTTTGCTGTG GCTGAGACCCAC AGGCAAAAAA GTCGAAGTCCC CTGGAGTCCC TGACCCCTCT TCCTCTCTAT AACGATTGGA AACTGTCCAA ACCAACTCCA GTAGTTCTGG GCTGATGAAT CATCCTCTTG TGGGGCGGAG AGTGGGGGTA ACCAACTCCA GTAGTTCTGG GCTGATGAAT CATCCTCTTG TGGGGCGGAG AGTGGGGGTA GGGTGGAGCA ATGTGGGCTA GGACCCAGG CAGGATCAAA ATCTCTGAAG ATGCAGAGCT CCCTCTGCCC TGGGAAGAAG GAAGCAGGAT TTATTATAAC ATTTAGCTCA CTGTCCAATC GACTAAAACA AGCTCTCCCA GGGCTCGGGC CAACTGTCGA CTCGAG	60 120 180 240 300 360 420 480 526
(2) INFORMATION FOR SEQ ID NO:1230:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 312 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:	
GAATTCGGCC TTCATGGCCT ACCATTGGC TATGACCTGA GGAGAATCAA GGTAGCTTTC TCAGGCCTCG TGGACATCGT GGATATAAGG AATGCTCTCG TAGGAGGGTA CAAGAACCCC AGCATGATTC CAATAGAGAA GGCCCAGGGG CCCATCCTGC TCATNGTTGG TCAGGATGAC CATAACTGGA GAAGTGAGTT GTATGCCCAA ACAGTCTCTG AACGGTTACA GGCCCATGGA AAGGAAAAAC CCCAGATCAT CTGTTACCCT GGGACTGGC ATTACATCGA GCCTCCTTAC TTCCCCCTCG AG	60 120 180 240 300 312
(2) INFORMATION FOR SEQ ID NO:1231:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 297 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:	
GAATTCGGCC TTCATGGCCT AGCTTTATCC ACTCTGGAAT CCTGGAGGAG CCGCTACAAC	60

CAAGTTGTAA AAGAAAAGGG AGACCTTGAG NTGGAAATTA TTGTCCTGAA TGACCGGGTA

CTGGTGGAGA C	TAAACCAACA ACAAACCCTG GAGGAGAAGA TGCGGGAA GACTACACCG TCAGACTGCT GAGTATTCCG CATTCAAG GCAGCTTTGC TCCAATGGAG GACAAACTCA ACCAGGCA	T GGAGAATGAG	180 240 297
(2) INFORMAT	TION FOR SEQ ID NO:1232:		
(i) S	EQUENCE CHARACTERISTICS:  (A) LENGTH: 360 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1232:		
AGCAGCACTG T GGAAAACTTG A CCTTTGGAAC C AACGAAGCCT T ATCTACCACA T	TTCATGGCCT ACGCAGCTCT ACCTGCTCCA GGGGCACCT TGCCATCCTC CTGCAGACTG AGCAGAACCA TGAGACCGC AAGACATTCC TGCCTTCTTT GAATTGGCCA AGAAGGTGT CAGGGTTCAA TTACTGCAGA GGTATCTACT GCTGGCACA TAAAGTTCCT GAACAAGGCA CGCAAGGACA GCACTTGGC TGGTGCAGAT CTGTCTGAAT CCAGACAACG AGGTTATGC TION FOR SEQ ID NO:1233: TEQUENCE CHARACTERISTICS:	T TCTGTGAAGT C TAGCCGGGTG AT AGGGCAGCCC G CCAGAGCGCC	60 120 180 240 300 360
(ii)	(A) LENGTH: 423 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  MOLECULE TYPE: cDNA		
	SEQUENCE DESCRIPTION: SEQ ID NO:1233:		
TTTTGCCTGT TAGGTGGTCTG ACCITCTTGT TAGGTATTAGAA TAGGGAGGAG T	TTCATGGCCT AGAAGGACTG AAATGATGTT ATACTAAGG TCTTTCCAGG TGTGACAGCC TTTTCTTTTC TTTCCAGGG AAGCCAAGGC CTCGCGGAGC TTCTTTGTGT GTCACCTTC TTTGTTTCTA CTGCTTTAGT TTTTTTTAAA GTTCTCCAC TCTTGCTGTA CCCAAGCAAG ACGTTAATTT TTCTTTTAA TGATAGCTTA ACTGCTGAAG CCAGGCGGG GTCTGCTGC TCCTCCACTG TACAATGTCA CAGACTATCT CTATCATCA	G GTTCGCTTTG C TTCCACGTTT CT GTCCCCAAGA C TGTTTTGGGG CA GGATTCCAAC	60 120 180 240 300 360 420 423
(2) INFORMAT	TION FOR SEQ ID NO:1234:		
(i)· s	EQUENCE CHARACTERISTICS:  (A) LENGTH: 475 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1234:		
GAATTCGGCC T	TTCATGGCCT AGCATGTAAA ACTTCAGTCC TGAACATT	TA TAGGGTTTTA	60

120

180

TAGAAGGGCA TCCTCCAGGG CTGGTCCATT CAGAGAAATG CTGCATGCTG CCGTCATGGA

ATGTGGCCCA CAGGACACCA GAGCCGTGAG AACCGGAGAG CAGACTTCCC TCACGGCTGG

CACAAGCACG ATATAAGGCC AACTACATTG	CCCTCCAAAG CCCTCCTCAC GCAGTT TGTTCTCACC TTTTTCCTAT GCCCTG ATCCTGACAT TGTTTCTGTG TTTCAA CTCCTAGTAG AACATTACCT TTAGGG TGCATGCTGC TCAGACCCCA AGTCAG	GACT AAGGTTTGGC AATT TGGATTTTA GACT AATTTTCCAT	CAGTGTAATC TTTACATTAG GGAGAACTAT	240 300 360 420 475
(2) INFORMA	ATION FOR SEQ ID NO:1235:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 301 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA	•		
(xi)	SEQUENCE DESCRIPTION: SEQ II	NO:1235:		
ATGTTTTTGT CTGCTTCTAT CATTGAATAT	TAGTAGCACT ACCTTCCAAG TGAGTC. CCACTGTTAT GATTNATCAT GTATCT GTATGGTGAG GCCTNGTTGT TCTAGG GCCAGGTAAA ATTTATGCAG TCAAGA AGTTCAAAAT TGTGCCCTTG TTTTAA	TACA AGAGCCACTC CTAG AATAAACTCT ATGA ATTATTTTC	AAGCAAGACT TTGTATGCCT TGACTAAAGT	60 120 180 240 300 301
(2) INFORMA	ATION FOR SEQ ID NO:1236:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 346 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ II	NO:1236:		
GTATTTTAAT GCTCTATGTG AGTCTCCATG TACTATCTCT	TTCATGGCCT AAGAGAAGAT AACATT TTCTTGGTCT CCGAAAACTC AGCTGTC TTTCCTCTAA CGCTAAAGGC ACAGCCC GAGTCTATTT TACAACCTCC TTTCCCC ATATACACAT TTTAAACATT ATTCTTC ATTCTTCATC TTCTTGGGAA ATGGCCC	GACT GCTTTCCATT CCCG GGAATCTACT CCCA TGCTTCCGCG CATT TGAAATTCCT	AACAGTTCCA GCTTCCTAAG GAGGAGTCTA	60 120 180 240 300 346
(2) INFORMA	TION FOR SEQ ID NO:1237:			
(i).	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 355 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ II	NO:1237:		
CAAGCGATTC	TTCATGGCCT ACTCACTATG TTGCTC TCCTGCCTTG GCCCCCAAAG TGCTGG	GATT ACAGGTGTGA	GTCATGGCAG	60 120

ATGAGCCCCT	CACAATTGGA	CACAGTTTTG	CAAAGGGGTA	AAAGGACAAG	AATCGGTAGC	240
TGTGACTGTG	GATGAGCCTC	TGAGCTTCAC	TTTCCCTCCC	TGAAAGGGGG	TGACAGTGGC	300
ACCTCCCTGG	AGGTTTTCGT	GGAGGGGAGG	AAACACATGT	AAAATACTTC	ACCCC	355

- (2) INFORMATION FOR SEQ ID NO:1238:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 560 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

GAATTCGGCC	AAAGAGGCCT	ACTAGACCTG	ATCACCACGT	TCAAAAGTTG	GCTTTCTCCA	60
TTTTAAGTTC	TTCCTTAAAG	CCTCTTTAAG	CAAAGTCCCT	GAAATGATAC	AGTAGAAAAA	120
		TGAATTCTAT				180
		AAGTGCTTTG				240
		GACATTCTTT				300
		TAACAGATTC				360
		CCATTTACCG				420
		AGTTCACTCT				480
CTCTGATAGA	GCACCTGTTT	TGCTACTGAC	AGTGTTAAGT	TCCATACTAA	TCAGCTCATC	540
TAGCCTAACG	ACAACTCGAG					560

- (2) INFORMATION FOR SEQ ID NO:1239:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 569 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

GAATTCGGNC	AAAGAGGCCT	AAGGAGAANG	AGGCTCAGAA	GGAGACGATT	AAGGATCTTC	60
CCAAGATGAA	CCAGGAGCAG	TTCATTGAGC	TGTGCAAGAC	GCTTTACAAC	ATGTTCAGTG	120
ANGACCCCAT	GGAGCAGGAC	CTGTACCACG	CCATCGCCAC	CGTGGCCAGC	CTCCTGCTCC	180
GCATCGGAGA	${\tt GGTGGGGAAG}$	AAGTTCTCAG	CCCGCACAGG	CAGGAAGCCC	AGGGACTGTG	240
CCACTGAGGA	${\tt GGACGAGCCA}$	CCAGCACCCG	AACTGCATCA	GGACGCAGCC	AGGGAGCTTC	300
AGCCCCCAGC	TGCAGGAGAC	CCCCAAGCCA	AAGCAGGCGG	AGACACACAC	CTCGGAACAG	360
CCCCACAGGA	GAGCCAGGTG	GTGGTGGAGG	GGGGCAGCGG	CGAGGGACAG	GGCTCACCCT	420
CCCAGCTGCT	GTCTGACGAT	GAAACCAAAG	ACGACATGTC	CATGTCCTCC	TACTCGGTGG	480
TCAGCACGGG	CTCCCTGCAA	TGTGAAGACC	TTGCAGACGA	CACGGTGCTG	GTGGGCGGG	540
AGGCCTGCAG	CCCCACAGCG	CGACTCGAG				569

- (2) INFORMATION FOR SEQ ID NO:1240:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 405 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

GAATTCGGCC	AAAGAGGCCT	AGAGACCAGC	CTGGCCAATA	CGGTGAAACC	CTGTCGCTAC	60
TAAAAATACA	AAAATTAGCC	AGGCATGGTG	GCTCACACCT	GCAGTCCTAG	CTACTTGGGA	120
GGGTGAGGCA	GGAGAATCAC	TGAAGCTTGG	GAGGCAGAGG	TTGCAGTGAG	CCAAGATTCC	180
ACCGCTTCCC	TCCAGCCTGG	ATGACAGAGT	GAGACTCCGT	CTCAAAAAAA	САААААААА	240
GTTACTTCAA	TAATGTACTT	TTTTTTTCA	AATTACAGAT	AATCTATAAG	GAATTAATCT	300
TGAAATTAAT	TCCAGGTTTA	ATTGTTAATG	AAATTTCAÇA	AGCCTAATTT	AACACTTGTC	360
TGGATAACTC	ATTTTGATAC	TGAGTAAATA	GTCACCGGTC	TCGAG		405

- (2) INFORMATION FOR SEQ ID NO:1241:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 542 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

GAATTCGGCC	AAAGAGGCCT	AGGGCTTTTG	TGAATAAATT	TTAAAAGAGA	CTACTGCCTG	60
TCCTTAAATT	CCTTTTTCTT	TTTATAAAAA	AAGAACTATT	AAAAATGATT	GACAAATTTT	120
GAGTTAAAAA	ATTGTTAAAA	CATTCTCTAT	${\tt ATTTAATTTC}$	AATTTTATAA	TAGATTACAG	180
GAAGATGCTT	ATGAAACAAA	TACATTTGTT	TCAGTACATG	TCTTTAAATG	ATAGACTTAT	240
AAGTATGTAA	ACAACTATAT	AATAAAAGGT	TTCCAAACGC	TGCCTGTAAG	AAATCAGGCA	300
AATTTTACCA	TAAGCAATAA	ACCATTCCAA	GCCTTCCAGA	CAGTCTCCAT	AGCCGCACCA	360
GCATGGCAAT	AAGCTTTAAC	CAAACGAAAA	CAAACAAACA	AAAGCACTTC	GCAATTTGTT	420
GCTGCAAAAC	AGGGAGAGAA	AAGAGTGTAC	AAACTTGATG	GAATCACAAC	AGTCAATATA	480
ATTTAAGGGA	CAATAAAGTC	${\tt AATAAGGTTG}$	${\tt ATGGTGTTTA}$	${\tt TTGTTTAAAA}$	AGTTAGGCCT	540
CT						542

- (2) INFORMATION FOR SEQ ID NO:1242:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 370 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

GAATTCGGCC AAAGAGGCCT	ACTGATACAA	TTGTTGACTT	TTCTTTTACT	ATGTGTAAGA	60
AATACCCCAA ACATGAAAAG	ATTGTTTTGA	TCATATGCAT	GTATGTAGAA	TATTTTTGCA	120
GAGCAGAAAG ATTATGTTAG	AAGTGTGATT	TTTATTTTCA	GAAGTCATAT	ACATGTAAGC	180
TACAATTTTG AGTGCTTTAT	AAACACTTAA	GATATATA	TAAATTTTAA	TTTCATAGCA	240
ACTTGTAAAA AATAAAATAC	TTGTTGAAAA	GCCTTTTTCA	ACATATCCCT	AAGCTAAGGG	300
AAGAGGAAGG AATAACAACT	CAGTGAAAAG	ATGGTCTCCA	GTTTCTGAAT	GAAAAAGCTA	360
CAACCTCGAG					370

- (2) INFORMATION FOR SEQ ID NO:1243:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 374 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

GAATTCGGCC .	AAAGAGGCCT	AGCCTCATCA	CGGGCAGGGC	TCTGGCCCAT	AGTGGCTGGA	60
CAGACACTGG	CACAGTCTTG	CTGGTCTGCT	GGGAGCACAC	AGACATTGGC	ACAGACTTGC	120
TGGTCTCTTG	GAAGAGGGCA	AGACCCCAAA	CCAGAGCAAA	ATACACTTCC	AGCTCTTAAC	180
CAGGCTCCTT	CCAGTCACAA	GTGTGCAGAA	TCAGAACAGA	AGTAGTACCA	ATCAATGTCA	240
CATGAACAAA	CAAGCTGCCC	CCAGGGTACC	ATTTGGGGAG	${\tt GGGAAATCTT}$	TTCTTTCTTT	300
CCCCCTTAAA .	AAAAAACACA	TCTGCCCCGA	ACACTTTCCC	ACTGTTATTC	TTTCCTCATA	360
CCCCAACGCT	CGAG					374

- (2) INFORMATION FOR SEQ ID NO:1244:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 468 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

GAATTCGGCC	AAAGAGGCCT	ACACACCAAA	CTGATTATCC	ACCAGACACT	CAGCGTCTTA	60
GAAGATATTG	TGGAGAATAT	CTCGGGGGAG	TCCACCAAGT	CTCGACAGAT	TTGCTACCAG	120
TCGCTGCAGG	AATCTGTTCA	GGTCTCCCTG	GCCCTCTTTC	CAGCTTTTAT	CCATCAGTCA	180
GATGTGACTG	ATGAGATGCT	GAGCTTCTTC	CTCACTCTGT	TTCGAGGCCT	TAGAGTACAG	240
ATGGGTGTGC	CTTTCACTGA	GCAAATCATA	CAGACTTTCC	TCAACATGTT	TACCAGAGAG	300
CAGTTAGCCG	AGAGCATCCT	CCACGAGGGC	AGCACAGGCT	GCCGGGTGGT	GGAGAAGTTT	360
CTGAAGATCC	TGCAGGTGGT	GGTCCAGGAG	CCAGGCCAGG	TGTTCAAGCC	CTTCCTCCCC	420
AGCATCATCG	CCCTGTGCAT	${\tt GGAGCAAGTG}$	TATCCCATTT	CGCTCGAG		468

- (2) INFORMATION FOR SEQ ID NO:1245:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 444 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

GAATTCGGCC	AAAGAGGCCT	AAGCTTATGG	GGAGGACACA	TATTTACTCA	AACATCCTGG	60
CAATTCATAT	CTAGGGCACT	CCCTCTGTGT	GTCAGACGCC	CTTGCATGTG	TCAAATGTCA	120
TCTGATAACA	TTGATGAAAA	ATATCATTCA	CTTCTTCTTG	GTGCAGAAGG	CATAGACCGG	180
ATTATGCAAT	CACTGAGAAG	TAGCTTCTGG	ATGTGTTTTC	TGGTGGCGTC	TTAACAATTT	240
CAGCCGACTG	AAGGCTCTTG	GACACTTGGA	ACATTTGTAG	GGTTTCTCTC	CGGAGTGGAT	300
GCGCTGGTGC	TCCTTCAGGC	TCCCCCTGTA	GGTGAAAACT	TTCTTGCAGT	CTTTACATTC	360
GAAGGGCTTC	TCCCCCTGTG	TGGCTTCTCT	TGTGACACTT	CAAGTAGGAC	TTCTGGGTGA	420
ACTGCTTAGG	CCTCTTTGGC	CGAG				444

- (2) INFORMATION FOR SEQ ID NO:1246:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

GAATTCGGCC	AAAGAGGCCT	AGTATTTTGT	ACTAGTTTTT	TAATAATTAT	AAGTCTTACA	60
CGTTCTCTAA	TTCTTCTTGA	ATCTGTTTAA	TTTTTCTCCC	TTGGGAATTG	TTAAGTGTAC	120
ATGTATTGTG	ATAACTGCTA	TAATTTTGCT	TTTATTGATT	TTTTTTGCTT	TATATCTGCT	180
ACAATTTGGT	TCCTCCAAAT	CCCATGTTGA	AATCTGATCC	CCAGTGTTGC	TGGGGGATCT	240
AATAGCAGGT	GTTTGGGTCA	TGGGAACAGG	TCCCTCATGA	ATGAATTAAT	GCCCTCACTG	300
GGAGGAGGGG	ATAAGTAAGC	TCTCACTCAT	TTAGTTCCCA	AGACAGCTGG	TTGTTTAAAA	360
GAGCCTAGTG	CCACTTCTCT	CTTGCTTCCT	TTCTTGCCGT	GTGATCTCTG	CACATGCCAG	420
CTCCCCTCGA	G					431

- (2) INFORMATION FOR SEQ ID NO:1247:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 389 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
    - •
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

GAATTCGGCC AAAGAGGCC	TTTTTTTTTA T	TTTTTTTTT	TTTTTTTTT	TCNGGGTGTA	60
GAACATTTAT TTATTTTTT	C CACAAATCAC	TGAAAGTTTA	GGTCAGTGGG	TTTTAATAAA	120
AATCAAATAA TTGTACATA	T TCTTCCCACA	TATCCTGCCT	TGTATTAGGA	AATGACATTG	180
TGATCCATTT CATTACAAC	T AAAATATTAC	AAAATATTTA	CAGGAAAATA	AATAAAAATT	240
CTCAAACACA AAAGGCAAG	A TGAAATAAAC	TGTTTTTTT	TCTCCAGAAA	TCTCTACTCC	300
AGTGCCCACA GCACACAAG	A GTCAAAACAA	ATAAGCAACT	AAGATCCCCC	GATCACAAAT	360
TTCCAAAGAA CTAGGCCTC	T TTGGCCGAA				389

- (2) INFORMATION FOR SEQ ID NO:1248:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 380 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

GAATTCGGCC	AAAGAGGCCT	AAAGGAAGGC	CACTTCTCAA	CTGGCAGAAC	TTCTGAAGTT	60
TAGAATTGGA	ATTACTTCCT	TACTAGTGTC	TTTTGGCTTA	AATTTTGTCT	TTTGAAGTTG	120
AATGCTTAAT	CCCGGGAAAG	AGGAACAGGA	GTGCCAGACT	CCTGGTCTTT	CCAGTTTAGA	180
			AGCTGGGACC			240
			GACAGTTTCA			300
			TATATACAGC			360
	TTTGGCCGAA	**				380

(2) INFORMATION FOR SEQ ID NO:1249:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 386 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

GAATTCGGCC	AAAGAGGCCT	GTTTGGTTTG	TGACTAGACT	TAAAAATACT	AAAATAAGCC	60
AAATAGATGC	TAACAATACT	AATTTGCACA	CAAGATTTGA	AAAAAGTACT	TCAAGTTTTA	120
TCTCTTATCC	CTAGAGAAAG	TAAATAAAA	GTGGCTCTTG	CAAAAATAAA	TGAAAACAAA	180
ACCACCAACA	AAAACTAATC	ATATAAGATA	CTGTTTTTCT	TTTTGAATAC	TTCAATTGGT	240
CCTATATTAG	GATAAGGTTT	TGATAGCAAG	GACTTCCTAG	CTTCTTCCTT	TATCTTCCAT	300
TCTCTAGTCA	CTTCCGTGTT	TTTATCAAAC	AAGGCTACGT	GTAGGCTTTC	CTACAAAGTC	360
AGATTGAATT	CTACCACCCT	CTCGAG				386

- (2) INFORMATION FOR SEQ ID NO:1250:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 428 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

GAATTCGGCC	AAAGAGGCCT	AACCATGTCT	GACCAGATCA	TTGGGAGAAT	TGATGATATG	60
AGTAGTCGCA	TTGATGATCT	GGAAAAGAAT	ATCGCGGACC	TCATGACACA	GGCTGGGGTG	120
GAAGAACTGG	AAAGTGAAAA	CAAGATACCT	GCCACGCAAA	AGAGTTGAAG	GTTGCTAATA	180
ATTTATACTG	GAATCTGGCA	TTTTTCCAAG	CCAAGAGAAG	ATCGAATGGC	TTTTTGCAGC	240
TAACTACTAT	GTGTAGACAG	GTTTTATATT	ATAAAGTATG	CATTCTTATC	ACCTAGTATA	300
TAGTTAGTTT	GTAGAGTGAT	TTCCCCCCAG	TTTCTTGAAC	ATGGTATCTT	CACATCTTGG	360
ACCTTGGTCA	GTTGTGCTAT	TCATTATTAA	ACACTAAAAC	TTTGGCGGTT	TAGGCCTCTT	420
TGGCCGAA						428

- (2) INFORMATION FOR SEQ ID NO:1251:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 264 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

GAATTCGGCC AAAGAGGCCT	T AAGAAAAGTA	GTATGAATGA	GTTTTTCTAC	ATATTAACTA	60
CAATTTATGG TAATTTGTGA	AATGTTTTC	CATTTTTAAA	TGTAAGAGTC	TCTATCTCCA	120
CTCACAAAGC AACAGGCAC	GCTAGGGGTC	TTAGGCTAAC	ATCTGCCACC	CCACCAGTCT	180
GCATGGCCCA TAAACAGGTC	CAGAGGACCA	GAGTTCACCT	GTCAGCAGCA	CCGCAGAATC	240
CAACTCTAGG CCTCTTTGGG	CGAA				264

(2) INFORMATION FOR SEQ ID NO:1252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 436 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

GAATTCGGCC	AAAGAGGCCT	ACTTTTTTT	TAATTTTCCA	CTTTCTTCTT	AACTTTACTT	60
CTCTTTTTGT	CCCCCCCAT	CTTACAGAAG	TTGAGGCCAA	GGGAGAATGG	TAGGCACAGA	120
AGAAACATGG	CAAACTGCTC	TGTGCTTTCA	AACCAAAGTG	TTCCCCCCAA	CCCCAAATTT	180
GTCTAAGCAC	TGGCCAGTCT	GTTGTGGGCA	TTGTTTTCTA	CAACCAAATC	TGGGTTTTTT	240
TCTTCTTTCT	TTAAACATAG	AGGTACCACC	ACAAGGGATG	CCCTACTCTC	TCGCAGCTCT	300
TGAAAGCATC	TGTTTGAGGG	AAAGGTCTCT	GGGCAAGCAA	GTGGTTATTT	GGATTGCTTG	360
CTTCCCTTTT	TCCACCTGGG	ACATTGCAAT	CATAAAATAA	CAGTAAATTC	CAAACCTCTA	420
GGCCTCTTTG	GCCGAA					436

- (2) INFORMATION FOR SEQ ID NO:1253:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 399 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

GAATTCGGCC	AAAGAGGCCT	AGGGTAGATC	ACTTGATATC	AGGAGTCGAG	GCGGGAAGAT	60
CACTTGACGT	CAGGAGTTCG	AGACTGGCCC	GGCCAACATG	GTGAAACCGC	ATCTCCACTA	120
AAAATACAAA	AATTAGCCTG	GTGTGGTGGT	GGGCACCTGT	AATCCCAGTG	ACTTGGGAGG	180
CTAAGGCAGG	AGAATTTCTT	GAACCCAGGA	$\tt GGCAGAGGTT$	${\tt GCAGTGACCA}$	GCAAGGTTGC	-240
GCCATTGCAC	CCCAGCCTGG	GCGATAAGAG	TGAAAACTCC	ATCTCAAAAA	ААААААААА	. 300
AAATTCCTTT	GGGAAGGCCT	TCTACATAAA	AATCTTCAAC	ATGAGACTGG	AAAAAAGGGT	360
ATGGGATCAT	CACCGGACCT	TTGGCTTTTA	CAGCTCGAG			399

- (2) INFORMATION FOR SEQ ID NO:1254:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 444 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

GAATTCGGCC	AAAGAGGCCT	ACCCGGTACT	TACTTCTCAA	TCCTAAAGAG	AGAAAACAGG	60
TGTTTGATCA	GTATGTAAAG	ACCAGGGCAG	AGGAAGAACG	CAGGGAAAAG	AAAATAAAA	120
ATGCAAGCCA	AGGAAGATTT	CAAAAAAATG	ATGGAAGAAG	CAAAATTTAA	TCCAAGAGCA	180
ACTTTTAGTG	AATTTGCAGC	CAAGCATGCT	AAAGATTCAA	GATTCAAAGC	AATTGAAAAG	240
ATGAAAGACC	GAGAAGCCTT	GTTTAATGAG	TTTGTGGCCG	CTGCTAGGAA	GAAAGAGAAA	300
GAAGATTCGA	AGACCAGAGG	TGAGAAGGTA	AGATGGTTTT	AGTTCCAGTG	GTGTGATTGA	360
TGGGAGTGTG	AATGGGAAAG	GTCTATGCTG	GTGTTATGTT	TCTAACCTTA	TTCATTGGCA	420
TAAATAATAG	GACGTACACT	CGAG				444

- (2) INFORMATION FOR SEQ ID NO:1255:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 284 base pairs
    - (B) TYPE: nucleic acid

(D) TOPOLOGY: linear

- (C) STRANDEDNESS: double
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

GAATTCGGCC	TTCATGGCCT	AAGAAGGACT	ACCCTGCACT	GCTTTCCTTG	GATGAGAATG	60
AACTCGAAGA	${\tt GCAGTTTGTG}$	AAAGGACACG	GTCCAGGGGG	CCAGGCAACC	AACAAAACCA	120
GCAACTGCGT	GGTGNTGAAG	CACATCCCCT	CAGGCATCGT	TGTAAAGTGC	CATCAGACAA	180
GATCAGTTGA	TCAGAACAGA	AAGCTAGCTC	GGAAAATCCT	ACAAGAGAAA	GTAGATGTTT	240
TCTACAATGG	TGAAAACAGT	CCTGTTCACA	AAGACAAACT	CGAG		284

- (2) INFORMATION FOR SEQ ID NO:1256:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 691 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

GAATTCGGCC	TTCATGGCCT	AGTGGGAGTT	TGCTAATGTG	AAACCTAATG	ATGTCTGAAA	60
ATGGTCCTGA	TGGGTATTAA	TAGCCATCTG	GAAAAATTTT	ACATCTTCAC	AAATAATCCC	, 120
AATAATTTAT	ATTGTGAAGA	TATTATCCTG	ATAGTCCTTC	TTTTCCTATA	TTCTTGTCGG	180
CTGTAGGATG	AGAGCAGTAT	GAAGCAAACA	GAAGACATTT	TGAAATTAAT	CACAAAATTC	240
CCATTGCTTT	GAAGCCTGCT	ATTATTATAC	TAAGCCTTCT	TATAGCTTTA	AAAATCAAAC	300
AATGCCAAAC	AGTATATCTA	ACATTTTTAA	TTTCCTTTGA	GCCAAACCAA	TTTGGTTTAA	360
ATTTCTCTGC	CTCCGTGAAG	ACAAGCTGGG	CTGGGGAGGA	CGGTGTCTAG	GAGGGATGAC	420
CCCACTCAGC	TCCAGGCAGT	GTTCTGCCGA	GACCCCAAGA	ACTCGGGGTG	TCAGAGGGCA	480
AAGGAACTAC	CTGCCTTTCA	CGGCTGCTGA	CTTCTCAGGG	CTGCAAGCAG	CACAGAATGT	540
TATCCTTACG	TCCTGAGCCG	GTTTAAGTCT	GTGGAAAAGG	AAGCACGGGA	GAAATCCACG	600
TAACCTTTGC	TTTCTTTTTA	AGGGAAGCGG	TTCCGCCGTG	AACTTGGAAC	CCTCAGCTCC	660
GGGTGTTCTC	GGCAGAAGGG	CAGCTCTCGA	G			691

- (2) INFORMATION FOR SEQ ID NO:1257:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 383 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

GAATTCGGCC TTCATGGCCT	AAGCTGATCC	ACGATCAGAG	TGCTCCCAGC	TGCCCCAGCA	60
GCTCCCCGTC CCCAGGGGAG	GAGCCTGAGG	GGGAAGGGGA	GACAGATCCG	GAGAAGGTGC	120
ATCTCACCTG GACCAAGGAC	AAGTCGGTGG	CAGAGAAGAA	TAAGGGCCCC	AGTCCTGTCT	180
CCTCTGAGGG CATCAAGGAC	TTCTTCAGCA	TGAAGCCGGA	GTGGGAGAAC	TTGAACCAGT	240

GGGACGCCAA	GCGCATGCAC ACGGCCGTGC GGCTGAACGA GGTCATCGTG AAGAAATCCC GCTTGTTTTG CTCAACATGC CTGGGCCTCC CCGCAACCGC AATGGTGATG GGAGTTTCTC GAG	300 360 383
(2) INFORM	ATION FOR SEQ ID NO:1258:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 418 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1258:	
CATTGCCTCC TTACAGCCTG GAATCTCCTT AACTCTTCCA TGATGACGAT ATCTCACCAT	GGACTAACTA CGACCATGAG ATTGGCAGTG ATTTGCTTTT GCCTATTTGG TCCCTCCCGG TGAAAGTGAC TGATTCTGGC AGCTCAGAGG AGAAGAAGCT CACCCAGATC CTATAGCCAC ATGGCTGGTG CCTGACCCAT CTCAGAAGCA GCGCCACAGA ATGCTGTGTC CTCTGAAGAA AAGGATGACT TTAAGCAAGA AGCAATTCCA ATGAAAGCCA TGACCACATG GACGACGATG ATGACGATGA GGAGACCATG CAGAGAACGA GGATTCTGTG GACTCGGATG AATCTCACGA TCCGATGAGT CTGATGAGAC CTTCACTGCT AGTACACAAG CAGTCGAG	60 120 180 240 300 360 418
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 189 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1259:	
TCTGTCACCC	TAATGCTTGA CTTTTTTTT TTTTTTTCTC TTTTTGAGGC AGGTTCTTGC AGGCTGGACT GCAACAGCAT GATCTTGGCT CACCTCCGCC TCCCAGGCTC CCCACCTCAG CCTTCAGAGT GGCAGAGACT ACAGGCTCAT ACCACCGCAC	60 120 180 189
(2) INFORM	ATION FOR SEQ ID NO:1260:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 278 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1260:	
TATAACAGGT TTCTTATGGT TGGGACAAGG	TCTAGCCTTT CCTCCGTTCA AGTAAATTTA GAAATTTCCT AAGTTTTCTT AGCCTAAATC TATATCATAC TTTTAAAATA AAAATCTAGG TGCAAATTTG TAAGGTTAAC ATGTACACTT CACAAACATT GAGACTTTTG TTTTGTTTTC TCTTGTTCTG TCTCCCAGCT GGAGTGGATA CAAGCATGGC TTGCTTCAGC CGGACTCAAG CGATCCCCCC CCCTCGAG	60 120 180 240 278

- (2) INFORMATION FOR SEQ ID NO:1261:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 265 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

GAATTCGGCC	TTCATGGCCT	ACTCACTGGA	TGCTGGGGGA	GGGCCCCTCA	GGTGAGCAGC	60
CCACCACTGA	CTTCAGCGTT	GCTGGCTCGG	TTATCAGACT	CTCATCCAAC	ACAAGCTCAC	120
AGGGAAAGCC	GTTCCTTGCT	CCTTGTGGAG	GGAGCTACCG	TCATTGCCCT	GAGACCACCA	180
GCCAAGAAAG	TAGGTATGTC	CAGGTAGGGA	ATTCAGAGGG	ACCCAGTGCA	TCCAATTATA	240
CAATTATACC	${\tt CAGAAAGTCC}$	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:1262:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 426 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

GGTCAGTATT	GAAGGTTGTT	TTCTGAGCCA	TTGTATGAAG	CTGCTGTTTT	GGCGTCCCTA	60
ATGCAGGGTG	AGATGGTAGT	GTGATTCTTG	TTGTGACATC	TCGTGACTGG	GCAGGACGCT	120
GAATACTGAT	TGCTGCAGAT	GGAGGATGCT	GGATAGACAA	${\tt GGTTGGCCTA}$	CTAAGTGCTG	180
AATCAGTAGC	ATGCGCCGCT	GTCGTAGTGA	TGACTGGAGA	CTGAGCTCTG	GTGGCTGAGA	240
CAGTTGCTAC	CACAGCAGGA	GGGATGGCAT	TGGAGGTGGT	CACAGGTGGC	CGAGACTGGA	300
TTGGTTGGTG	AATGATGTGC	${\tt TGTACTGCTG}$	GCTGAGCAGT	AGCAGCATTT	GGCAGCTGTG	360
AGGTCGGCCT	CAGGACTGTG	GTTACTTTAG	AACTGGACAT	CACAGCAGCA	GCAGCTGCAC	420
CTCGAG						426

- (2) INFORMATION FOR SEQ ID NO:1263:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 398 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

${\tt GAATTCGGCC}$	TTCATGGCCT	AGGCCGGTGT	TTATGCACGA	TGGCGTTGAA	AGCTAGTCCA	60
TCTCTCCAGC	${\tt TGGTGGTGAA}$	GTTGTGTACA	TTGACGTTGG	GATAACCTGC	AGTCTTCATC	120
TGGCACCACA	GAAGCAGGGC	ATCCTTGGCT	GACTTCTTCT	CCTTGTTGTC	TTCTGTCTCC	180
ACACTGATGT	CTTGGATCTG	GAATCGAAGG	ATGATGGTCC	AGACCAGCCC	AAGGGTCAGT	240
CGGTGGTTTC	CGTCCACAAT	GTCATGGGAG	CCCATGTTTT	CCAAGTGCAC	TTTCTGCTCC	300
TTGAGGAACT	GCAGTGCCTT	GTCCACGTTC	TCCAGGCAGT	GGATCCGCAT	GCGGCCCTTT	360
GTAGGCTTTG	GCAGTATCTC	TCCCGAGAGC	ACCTCGAG			398

ì	(2)	INFORMATION	FOR	SEO	TD	NO - 1264 -

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 256 base pairs
  - (B) TYPE: nucleic acid
  - (C) ·STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

GAATTCGGCC TTCATGGCCT AAAAAAAGC	T GTTAAGAAAA	TATGTTTTAA	AAATTTGCCC	60
AACAGGAAGG AGAAAATTAG AATCTAATA	G CAAACTTGTG	TCAAAGCAGG	GGAGACCACA	120
TGATCTTCCT CTTTGAAAAT CTGTCCTGG	G TGATGACCAT	ATGCTCTCTA	AACAGGTTTT	180
CTGTGTTTTA GGGAAAGAAG CTCAGAAAG	G ACCCCTGCTC	TTTGATGACC	TCCCTCCGGC	240
CAGCAGTAAC CTCGAG				256

- (2) INFORMATION FOR SEQ ID NO:1265:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 249 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

GAATTCGGCC	TTCATGGCCT	ACAGAGTCTA	ATTAGCCATA	TTTATATGAT	AATAATAAAC	60
ATTTTGGCTA	CAGTCCTACC	TAGATTTTTT	TTTTTTAGAT	${\tt GGAGTCTTGC}$	TCTGTCGCCC	120
AGGCTAGAGT	GCAGTGGTGC	GATCTTGGCT	CACTGCAACT	TCTGCCTCCC	AGGTTCAAGC	180
AACTCTGTTG	CCTCAGCCTC	CCAAGTAGCT	GGGATTACAA	GCGCACATGA	CCACGCCTGG	240
CAGCTCGAG						249

- (2) INFORMATION FOR SEQ ID NO:1266:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 265 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

GAATTCGGCC	TTCATGGCCT	AGGTTATATA	GCAGTGATGC	TTTCATAGTA	TTTTTCTTGA	60
ATAAGGTCCC	CAAAACCTTA	TTAAGTTCCT	GGTAGGCATG	GAGCATTGAA	GATGGCAGAC	120
ATGGTGCAGT	CTCTCAAGGA	GTTTACGCTC	TAGTGGAGAA	AACAATCAGA	CAGCCTTAAA	180
ATACATGTAT	GGCTACTATA	ATAAATACTG	TGAAGCAGGA	GTGCACCACG	AAACCTGGAG	240
TCCTCTCCAT	CCTCCCCTTC	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:1267:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 293 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

GAATTCGGCC TTCATC	GCCT ACTAGACCTG	CCTCGAGATT	AGGGGGGTTA	GACTCAGAAT	60
TCTGTCCAAA CTCCTG	GACG ACCTCTTGAA	ATTAAGTCAG	GGATTTTATG	TACTGGGTTA	120
ATTTCGTAAC CTCTGG	GTAT AATATTAGGT	TTGCATGTAG	AAAGGGTCTC	CAGTATAGGA	180
CTTCAAAGAA ACTAAG	CCAT AGACGTAATT	TAAGGGCTGT	TCTGATCTGA	AGAAGTGCCA	240
TGGGTAGAAG TTTTAG	CCAT GGTAAAGAGG	CTTCCTGGCA	TCATTTGCTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:1268:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 501 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

GAATTCGGCC TCATGGCCTA	CTGGTCCAAG	CTGATTACCC	TCATAGTGTC	CATCATTGAG	60
GAAGACAAGA ATTCCTACAC					120
AAAATCAGCG CTGAAGTGAT					180
GAGCACGACA AGCATCGTCT	ATGCAAGAGT	GCCGACTACA	TGAACCTCCA	CTTCAAGGTG	240
AAATGGCTCT ACAATGAGTA	TGTGACGGAA	CTTCCCGCCT	TCAAGGACCG	CGTGCCTGAG	300
TACCCTGCAT GGTTTGAACC	CTTCGTCATC	CAGTGGCTGG	ATGAGAATGA	GGAGGTGTCC	360
CGGGATTTCC TGCACGGTGC	CCTGGAGCGA	GACAAGAAGG	ATGGGTTCCA	GCAGACCTCA	420
GAGCATGCCC TATTCTCCTG	CTCCGTGGTG	GATGTCTTCT	CCCAACTCAA	CCAGAGCTTT	480
GAAATCATCA AGAAACTCGA	G				501

- (2) INFORMATION FOR SEQ ID NO:1269:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 330 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

GAATTCGGCC	TTCATGGCCT	AGGCCCCTGC	TCCACCTGGG	GGGACTGGGA	GTGTGAGTGT	60
GCATGGCATG	TGTGTGGCAC	AGATGGCTGG	GACGGGTGAC	AGTGTGAGTG	CATGTGTGCA	120
TGCATGTGTG	TATGTGTGTG	TGTGTGTGGC	ATGCGCTGAC	AAATGTGTCC	TTGATCCACA	180
CTGCTCCTGG	CAGAGTGAGT	AACCCAAAGG	CCCCTTCGGC	CTCCTTGTAG	CTGTTTTCTT	240
TCCTTTTGTT	GTTGGTTTTA	AAATACATTC	ACACACAAAT	ACAAATTGAC	AGGTCAAAAT	300
CCATGAAATG	AGATCCCCCA	GCGGCTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:1270:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 502 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

GAATTCGGCC	TTCATGGCCT	AAAAAAAAA	TACTGATTCA	CTTTTGCAAT	TTTTCAGATA	60
CTACTTGATG	TGACACCTCC	CCTAGGCTTG	CTGTGGGTCT	CTTGGAAGAT	AGAGCTATAT	120
TAACTCCTTG	ACTTAAAGGG	CAGCAGACTA	TATAAGGTCT	CTTTACAGAC	AGAGTAGGGA	180
GAATAATGAA	AAACTTTTTG	ATTTCTAGAG	AGAAGAGAGA	AGACATAGCA	ATGGAACTGT	240
TCTTAGCTTT	GTTTGCTACA	ACTCTTCAAA	GTTTAATTTT	AGATTCAGTG	CATTTATTCA	300
TAGAGCATGA	AACATATAAT	CATGCCTTTT	ACTAATTGCG	GATACTTAAA	TTATATATTA	360
TTTGACCTAC	TGTGTTATGG	TCAATTTGAA	AAAGAATGGT	TTGATTATAT	ATTATTGTCT	420
GTAGATTCCC	TGTACTATTC	TAGGATCATA	TGACATATTA	TCATTACTAA	ATATAGCACT	480
AATTATTGAT	GCTCCGCTCG	AG				502

- (2) INFORMATION FOR SEQ ID NO:1271:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 285 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

GAATTCGGCC	TTCATGGCCT	ACCCCTGACT	ATTCAGTAGG	AGAAGAAATC	AAAAATCCAT	60
TCTTTTCTCC	TTCTCTCCCT	CCAACAGTGG	CCAGGGGAAG	GGGAAGTGAG	GGCAGGGGCA	120
AAAAGATTTG	GGAATTTTTA	TTTATTTATT	TATTGTGACT	TTTCATTTTT	TTGGTATTTG	180
GCTTTACTGG	AATAGGAGGG	CCCCTGCCCA	CTGTGCCCCG	TTTATCCCTT	ATTCCCCAAA	240
CCCTGCTCTC	CCCAACACCT	ACTCACTTAA	GCACTTGTCC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:1272:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 405 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

GAATTCTAGA CCTGCCT	CCA ATTTGAAGAT TTAT	TTCTCT CTTTGGATAT	AGAACAAAAT	60
AACTTTATGT ACATTTT	ATT TCACTTTATT TTAC	TATTGG GTTGGTGCAA	AACAAATTGC	120
AGTTTTCCCA TGAAAAG	TAA TGGCAAAAAC TGCA	ATTACT TTCGCACCAG	CCCAATATTT	180
TATTTTGAGA CAGAGTO	GCA CTCTGTCACC AAGG	CTGGAG TGCAGTGGTG	TCATCCCAAC	240
TCACTACAGC CTCTGCC	TCC TGGGTTGGAG AGAT	TCTTGT GCGTCAGCTT	CATGTGTAAC	300
TGGAATTACA GGTGCAC	GCC ACCACGCCCA GCTA	ATTTTT GTATTTTTTG	TAGAGATGGG	360
GTTTCGCCAT GTTGCCC	TGG CTGTTCTCAA ACTC	CTGACC TCGAG		405

- (2) INFORMATION FOR SEQ ID NO:1273:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 412 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

GCGATTGAAT TCTAGAC	CCTG GCTCGAGGCA	GGTCTAGAAT	TCAATCGGCT	TCCTGGCAGT	60
GCCCTCTCCC AGATGAC	SACC TGATCTCTTT	TTTGTTTTTT	GTTTTTTGTT	TTGAGACAGA	120
GTTTTGCTCT TCTTGCC	CAG GCTGCAGTGA	GTTGAGATCG	CACCACTGCA	CTCCAGCCTG	180
GGTGACAGAG TGAGAC	CCA TCTCAAAAAA	AAAAAAAAA	ATCTGGCCTT	ATGGACTGTG	240
TACTACACTC TAGTGGG	GGT AAGAGGCAAT	GGGTAAATAG	GTAAGTAGAT	TATTGGATGT	300
ATTAGAAGGG GCATGGG	GAA TGTGGGGTCA	AGGTTATAGT	TTTAAATAGG	GTGGTCAGGG	360
AAAGCTTTCT GAGAAGG	TGA CATTTGAAAC	AAATACTTGA	${\tt AGGAGTCTCG}$	AG	412

- (2) INFORMATION FOR SEQ ID NO:1274:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 285 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

GAATTCGGCC	TTCATGGCCT	AGCTATTTTT	AAACAATATC	TGAGATTATT	CATTCAACTA	60
AAACTTATTA	AGCATTTAAT	ATCTGTCTGG	CATTCTTCAG	GCACCAAGGA	TATTTCGTTG	120
AACAAAACAA	AATCTTTGTC	ACTATGGAGT	TTACGTTTTG	TGGTGGCATT	GGAGTGAAGA	180
GCTAGGGAAT	AAAAAAACAA	GTCAATATGT	AGTATGCCAC	TTGGTGGTAA	GTCATTTGGA	240
GAATGATGTA	GTAGGGAAAG	AGGAAAAGGG	TGTAGGCATC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:1275:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 280 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

(	BAATTCGGCC	TTCATGGCCT	ACTCCACACA	TTCATCTCCC	AAAGGACTCC	TTGAATATTT	60
C	CCCCAAAAC	ATCAGCTCCC	AGAAAACACC	CCTCCCAGTC	ACACACACAC	CCAAATTCTC	120
						CCTTCTCTCT	180
						TCCCTTCCTT	240
				CCCACTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:1276:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 220 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

GAATTCGGCC	TTCATGGCCT	ACGAGTGGTG	CGATTTTTTT	TTCTTAGCTT	ATCAGCTATG	60
GTTAGTGTTA	GCGTATTTTA	TGTGCGGCCC	AAGACAATTC	TTCCTCTTCC	AGTGTGGCCC	120
AGGAAAGCCA	AAAGATTGGA	CACCCCTGGT	AGAGGCAGAA	ACTCACTGGG	TTAGTTCCAC	180
AGCATCTGAT	CAAAGATATG	AGGCCAAAGA	GCCTCTCGAG			220

- (2) INFORMATION FOR SEQ ID NO:1277:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 246 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

GAATTCGGCC TTCATGGC	CT ACGAGCTGAG	ATTGCGCCAC	TGCACTCCAG	CCTAGGCAAT	60
AGAGTAAGAC TCCATTTC	AAAAAAAA AA	AAATGTTGAT	CAAAAGAAGC	CAGATGACAG	120
AGTACTCACT GTGTGAGT	CC ATTTATTTGA	AATTCTAGAA	CAAAAAATAA	ATATCCATTG	180
ATAGAAATGG GAACAGTG	TT GGCCTATGAA	GAATGGAAAT	TGACTGGAAG	GAGGCCTCTG	240
CTCGAG	•				246

- (2) INFORMATION FOR SEQ ID NO:1278:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 499 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

GAATTCGGCC TTCATGGC	CT AGCTGGGCGT	GATGGCGGGC	GCCTGTAGTC	CCAGCCACTC	60
GGGAGGCTGA GGCAGGAG	AA TGGCGTGAAC	CCGGGAGGCG	GAGCTTGCAG	TGAGCCAAGA	120
TTGCGCCACT GCACTCCC	GC CTGGGCCACA	GAGAGAGACT	CCATCTCNAA	AAAAAAAAA	180
GAAAGAAAAA AAGAAAAT	AA ACAAAGAAAA	AATTAAGATT	TTTGAAATAA	AAACAAATAT	240
TAAAAATTAT TGAAATAT	AT TGAAAGTTTT	TTCACCATAT	ATATTTACCT	TTTAAAAGGA	300
TATGAATTCA ATTATTTT	AT TIGCTTATGG	AAAATAGATC	CACTGCTCTA	AGATGCTACT	360
AATCATGCTC AGAGGATT	CA CAACAAACAG	ACTGATAAGG	TATTACTTAA	AGCGCTCTAC	420
ATTAAATAGA GCATTCCA	ST TTTCTAGGGC	ACACTACTTG	CTGTATTTCC	AAGGTCAAGC	480
AAAATAGCTT TCGTTCGA	3				499

- (2) INFORMATION FOR SEQ ID NO:1279:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 317 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

GAATTCGGCC	TTCATGGCCT	AATGAGCTAA	AAGCAGTGTC	ATCTCCGCAT	GTTGGAGCAG	60
CCAAGAAATA	GTTTGGTACT	ACCGACATTG	TCTAATCCAT	GTCACATCCT	CATACAATTT	120
AATTGCTCAA	CCATGCATTT	AAAACTCCTC	AAGAAAGGAT	TGGTACTGCA	ACTGTAGGTA	180
AACTGAAAAA	AAATAAGAAA	${\tt GAAAGAGTTG}$	GATGAAAATG	TGAAAGCCCA	AGTTTAGATG	240
TGCATTAAGT	ATTAAATAGC	ACAGTATCTT	CTTCATGGAG	CCTTTTTTCC	TCCCCCATCC	300
CCTGCAGCTA	CCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:1280:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 407 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

GAATTCGGCC	TTCATGGCCT	ACTTCCTTTC	ATTTTGAAGC	AACAGTTTAT	AAACAGGAAA	60
GTCTACTGGT	TTCATAGAAT	CTGTCAGATT	TGCTTATTTG	CTACTGGTTT	CACGCGCGTG	120
GACTATATTC	CAGTGTTTCT	AGTCAAAGAC	CTTTATCCTC	AAATCATGAG	ATTAGAGTAA	180
AACAACTGCT	GTAAGGTTGA	GCATTTCATG	ACCAATGACT	ATGAAGGCAC	ATTCACCAAA	240
CACAGGCACT	TTAAGGGCAT	CCTTGATTAA	TTTGCTAATT	GCTATTTTT	GTTGGTATGT	300
GAATTCCTGC	TAGGAGGCCG	AGGCTAGTAG	GCAATGAAAA	AGACAGAACA	ATGGTAAAAT	360
GCAGCCCCGG	TCCTCTACAA	ATTGACAGTA	TAATTTAGGG	GCTCGAG		407

- (2) INFORMATION FOR SEQ ID NO:1281:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 281 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

GAATTCGGCC TTCATGGCCT	AAGATTGACA	AAGAAATAGA	GCTTCACAGA	ATTCTTCATC	60
ATAAGCATGT AGTGCAGTTT	TACCACTACT	TCGAGGACAA	AGAAAACATT	TACATTCTCT	120
TGGAATACTG CAGTAGAAGG	TCAATGGCTC	ATATTTTGAA	AGCAAGAAAG	GTGTTGACAG	180
AGCCAGAAGT TCGATACTAC	CTCAGGCAGA	TTGTGTCTGG	ACTGAAATAC	CTTCATGAAC	240
AAGAAATCTT GCACAGAGAT	CTCAAACTAG	GGAACCTCGA	G		281

- (2) INFORMATION FOR SEQ ID NO:1282:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 250 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

GAATTCGGCC TTCATGGCCT AGTAGTTTAT TATATAGAAA TTATTTGTCC TTGTCTTAGT TGTGCCCTTT GACTCAGCAA TTCCCCTTCT ATAAAATTTT CCCAAGCAGA TGATTATGGA TATATGCACC AATTTGGAAA CAGGGATGTT TATTGTTTAT AGTAGCACTC AACTGAAAAC AACATAGTTG TCTTCAGGAG CGGGGACTGA TTAAATTATG ACATGAAGCA GAATAATGCA AAATCTCGAG	60 120 180 240 250
(2) INFORMATION FOR SEQ ID NO:1283:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 257 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:	
GAATTCGGCC TTCATGGCCT AGCTGAAGAA GGCCTTCACA GAGCTTCAAG CCAAAGTTAT TGACACTCAA CAGAAGGTGA AGCTCGCAGA CATACAGATT GAACAGCTAA ACAGAACGAA AAAGCATGCA CATCTTACAG ATACAGAGAT CATGACTTTG GTAGATGAGA CTAACATGTA TGAAGGTGTA GGAAGAATGT TTATTCTTCA GTCCAAGGAA GCAATTCACA GTCAGCTGTT AGAGAAGCAG TCTCGAG	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:1284:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 434 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:	
GAATTCGGCC TTCATGGCCT AAAGACTAGC ATATTTATCT TTGACTTGAT TAATCAGACC TAATTTGCAT TCGCAAATGA GACTGATAAA AATGGATTTA CCTTTTAACC TTTAGAGGAG GAAAGGTATT TCTCTGCAAG ATTTCTGGGG CTATCGTTTC TTAACCGATA AGAAGCCACT CCTTTATCAA TAAAGATGAA AATCCGCAAT TTGCATTAGT GAATGGGACT GATTATTATA TAGTTAATTA GCATCTGGAA ATGAGGATTA TCTTAATTAC AAAGCACAAT TTCCCTAATA GCTACAAAAAC TGTAAGTTTG ATCCATGTGG AAATTGGTAA CATTATTATG TAATTAGTGA TAACATTAAT AGTGTAGAAT ATTTAGATGT AATTTGCATA TGCAAATGTG ATTTACCTGA GCCAAAAAACT CGAG	60 120 180 240 300 360 420 434
(2) INFORMATION FOR SEQ ID NO:1285:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 302 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:	
AGCAATATTT ATTTTAGACA GACTTCTGCG TTATGACCCG GCTGCTGGGC TACGTGGACC CCCTGGATCC CAGCTTTGTG GCTGCCGTCA TCACCATCAC CTTCAATCCG CTCTACTGGA	60 120

GCTTCACGCA GGCCATGCTG AGCCAGCCCA GGATGGAGAG CCTGGACACC CCCGCACTCG AG	180 240 300 302
(2) INFORMATION FOR SEQ ID NO:1286:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 245 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:	
GAATTCGGCC TTCATGGCCT AATCTTTTCT AATTTGTCTT AATGCTTTAT AATTTTCTAT GCAGAGGTCT TGTAGATCTC TTTCCAAGAT ATTTGATGTT TGTTTTGTT TGTTTTTTGA GACGGAGTCT CACTCTGTTG CCCAGGCTGG AGTGCAGTGG CGTGATCTTG GCTCACTGCA ACCTCCGCCT CCTGGGTTCA AGCAATTCTC CTGCCTCAGC CTCCCAAGTC TCGAG	60 120 180 240 245
(2) INFORMATION FOR SEQ ID NO:1287:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 232 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:  GAATTCGGCC TTCATGGCCT AATTTTTTT CTCCTCTTTC TTCTAGTACA TATTGATAGG TATAACATAA TTAAGGTTTA AAAAAAATTA GACATAGTTA TTCAGATTTA GGACCAGTAA GGATAGAACT TTCTCTTATT TATGAAAAAA AATGCTAATA ATTTTGGGGC AGTTTTTCC TTTAATTATT TTTTCAATT TCAAGTTTAA TTTTATTTTA	60 120 180 232
GAATTCGGCC TTCATGGCCT AATTTTTTT CTCCTCTTTC TTCTAGTACA TATTGATAGG TATAACATAA TTAAGGTTTA AAAAAAATTA GACATAGTTA TTCAGATTTA GGACCAGTAA GGATAGAACT TTCTCTTATT TATGAAAAAA AATGCTAATA ATTTTGGGGC AGTTTTTTCC	120 180
GAATTCGGCC TTCATGGCCT AATTTTTTT CTCCTCTTTC TTCTAGTACA TATTGATAGG TATAACATAA TTAAGGTTTA AAAAAAATTA GACATAGTTA TTCAGATTTA GGACCAGTAA GGATAGAACT TTCTCTTATT TATGAAAAAA AATGCTAATA ATTTTGGGGC AGTTTTTCC TTTAATTATT TTTTTCAATT TCAAGTTTAA TTTTATTTTA	120 180
GAATTCGGCC TTCATGGCCT AATTTTTTT CTCCTCTTTC TTCTAGTACA TATTGATAGG TATAACATAA TTAAGGTTTA AAAAAAATTA GACATAGTTA TTCAGATTTA GGACCAGTAA GGATAGAACT TTCTCTTATT TATGAAAAAA AATGCTAATA ATTTTGGGGC AGTTTTTCC TTTAATTATT TTTTTCAATT TCAAGTTTAA TTTTATTTTA	120 180
GAATTCGGCC TTCATGGCCT AATTTTTTT CTCCTCTTTC TTCTAGTACA TATTGATAGG TATAACATAA TTAAGGTTTA AAAAAAATTA GACATAGTTA TTCAGATTTA GGACCAGTAA GGATAGAACT TTCTCTTATT TATGAAAAAA AATGCTAATA ATTTTGGGGC AGTTTTTCC TTTAATTATT TTTTTCAATT TCAAGTTTAA TTTTATTTTA	120 180

(i) SEQUENCE CHARACTERISTICS:

<ul><li>(A) LENGTH: 227 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:	
GCGATTGAAT TCTAGACCTG CCTCGAGCCA TACCCATGGT CAGCCTCTTC CTCGTGTTCA CGGCCTTCGT CATCAGCAAC ATCGGCCACA TCCGCCCGCA GAGGACCATT CTGGCTTTTG TCTCTGGCAT CTTCTTCATA CTATCGGGCC TCTCCTTGGT GGTGGGCTTG GTTCTTTACA TCTCCAGCAT CAACGACGAG GTCATGAACA GGCCCAAACA GCTCGAG	120
(2) INFORMATION FOR SEQ ID NO:1290:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 264 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:	
GAATTCGGCC TTCATGGCCT AGACAACTCT TAGCTAAATG TGGTTTGGTT	120
(2) INFORMATION FOR SEQ ID NO:1291:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 323 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:	
GAATTCGGCC TTCATGGCCT AGGTGCTCTC AAGGATCAGT ACTGGGTAAC AATAATCAAA CTTTGAATTT AAACATGCAT CTATTATTTG TGTTTTTTGT TTTTGTTTTT GAGGCAAAGT CTCACTCTGT CACCCAGGCT GGAGTGAAGC AGCCCAATCT TGGCTTACTG CAACCTCCAC CCCCTGGGTT CAAGCAATTC TCCTGCCTCA GTCTACCTAG TGGCTGGGAT TACAGGCGCC CGCCACCACG CCCAGGTAAT TTTTGTGTTT TAGTAGAGAT GGGGTTTCAC CATGTTGGCC AGGCTGGTCT AGAATTCAAT CGG	60 120 180 240 300 323
(2) INFORMATION FOR SEQ ID NO:1292:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 289 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

GCTCGAGAAA	CTTCTGCTGC	ACGTGCGTCT	TCCCCTCCAC	CTTCACCCCT	TGTGGCTCAC	60
TCACGCACCC	ACTCTCCAGT	CCACCCCTCC	TCAGAGACCC	TGTCCACTCA	TCCATCTCTC	120
TCCCATTGCG	CTTCCTCTTC	ACTCCGTTCC	TTCTGCCTCC	CACCATATGC	AAATCTTCTC	180
CATCCTTAAA	AGCCTGATTG	CCTCCTCTGG	ATTTTTCCAC	ACTCTTGGGG	AACTTCCTGT	240
GACTCCCTGC	CCTTCACCAC	CAGCCTTTCC	CAAAGAGAAA	TCCCTCTCA		289

- (2) INFORMATION FOR SEQ ID NO:1293:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 421 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

GAATTCGGCC	TTCATGGCCT	AGTTGAAATC	TTTAGGAATG	AACTTCTGAG	GGCCAAAAAA	60
TGTGACTGAC	GGGAACAATT	CTTAAACTGA	TTAACTAGCT	GTAATATAGT	TTTGTGAATT	120
TATTGCACTG	ATGTTGTACC	TTGTGGTATA	TCTGTCCCTA	TTAAATAAGT	GTTGTTTTCT	180
CCTCTTTAAT	ATTGCTGTGA	ACAGTGGTGC	CCATTGTAGC	ATATGTTTGA	TTTTTTTTTA	240
TTATTTCATA	AGAAAACTAC	GTTAATTTTA	CCTTACTTTC	ATTGTAAATA	AGCCTGTCTT	300
CCTATCTGGA	TTTTTTGTGT	GCATACATAT	TCTACTGATT	AACTACTTTT	GCAGTTTTAA	360
TCCTGTATTA	TTTCTTCTAC	TTTGTTTTGT	GTAAAAGGGG	AAAAAATAAA	AAAAGCTCGA	420
G						421

- (2) INFORMATION FOR SEQ ID NO:1294:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 408 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

GAATTCGGCC TTC	CATGGCCT ACAGGTGTAT	GTCACCATGC	CTGGCTAATT	TTGTTTTTCT	60
TTTCTTTTTT TTT	TTTTCCT AGAGACAGGG	TCTCACTATG	TTGTCTGTCC	TGGCTGGTCT	120
CAAACTCCTG GGC	CTCCATCT TCCCGCTTCG	GCTTCCTGAA	GTGCTGGGAT	TACAATAGGC	180
ATGAGCCACT ATG	SCCCATCC TAAAGTTTTA	CAGCCCAATA	ATAGTAATAT	TCCATCACTA	240
CAGCTATCAT TGA	AGTTTCAG AAGTTAGACT	GTTAAAAGTT	TCAGTAAAGA	GCTTTAACCA	300
GTTTATTGTG GCA	AATACTGT GTACACAATT	ATTTTTTGTA	AAAGGAAGGA	GATTTCTGTC	360
TTAAATAGCT TTA	ANTANAGT TTCAGTTTCA	TATACAGGAA	ACCTCGAG		408

- (2) INFORMATION FOR SEQ ID NO:1295:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 259 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

GAATTCGGCC	TTCATGGCCT	ACAGGCACTC	CAGTTATAAT	TATGTGCCTT	TCTTCCATTT	60
CTACCACTTT	CTCTGATACT	TCTCACTTCT	TTCTCTGGTA	CTTCTCACTT	CTTTCTCTGG	120
TATCATTTTC	ATTCTTCATC	ATTGTTTTAG	TGCCTTTACT	TCAATTCCTT	CATTATTTGA	180
ATTTTTCTTT	TTATCATCTT	GTGATTCAGT	TTTTATTTAT	TTTTTGATAG	TATTCTCCTT	240
TTCTTCCATT	CCACTCGAG					259

- (2) INFORMATION FOR SEQ ID NO:1296:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 257 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

GAATTCGGCC	TTCATGGCCT	AGTGGAGAGT	GCTATCATTA	ACACCTGAAC	TCTGGGCCAG	60
CTTAAGTGTA	TATTCTGTAA	AAAATTTGAA	ATCCCCCAAA	TGTCACATGC	TATGACAGTC	120
ACTTTCTTTA	GTACTTTGTA	ATCATACAAA	ATGGTGTATG	${\tt GGCTAAATAT}$	TGCAGCACCT	180
ATGTCGTCAT	CCTCCATGTT	GCTTATTGAT	CATGGAATGT	TAATTTAGCA	ATAATTTTCT	240
CTGTGTGTGC	GCTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:1297:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 327 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

GAATTCGGCC TTCATGCAAG	TAGGGTATGT	AGGCTTCAGT	TGGTTCTACT	TTCAGAGAGT	60
TAAGATGGAA TGAGGCAGCT	CATGGCACTA	CAGGTCAGTT	GCCTTCTCTC	CAAAATGTTC	120
ACTCATGCAT GTGGGCACTC	ATTGTATTTG	AATAACAGCA	ACAGTGCCTC	CCTCAGTTTG	180
GAACCTCTAG TCCACTTGCT	CACTCATGGT	CCCTGCCTTA	ACCCCAGTCA	AGTTCAAAGC	240
CATAGGCATC ATTTGTCCGA	CTGACATATT	AGGGCATCTA	CCAGTCAAAG	GGTGATTGTT	300
GTAGATGACC TTTGGCCCGT	TCTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:1298:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

GAATTCGGCC TTCATGGCCT ACACTCTCAT GTTTGTTGCA GCATTATTCA CAATAGCCAA	60
GGTATGGAGT CAACCTGAAT GTCGAACACA TGAATGGATA AAGAAAATGT TCACACACAC	120
AATGAAATGT GATTTAGCCT TTAAAAAGAA GGAAATCCTG CCATTTGGAA CAACATGGAT	180
GAACCTGGAG GGCATTGTGC TAAGTGAAAT AAACCAGACA CAGAAAGACA AACACTGCAT	240
GACCTCACTT ACTGTGGAAC CCCTCGAATT CTGGATCTCC CTCGAG	286
(2) INFORMATION FOR SEQ ID NO:1299:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 285 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(5) 3333333	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:	
GAATTCGGCC TTCATGGCCT AATGAATTTA GTATTATTTC TATCATTTCA ATTGCAAATT	60
GTCAGTATCC CCTGCTACGT TTCTACTAAT TTACCATCGC TTCTTCAAAA AATTGTGTTC	120
AGAGTGCTAC AATTTCAGAC TTTGAAATGA ATCACTATAA CTTTTAAAAA TTAGAGATTT	180
TAAAAACTGG AGATTGAATA TATATAAAAA ATACAAAATT TGACATTTAA AACCTCATTG	240
AACTTTTAAA AAAGCCAGAC TCATATTAAG GCACACACCC TCGAG	285
THE TANKE THE PROPERTY OF THE	205
(2) INFORMATION FOR SEQ ID NO:1300:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 292 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:	
(AI) DEGEMENT DEDOCATE TOWN, DEG ID NO. 1300.	
GAATTCGGCC TTCATGGCCT AGGGCCAATG GCCAGGATCT CTGGGGACTA GAAGGGTGGA	60
TTCCTGAACC TGGGTAACAA CGAGACAAAC TCTAGCAATC TGAGCAAGGG AAGGGTCATC	120
AAAGTCCCAA AATCTAGCCC ACTAGCTGCC TAGCCAGGTA AACCAAGGCT TAGGGAGTTT	180
AGACCCTTTC ACATAAAGAA GCTTAATAAA AAGTGTTGGG TGAAGAGATA AACACATGAA	240
GGGGTTGGCT AAAGTCAAAA GAAGATCCGA GGCAGGTCTA GAATTCAATC GG	292
(2) INFORMATION FOR SEQ ID NO:1301:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 548 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(2) 101020011 1111011	,
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:	
GAATTCGGCC TTCATGGCCT ACTCCTCATT TGCCACCACC AGGCCAGTTT GTCCCTTTCC AAACACAGCA ATCACGATCG CCTCTGCAAA GGATAGAAAA TGAAGTGGAA CTCTTAGGAG	60 120
AABI AI AI-I A AII AI-IAI II TUTUTUTUTUTAAA GGATAGAAAA TGAAGTGGAA CTCTTTAGGGAG	140

180

240 300

AACATCTTCC AGTAGGAGGT TTTACTTACC CTCCATCAGC CCACCCCCCA ACATTACCTC

CATCAGCTCC CTTGCAGTTC TTAACACATG ATCCTTTGCA TCAGGAGGTG TCCTTTGGAG TACCTTATCC TCCATTTATG CCTCGGAGGC TTACAGGATA GTAGATACCG ATCCCAGCAG

GTGCCACCTG CAGTGGGCCC AACTTTCAGC GAAAATTACG AGGCCCTGTT AAACCTGGCA	TTACTGCCAT ATGTGTTATC AATGCTTCCA 360 TTTGAATTAG ATGTAGAAGA TGGAGAAGTA 420 GAGCGACTGG GAGAGGCAAA GCCTCGTGGA 480 TCTTATCGGT TCAATCCTAA CAACCACCAA 540
(2) INFORMATION FOR SEQ ID NO:130	22: .
(i) SEQUENCE CHARACTERISTI  (A) LENGTH: 384 bass  (B) TYPE: nucleic as  (C) STRANDEDNESS: do  (D) TOPOLOGY: linear	e pairs cid cuble
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION:	SEQ ID NO:1302:
GAATTCGGCC TTCATGGCCT AGTATCTATC TCCGCTGCTT CCCCCATTTTC CTTCTGTCCT ACATGGGGTT CCTCGGAGGA GCAGAGGTGG CTGCGTCATT TTTCCTTTGC TTTCTCTTTA CCTTTCATTC CCTCAGTGCT TCTCTTCTGA TTCCAACAAA AACCAGAGTC ACTGACAGAG TGTGATGGAT ATAGCGATCT CGAG	TTTTCTCCTG CTCCTTGTTT TCCCAGCAGC 120 CCGCCGTGGG GGGGCGTTTG GGCTGCGGTG 180 CTTTAGACAC TGGCCCAACT CCAGGCGTTT 240 CCTGCATGTT GAGTTCTGTA TTGCTGGGGC 300
(2) INFORMATION FOR SEQ ID NO:130	3:
(i) SEQUENCE CHARACTERISTIC  (A) LENGTH: 140 base  (B) TYPE: nucleic ac  (C) STRANDEDNESS: dc  (D) TOPOLOGY: linear	pairs aid puble
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION:	SEQ ID NO:1303:
GAATTCGGCC AAAGAGGCCT AGGGTACGTG AATCTGGTGT GTATTTTATA CTTATAGCAT ACCTGCCTCA AGAGCTCGAG	
(2) INFORMATION FOR SEQ ID NO:130	4:
(i) SEQUENCE CHARACTERISTI(	pairs aid puble
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION:	SEQ ID NO:1304:
GAATTCGGCC AAAGAGGCCT AAATAAGTTT GGTCTGAATA TTGACAATCA GTATGCATTA CTGTGTGTGC CAGGCCCTGG GTTCAATGCT TGACAACCT GAGATGGTAT AGCCACCTCA	TGAAGCTACC TGGCTAACAT TGTGTACTCA 120 CTACATGCAC TTATATTTCA TTTAATTCTC 180

GTGTCTGACC	ACCAGTTCGT	GTTCTGACGG	CAGGCTAGTC	TGCATCACAG	AGTGTGGAGT	360
AGATGGTGCA	TGCCTGCTAG	GATGGGCTAG	GTATCACTGT	AGGTAAGAAA	CAGCCCCAAA	420
CTATGGAAAT	GTACACCACC	GAAGGCTCTT	TTCCTGCCCA	TGCTGCACAT	CCTCCATGGC	480
TCTCCTGTGC	CCTGTGCCCC	ACATGCCCTC	ATCCTGCCAC	GAGAATAAAG	GAGCAGCCTC	540
CATATGGGAG	CTGTCAGCTG	CTCTAAGAGA	TGAAGGAGAG	AGTGGCCCGT	CTCAATGGCT	600
CCCAACTCTT	CTGCCTCGAG					620

- (2) INFORMATION FOR SEQ ID NO:1305:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 736 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

GAATTCGGCC	AAAGAGGCCT	ACTTTTGGCT	CAATGTTTTC	CAAACTTATT	TGACCCCAAA	60
ACCTTTTTCA	TATACCCAAT	AATAAGCTAC	AGAACTAATA	TTCTGCAAAT	GTCTCTTGGA	120
ACACACTGCC	TTAAACAGAT	ATTTCTATAG	CTGTCAGTAT	AGTTATGTTG	CTCCCAAGCC	180
TAGTTATCTC	CAGTTGTTTT	AAGGGTGTTA	TGAAAAATTC	TTAAAATATA	TATGAATTTG	240
TGTAACACAC	ACAGAGACAC	ACACACATAC	TACTTTAAGG	GGGTGAGGAT	CATTAATTCA	300
GATAATTTTT	AAGTTTCCTA	GTGATTCTCA	ATCTCTTTGA	ATTTTACTTA	CATTTACACA	360
CACACGCACA	CACATATGTA	TATACACATA	TCATTTTAAG	AAGCTGAGGA	TCACTAATTC	420
AGATAATGTA	TAAGTTTCCC	AGTGATTCTC	AACCTCTTTG	AATTTTACTT	ATAATTACAT	480
ACACACACAC	ACTGCTACTT	ATATAAATGT	TCTCATGTAA	TCATGGTAAC	AGCTCAAATT	540
CCCAAAGCAA	GGGAAGACTT	CTCATTGTCA	GTTAAACCTG	TTAAAACATG	AAAATATTCA	600
TTGAGCCTAG	TTCCTTGTTA	TAAAATACAA	GAAATAAGAC	ATTCAGGCAT	TTTCCCTTTA	660
TGAAGATGTT	CAGTCATCCT	TTCCTTGAAC	TACAATTAGG	AAAAGTATAT	GTCTTTATTC	720
CATTGAAGTT	CTCGAG					736

- (2) INFORMATION FOR SEQ ID NO:1306:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 511 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

GAATTCGGCC AAAGA	GGCCT ACAGCAATAT	GCATCTTGCA	CGTCTGGTCG	GCTCCTGCTC	60
CCTCCTTCTG CTACT	GGGGG CCCTGTCTGG	ATGGGCGGCC	AGCGATGACC	CCATTGAGAA	120
GGTCATTGAA GGGAT	CAACC GAGGGCTGAG	CAATGCAGAG	AGAGAGGTGG	GCAAGGCCCT	180
GGATGGCATC AACAG	TGGAA TCACGCATGC	CGGAAGGGAA	GTGGAGAAGG	TTTTCAACGG	240
ACTTAGCAAC ATGGG	GAGCC ACACCGGCAA	GGAGTTGGAC	AAAGGCGTCC	AGGGGCTCAA	300
CCACGGCATG GACAA	GGTTG CCCATGAGAT	CAACCATGGT	ATTGGACAAG	CAGGAAAGGA	360
AGCAGAGAAG CTTGG	CCATG GGGTCAACAA	CGCTGCTGGA	CAGGTTGGGA	AGGAGGCAGA	420
CAAACTGATC CATCA	TGGGG TCCATCACGG	GGCCAACCAG	GCGGGAAGTG	AGGCAGGGAA	480
GTTTGGCCAG GGAGT	CGACA ATGCACTCGA	G			511

- (2) INFORMATION FOR SEQ ID NO:1307:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 219 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (D) TOPOLOGI: IInea
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

GAATTCGGCC	AAAGAGGCCT	AATTTTTCCC	CACACCACAC	CACTGTCCTC	TGTGCCTGTG	60
GAAACCACTC	AAATGCCTCT	CCCCAAGCCT	TCTTTCAGTA	ACAACCATCT	CATCCGGTTG	120
ATTACTGTAG	CTTTCGGCCT	GTATAACCCC	TCCTTATGTC	ATGCCTGTAC	CAGATGTTCC	180
ACTGCATCTG	TATCCCACCA	GATTGCACAT	ACTCTCGAG			219

- (2) INFORMATION FOR SEQ ID NO:1308:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

GCACTGCGCC	TGGCCCTTGT	GGATACTTTC	TAGGTGATTT	GAGGAGGAAA	GGCACAGCCA	60
TGTCTCCTAA	AGTTAACAAG	CACTAAGCTT	TCCCAAGTAG	TGAAATGTCA	AGCCTCTGCT	120
TCTGTCACTT	ATTTGTTCAT	TCAGCAGAAA	GTCACTGAGA	GCCTTCTGTA	CACCAGGCAC	180
AGTGCTGGGC	AGTGAAAGAG	ACAGACATGT	CCCTGGATCC	AGGGAGGAGA	TGACCAAGTG	240
ATGGCTGTCA	GGCCCAGACC	TTGCTGTTTG	TCTGCAGCCT	CTTCCCTCAG	GCAACTTGTT	300
CTCTATCAGG	AGAAATGAAA	TAATTATTAT	CTGGAGCTCT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:1309:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 565 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

GAATTCGGCC TTCATGCCTA	AAAAGGGTCA	GAGGAAGGCA	GTATCCTTGG	GGTGTTGCTG	60
AAGTTGAAAA TGGTGAACAT	TGTGATTTTA	CAATCCTAAG	AAATATGTTG	ATAAGAACAC	120
ACATGCAGGA CTTGAAAGAT	GTTACTAATA	ATGTCCACTA	TGAGAACTAC	AGAAGCAGAA	180
AACTTGCAGC TGTGACTTAT	AATGGAGTTG	ATAACAACAA	GAATAAAGGG	CAGCTGACTA	240
AGAGCCCTCG AGTTGCAGGG	AGCCCAGATC	ATGCCACTGC	${\tt TCTCCAGCCT}$	GGGTGACAGA	300
GCAAGACTCT GTGCCCCCCC	CCCACCCCAA	AAAAAAAGAA	AACAAAAATT	AAAATCTTTA	360
GTTACTGTAT TATTCAAAAA	TGTCTACTTT	CAAGAAAAAC	TACAGCCATG	CAAAGAAACA	420
GTAAAATGTG ACCATACTCA	GGAAAAAAAG	CAGACAATAG	AAATGGCTTC	TCAGTAGGGC	480
TATATGTTGG ATTTAGCAGG	CAAAGACTTC	AGAGGCCTTT	TAATAAGTAT	ATTCAAAGAA	540
TTACAGGAAA ATATGAAAAC	TCGAG				565

- (2) INFORMATION FOR SEQ ID NO:1310:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 104 base pairs
    - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:	
TGCACAGCTG TAGTACCCCA AGAAGAAAAT GTTACTTCTC TCATCTGGGC AAAACCCACA GAAGACTTCC CAGCTTCTGC CACATAAAAG ACACAGAACT CGAG	60 104
(2) INFORMATION FOR SEQ ID NO:1311:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 105 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:	
GAATTTTGCG TTCTGTTTAG CATGCTATCC TGTGTGAAAG AAACTGAAAT CCAATATTAT GGAGAGTATG TTAAAGCCAC CTCTGAAATG AAGACCACTC TCGAG	60 105
(2) INFORMATION FOR SEQ ID NO:1312:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 407 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:	
AGATTCGGCC TTCATGGCCT AAAGGAAGG GAGGTGTGAG GAGGATGGAG TAAGAGTGAG GAGGTCCTAAG AACATGGAGG GAGGCTGTGT GTGATCGATG GAGAAATATG GTCCTGAGAG ATTCCTTGTA GTCAAGAATG GCCAATACAT GTCTACCTTT AACTGGTATT GGAAGGAAGT GAGTTCCTGC TCTGTGCTCT AAATACTCTC TATTACCCTC AAGATGTCAG CAAAATGTGA GACATAGCAA TCTTGTGTTA GAGGATGCTT AGGAATTGCA GAAAAACCAT GCTATCAAGT GGTAGGGAAG TGAGTGGCAA GAGGATGCTT GTCACAGAAA CTAGGGATAG AGGGGCTGGC AATGGCAGAA ATGCAGGATG AGTGGACTGA TTAAGGGGAG TCTCGAG	60 120 180 240 300 360 407
(2) INFORMATION FOR SEQ ID NO:1313:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:	
SAATTCGGCC TTCATGGCCT AGGTCTTGCC ACATTGGCCA GGCTGGTCTC GAACTCCTGG	60

GTTCAAGTAG T	TCCTCCACCT CAGCCTCTCA AAGTACTGGG ATTACAAGCG TTGAGCC	CACC 120
CICCCAGCCI I	TTGCCTTTTT TTTTTTTTT TTTTTTTTA GGAGGAGAAT TAATTG	ATAC 180
ATAGACCCCT T	TAAGAGAAGG GATGCTATGG GCAGGAAGAG ATTGAAGGTA AAGGAA	AAAG 240
GATTCAGCAC C	CCAAGCAAAA CAATTGGCCT GTGATAGAAG GGCGATCTCG AG	292
(2) INFORMAT	FION FOR SEQ ID NO:1314:	
(i) ci	EQUENCE CHARACTERISTICS:	
(1) 5		
	(A) LENGTH: 309 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii) !	MOLECULE TYPE: cDNA	
(wi) (	SEQUENCE DESCRIPTION OF TO NO 1211	
(XI)	SEQUENCE DESCRIPTION: SEQ ID NO:1314:	
GAATTCGGCC T	TCATGGCCT AGATCCAAGA AGCTCAACAG ACCTCAAGTA GGATAAA	ACAC 60
AAACAGATCT T	CACTAAGTC CTACTGCTGA AAGACAAAGA CGAGGAGAAC ATCTTGA	CAC OU
CACTCACACA A	ANACANCIO CINCIGCION MAGACAMAGA CGAGGAGGAC ATCITGA	AAAG 120
CAGIGAGAGA A	AAACAACTC ATTATGGAGA GAGCAATGAT AAAATTCTTA TCAGAAC	LAGT 180
GGAGGCCAGA A	AGGAAATAGA GTGACATATT CAAAATGCTG AAGGAAAAAT TTGCAAC	CTAC 240
AAGTTCTAGA T	CCAGCAAAA TTATCCTTCA AGAATGAAGG TTTAGTAAAG ACATTCC	CAG 300
ACCCTCGAG		309
(2) INFORMAT	TION FOR SEQ ID NO:1315:	
(i) SE	EQUENCE CHARACTERISTICS:	
	(A) LENGTH: 469 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	,	
(ii) M	MOLECULE TYPE: cDNA	
(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:1315:	
GGCCCCAGCT C	CTGAGTAGC TGGGATTACA GGCATGCACC ACCACACCCA GCTAATT	TTG 60
TATTTTTAGT AG	GAGACAGGG TTTCACCATG TTGGTCGGGC TGGTCTCAAA CTCCTGA	CCT 120
CAGTGATCCA CO	CCGCCTTAG CCTCCCAGAG TGTTAGAATT ACAGGCGTGA GCCACTG	CAC 180
CCGGCTGGGA A	ACATTTTA AAACGGCGCA GGGTTGTCCT TGAAAGTCCC AGGTTTC	CTC 240
ATTGGCCCTG C	CATTGGCGG GTGGGTGATT TCAGGCAGGA CACGCAGTGT CTGGGGA	CIC 240
TCCCTTTTCTC	CTCCAACAC CATTOOTTATIC CTCCAGGCAGGA CACGCAGIGI CIGGGGA	CCC 300
TOUCITICIC A	CTGGAAGAC GATTGTTATG GTCCAGAGGG TGGTAACTCA GGTGTTC	ATG 360
TCTGATTCTG GA	ATGTTCTCT GCAGCTGCTG GAGTCTCCTG ATTGGAGAGC AGCAAAT	
TGTTCAATGA C	AGTTCTAGT TGTACCTCTA GCACCCCCAC TCGCTCGAG	469
(2) INFORMAT	ION FOR SEQ ID NO:1316:	
(3) 05	FOLIENCE CUADA COURT CO	
(1) SE	EQUENCE CHARACTERISTICS:	
	(A) LENGTH: 262 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

60

120

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

GAATTCGGCC TTCATGGCCT AATCTATGTG TGTCAACTTT CATAGAACCC TACACCAAAA

AAGGTGAATT TTATTTCGTG ATAAATTAAA AAGTAAAACA AAAGAGACAA AAATAGTAAC

CAGGGAAGCT	TTCAAAAAAT	ATATGTTCTT	GTTCAAGACC	AGCATGGCCA	ACATGGCGAA	180
ATCCCATCTC	TAAAAAAAT	AGAAAAATTA	GCCAGGCGTG	GTGGTGGCG	CATGTAGTCC	240
CAGCTATCCA	GCACCGCTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:1317:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 497 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

		AAAGGAATGG				60
		GATGCAAGAA				120
		CATGGATGGA				180
		AGACAACCAC				240
		TATTTGAAAG				300
		AACCTACTCA				360
		CGGGTTTGAG				420
CTCATTCTGC	ACCACGTGCT	GTCAGCCAGG	CAGCCAATGT	GGACTTGGAG	GCTGGCATCT	480
GCTGGGCACT	GCTCGAG					497

- (2) INFORMATION FOR SEQ ID NO:1318:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 451 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

GAATTCGGCC TTCATGGCCT	AATCTGGATG	TCTGTCCAAG	GCCTGACTGC	TGAACTCCTA	60
CTTTTCCTAC AAAACCCTAC	CCACATGGCC	CTTCCTGCGG	GAAGAGATCT	TGAGCCTCCC	120
TGGCTATTAA GACTCTGCTG	TGCAGCCTTC	TTTTACTGGA	CTCAGGGCTA	TCTTCCCCAG	180
ACTAGGGCCT TCTTGAGGAC					240
GTAGTTGGTC TTCCTGGTTG	CTTCTTGCCC	CTGTGGCTCC	CTTGGGAGAC	TGAAACTCAG	300
AGGACAGCTT CTGGTCTGCT	GTTACATGGC	TCCCACAGGG	AGACTGGCCC	CACCTGTGCC	360
CCACCCATCA CAGCTAGGGC	CTGGGATGGG	TCAGACACTG	GAAGAGCCTC	CCCCTAGGCC	420
ATGCATATGG ATCGTGCCCA	CACGCCTCGA	G	•		451

- (2) INFORMATION FOR SEQ ID NO:1319:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 477 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

GAATTCGGCC TTCATGGCCT ACACTACGGT ACTCCCAGCA TATCACCCTT AATGTAACTT TAAATAACAT GGCCATTTT TAAAAAGGAC ACAGGAACTA CATAACATTT TTTTTCAGAT TTTGGAAAAT TCTAAATATG TCTAGAAAAA CTTTTCTTTC TGTTCCATTC TCCTCTAT TCTCCATGAC CCCCTCCCCG CGGACTGTAT CAGGTACAGC CTGTTGGAAA TCCAGCACCG CACATTAGGC ACACCAGTGG TAAGTTTACT TGTTGAGTTA TCACCTTTTT TTTCCTTTTA ATCAGAGAGG CAGCTCTGT TTGAAGATGC TAGGTAGTGA TGGAAAAGAC ATTAGGAAAA TTTGTTACCG TGGTAACCGG GGATGGACAT CATGACCTTT TGTGATATGC ATGCTGTGGC CTTGGTAGTC TCTTCCCCTA ATTAACATCC TGTGAGAAAC GTGAGAGATG ACTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:1320:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 284 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:	
GAATTCGGCC TTCATGGCCT AGACGAGGC TGGAGATTCA CATGGGGCGA GGAGTTGCAG ACCAGCCTGG GCAAAGCATG GTGAGGCCCC GTCTCTGCAG AAATGAGAAA ATGAGCTGGA TGTAGTGGCA CCGACATGTG GTCCCAGCTG CTGGGAGGGC TGAGGTGGGA GGATTGCTTG AGCCTAGGAG TTCAAGGCTG CGGTGAGTAG ATCGTGCCAC TGCGCTCCAT CCCTGGCAAC AGAGCAAGAT CATTTCTCAA AAAGAAAAAA AAAGCCATCT CGAG	60 120 180 240 284
(2) INFORMATION FOR SEQ ID NO:1321:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 254 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:	
GAATTCGGCC TTCATGGCCT AGGGAAATGT GTGATTGGGA AAGAGGCAGC TTTTAAAAAT GTGTCTGGCC TTTGACCACG CAATTTCACT TTCCAGTATT TATTCTAGGA AAATACTCAT ACTATTGCAA AGTTTATATA TAAAGATAGT TATAACTGCA TTGTTTATCA TTTACAAAAA GAAAACATCT GAAGCCCAA CAAGACGGAA CTGGTTATTC CACATTGGCA CATTCATACA AGGCAATGCT CGAG	60 120 180 240 254
(2) INFORMATION FOR SEQ ID NO:1322:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 352 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:	
GAATTCGGCC TTCATGGCCT AGGCACAGAA AAATTGGAAA GGATTGGTGG TCGTACATCT TGCAGCTCAC TTAGTAGCTG CATGCATGTA GACCGGGTGG TGTTGATGCA GTGTTGACTT	60 120

GCTGGCATTG GGGTGGTGG TAGCATGGTC AAGCTGGCTG AGTGATGGGA TATTGTC GAGGTTGGTG CAGGGAAACT CTGTGGGTGT GTCTAATGCA AGGATAATGA CAATGTC GCTGCCTGGT CTTTGGGGGG TCAGGTGGAG ATGTCCTTTT GGAAAGGCAG CCATTCTC GGAGTGTCCA GAGGGCATGG TGCAGGCACA TGGATTGAGT GGAGGACTCG AG	CTG 240
(2) INFORMATION FOR SEQ ID NO:1323:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 440 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:	
CATTCAGCC TTCANGGCCT ACTGTGTA GAATTCTGTT TTCTCATGAT ATTGAAGA TATTCCAGT ACTTTGACTG CTAGTATTGC TGTTGAAAAG TCTTAATTGC CCTTCCTT TAGGTAATAA CCCTTTTATT TGGCTGTGTT AAGCCTTTTT TTTTCCTTCC CATTTAGT TGTGAATCCCA CTTGGGATTC TTTGGGCTTC CTGGATCTGA GGATAATAAT AATGTCTT TATAACTCT AATTAGACAT ATAGTCTATT TTTCATGTA CTTATGCCTT TTCATCCT TCGTCTCCA CATACTCGAG	TTG 120 TGT 180 TT 240 TTG 300
2) INFORMATION FOR SEQ ID NO:1324:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 280 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:	
AATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCC TAAAATGCCC AGTTACCT ATTGTATAA ATTCTTGCCA AAAGTGTTTG AACTTAATAC AAACTTCCCA TCTCTTAC TTAGCACTG TGCTCATCTT GAGGGGACAT AGTCCCAATT TTGTATTTTA TATAATAC TAATGAATA TGTGTAGACT TCATATGGTT GTGGGTAAGA GAATACTGCA TTCAGATA AAGATGCTA TATAGCTAAG TTGATCCGCG GATCCTCGAG	CT 120 TG 180
2) INFORMATION FOR SEQ ID NO:1325:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 281 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:	
TTTCCTTTT CTACTTACAA AGAAAATAAA TAGAAATAGA TTTTACATGC TTTATTTC GAGACAAGC CATTGTAAAT TGTTACTAGA CTAAGTAGTA GTATACCAGT CATTGACT CTTTTCAAC TCCACTCAAA TTTGTAAAAA GCAATTCCTC TTATACTATC ATCTTTTT	GG 120

TTTTTTAAGG TTTTTGTTGT TGTTTGGTTT TTTGGCAAAA CATGATACAT TTCTCATGCT TGATCTAAAG AGGCTTTACA TAAGAGACAG AGTCGCTCGA G	240 281
(2) INFORMATION FOR SEQ ID NO:1326:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 348 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:	
GAATTCGGCC TTCATGGCCT ACTATCTTGA ATGTCCAACT CCAACTCCTA ATTATTTTAA AAATCTATGC ACTTCTTCA CTTGAATTTC TATGCCCTCA TAGACTTTAC AGGCACATGT CTAATCACCA ATTAAGAGAA ATTTAACTTA CACATTTTAC AACTTATACA TGCAATTTGG CTGAGCTTAT ACAGCACAGA TCAACATTAC AATCAATTTA CTGCCATGTT AAAAAAAAAA	60 120 180 240 300 348
(2) INFORMATION FOR SEQ ID NO:1327:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 680 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:	
SAATTCGGCC TTCATGGCCT ACACGGACTT ACATCCTCAT TACTATTCTG CCTAGCAAAC	60
CAAACTACG AACGCACTCA CAGTCGCATC ATAATCCTCT CTCAAGGACT TCAAACTCTA	120
TCCCACTAA TAGCTTTTTG ATGACTTCTA GCAAGCCTCG CTAACCTCGC CTTACCCCCC	180
ACTATTAACC TACTGGGAGA ACTCTCTGTG CTAGTAACCA CGTTCTCCTG ATCAAGTATC	240
ACTCTCCTAC TTACAGGACT CAACATACTA GTCACAGCCC TATACTCCCT CTACATATTT	300
ACCACTAACC CTCGAGACCA CTTCATATAA ATACTTATTT ATTTCCTATT TCCCCTGACT	360
AGAAATATAA GCTCCATGGT AGCAGAGATT CTGATTGCTG CCTACTCTAT CCCCAGCTCC	
AND CONTROL OF THE PROPERTY OF	420
CATACTAGGC ACCATGAGTA CATGATCAGA AAATATTCAT GGAAAAAAAT ACATAAATGT	480
TAACAATCT TCATTTGTGA GTAAGAAGAT GGGCTCTGGA ATCAGACTGC CTGGATTGAA	540
TCCTAACTT CATCACTTAC TAGTCATGGG ATATTTTACC TCAGTTTCAC TTTTTGAAAA	600
GAAGATAAT AATGTCTACC TTATAGTATT GTGAGGATTA AGTGAATTAA TGCACACAAA	660
NTTAGGCCAT GAAGGCCGAA	680
2) INFORMATION FOR SEQ ID NO:1328:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 499 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(c) strumpenteps: doubte	

(ii) MOLECULE TYPE: cDNA

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

PCT/US98/06956 WO 98/45437

> GAATTCGCGG CCGCGTCGAC TGTCACTGAG CTTCTTGGCT CTCTTATATA TATTCTTTAT TGTCATTTAC TTTGGTGGAC GAAGAGAAGG AGAGAGTTGG AATTGGGCCT GGGTCCTCAG

120

CACTAGATTG GCAAGACATA TTGGATATTT GGAACTCCTC CTTAAATTGA TGTTTGTGAA TCCACCTGAG TTGCCAGAGC AGACTACTAA AGCTTTACCT GTGAGGTTTT TGTTTACAGA TTACAATAGA CTGTCCAGTG TAGGTGGAGA AACTTCTCTG GCTGAAATGA TTGCAACCCT CTCGGATGCT TGTGAAAGAG AGTTTGGCTT TTTGGCAACC AGGCTTTTTC GAGTATTCAA GACTGAAGAT ACTCAGGGTA AAAAGAAATG GAAAAAAACA TGTTGTCTCC CATCTTTGT CATCTTCCTT TTTATCATTG GCTGCATTAT ATCTGGAATT ACTCTTCTGG CTATATTTAG AGTTGACCCA AAGCTCGAG	180 240 300 360 420 480 499
(2) INFORMATION FOR SEQ ID NO:1329:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 200 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:	
GAATTCGCGG CCGCGTCGAC CGCTGCCAAA TGCTTCACTC CTATCTACTC TCCCGATTCC TTATACTTCT GAACCTCCTC AACAGAAATC TTGCTCTCTC CCTAAATCCT CAGTGCAACA TACGTCCGCA AAAACTAAAT GATCCCTCCT CAGCCAGACA GAAAACTCTC AACATATCAA CACTCCCAAG GCGTGGACAG	60 120 180 200
(2) INFORMATION FOR SEQ ID NO:1330:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 158 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:	
GAATTCGGCC AAAGAGGCCT ACAGTCTTTT TAGGCATGTT TTTTTTTTTT	60 120 158
(2) INFORMATION FOR SEQ ID NO:1331:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 552 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:	
GAATTCGCGG CCGCGTCGAC GATCATGAAG CGCTCGGTAG CCGTCTGGCT CTTGGTCGGG CTCAGCCTCG GTGTCCCCCA GTTCGGCAAA GGTGATATTT GTGATCCCAA TCCATGTGAA AATGGAGGTA TCTGTTTGCC AGGATTGGCT GATGGTTCCT TTTCCTGTGA GTGTCCAGAT GGCTTCACAG ACCCCAACTG TTCTAGTGTT GTGGAGGTTG CATCAGATGA AGAAGAACCA	60 120 180 240
522	

```
ACTTCAGCAG GTCCCTGCAC TCCTAATCCA TGCCATAATG GAGGAACCTG TGAAATAAGT 300
GAAGCATACC GAGGGGATAC ATTCATAGGC TATGTTTGTA AATGTCCCCG AGGATTTAAT 360
GGGATTCACT GTCAGCACAA CATAAATGAA TGCGAAGTTG AGCCTTGCAA AAATGGTGGA 420
ATATGTACAG ATCTTGTTGC TAACTATTCC TGTGAGTGCC CAGGCGAATT TATGGGAAGA 480
AATTGTCAAT ACAAATGCTC AGGCCCACTG GGAATTGAAG GTGGAATTAT ATCAAACCAG 540
CAAATCCTCG AG
```

- (2) INFORMATION FOR SEQ ID NO:1332:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 760 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

GAATTCGCGG	CCGCGTCGAC	CTCAGAACTA	TTTAAATTTA	GTTAAATTAC	TATTATATTT	60
TATAGTAAAT	ATTGGTCCAC	TTTATAGCTC	AGAACCTAAA	AAGAGAATAT	GTACCCAAAC	120
TTCTCTATGT	TTACAACCAA	CCCAGAGTTT	AAGATTCTGA	ATTGTGCTTT	GTTTTGTTAA	180
AAATTTAACC	AAGGGTCAGG	CACAGAGGCT	CATGCCTATA	ATCCCAGCGC	TTTGGGAGGC	240
CGAGGCGGGT	GGATCACTTG	${\tt AGTTCAGGAG}$	TTCGGGACCA	GCCTGGCCGG	CATGGTGAAA	300
CCCCGTCTCT	ACTAAAAATA	CAAAAGTTAG	CCGGGTGTGG	TGGCATGTGC	CTGTGGTCCC	360
	GAGGCTGAGG					420
GCAGTGAGCC	GGGATTGTGC	CATTGTACTC	CAGCCTAGGC	AACAAGAGCG	AAACTCTGTC	480
AAAAAATT	AAAAGAAAAA	AAAATTAACC	AAGGTTCTCC	TTTCTCTAAA	TCTAGCAATT	540
TGTTCTATTT	TTCAGAAATA	AACTTAATAA	TTTTAATACA	GATTTTAGCT	TTGGCTTTTT	600
TCTTACTTTT	TAGTTTGCAA	ATTATTTTAT	GGTATTCCTA	CAAAGTAGAT	ACAAATTTGC	660
ATTCAGAATG	CACCTTTTGT	TTTTCTGGGT	TTTTTTTTTT	GTTTGTTTGT	TTTTTCAGAA	720
AACTCATGGA	AAAGTACACT	GTTCACCTCA	GCATCTCGAG			760

- (2) INFORMATION FOR SEQ ID NO:1333:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 579 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

60
120
180
240
300
420
480
579

- (2) INFORMATION FOR SEQ ID NO:1334:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 521 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

GAATTCGCGG	CCGCGTCGAC	CAACAAGGGC	AAAGGCCTTG	AGACACAAAC	CAACTGTGTG	60
GGTGTAAAGG	TAAGAAAGGC	CAGTGAGGCC	AGCATGATGA	ACTGGGGGAG	CATGGTGGCT	120
GATTTGGTCA						180
					TGGAAGTGAT	240
GTGACCTGAG						300
GGGCAAAAGC						360
AGTGATCATC	TTGACTAGGG	TGGTGGTGGT	AGAGGAGGTG	AGTGGTGGTC	AGGACTGAGA	420
GGAGCCAACA					TGAGAATCCA	480
AGATGGCACC	AAGGCTTATA	CCCTGAGCAA	CTGAACTCGA	G		521

- (2) INFORMATION FOR SEQ ID NO:1335:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 775 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

GAAATTCGCG	GCCGCGTCGA	CGCTCTTGAG	TGAGACCCAA	CAAGCTGCTT	TTCACCAAAT	60
TGCAATGGAG	CCTTTCGAAA	TCAATGTTCC	AAAGCCCAAG	AGGAGAAATG	GGGTGAACTT	120
CTCCCTAGCT	${\tt GTGGTGGTCA}$	TCTACCTGAT	CCTGCTCACC	GCTGGCGCTG	GGCTGCTGGT	180
GGTCCAAGTT	CTGAATCTGC	AGGCGCGGCT	CCGGGTCCTG	GAGATGTATT	TCCTCAATGA	240
CACTCTGGCG	GCTGAGGACA	GCCCGTCCTT	CTCCTTGCTG	CAGTCAGCAC	ACCCTGGAGA	300
ACACCTGGCT	CAGGGTGCAT	CGAGGCTGCA	AGTCCTGCAG	GCCCAACTCA	CCTGGGTCCG	360
CGTCAGCCAT	GAGCACTTGC	TGCAGCGGGT	AGACAACTTC	ACTCAGAACC	CAGGGATGTT	420
CAGAATCAAA	GGTGAACAAG	GCGCCCCAGG	TCTTCAAGGT	CACAAGGGGG	CCATGGGCAT	480
GCCTGGTGCC	CCTGGCCCGC	CGGGACCACC	TGCTGAGAAG	GGAGCCAAGG	GGGCTATGGG	540
ACGAGATGGA	GCAACAGGCC	CCTCGGGACC	CCAAGGCCCA	CCGGGAGTCA	AGGGAGAGGC	600
GGGCCTCCAA	GGACCCCAGG	GTGCTCCAGG	GAAGCAAGGA	GCCACTGGCA	CCCCAGGACC	660
CCAAGGAGAG	AAGGGCAGCA	AAGGCGATGG	GGGTCTCATT	GGCCCAAAAG	GGGAAACTGG	720
						775
	TGCAATGGAG CTCCCTAGCT GGTCCAAGTT CACTCTGGCG ACACCTGGCT CGTCAGCCAT CAGAATCAAA GCCTGGTGCC ACGAGATGGA GGGCCTCCAA CCAAGGAGAG	TGCAATGGAG CTCTTCGAAA CTCCCTAGCT GGTGGTGCT GGTCCAAGTT CTGAATCTGC CACTCTGGCG CAGGGTGCAT CGTCAGCCAT CGTCAGCCAT GAGCACTTGC CAGAATCAAA GCCTGGTGCC CCTGGCCCGC ACGAGATGGA CCAACAGGCC GGGCCTCCAA GGACCCCAGG CCAAGGAGAG AAGGGCAGCA	TGCAATGGAG CCTTTCGAAA TCAATGTTCC CTCCCTAGCT GTGGTGGTCA TCTACCTGAT GGTCCAAGTT CTGAATCTGC AGGCGCGGCT CACTCTGGCG GCTGAGGACA GCCCGTCCTT ACACCTGGCT CAGGGTGCAT CGAGGCTGCA CGTCAGCCAT GAGCACTTGC TGCAGCGGGT CAGAATCAAA GGTGAACAAG GCGCCCCAGG GCCTGGGTGC CCTGGGCCCC ACGAGATGGA GCAACAGGCC CCTCGGGACC ACGAGATGGA GAACCCCAGG GTGCTCCAGG CCAAGGAGA AAGGCCACAC AAGGCGATGG	TGCAATGGAG CCTTTCGAAA TCAATGTTCC AAAGCCCAAG CTCCCTAGCT GTGGTGGTCA TCTACCTGAT CCTGCTCACC GGTCCAAGTT CTGAATCTGC AGGCGCGCT CCGGGTCCTG CACTCTGGCG GCTGAGACAA GCCCGTCCTT CTCCTTGCTG ACACCTGGCT CAGGGTGCAT CGAGGCTGCA AGTCCTGCAG CGTCAGCCAT GAGCACTTGC TGCAGCGGGT AGACAACTTC CAGAATCAAA GGTGAACAAG GCGCCCCAGG TCTTCAAGGT GCCTGGTGCC CCTGGGCCCA TGCTGAGAAG ACGAGATGGA GCAACAGGC CCTCGGGACC CCAAGGCCCA GGGCCTCCAA GGACCCCAGG GTGCTCCAGG GAAGCAAGGA CCAAGGAGA AAGGCCACA AAGGCGATGG GGGTCTCATT	TGCAATGGAG CCTTTCGAAA TCAATGTTCC AAAGCCCAAG AGGAGAATG CTCCCTAGCT GTGGTGGTCA TCTACCTGAT CCTGCTCACC GCTGGCGCTG GGTCCAAGTT CTGAATCTGC AGGCGCGCT CCGGGTCCTG GAGATGTATT CACTCTGGCG GCTGAGGACA GCCCGTCCTT CTCCTTGCTG CAGTCAGCAC CAGACTCCA GGCCCAACTCA GAGCACTGC TGCAGCACT GAGCACTCA GAGCACTGC TCTCCAGGACC CAGAATCAAA GGTGAACAAG GCGCCCAAG TCTTCAAGGT CACAAGGGGG GCCTGGTGCC CCTGGCCCG CGGGACCAC TGCTGAGAAG GAGCAAAGG CCCAGGGCCCA CCGGAGTCA GGGCCCACC CCAGGCCCAAGGC ACGAGATGAA GCAACAGGC CCTCGGGACC CCAAGGCCCA CCGGGATCA GGGCCCACC GGGAGTCA GGACCACTGCAAAGG AAGGCCCAA GGACCACTGCAAAAG GCCACTGGCAAAAG GCCACTGGCAAAAG GCCAAGGCCAACCCAAGGCCAACCCAAGGCAACCCAAGGCAACCACACCAAGGACCAACCACACCAAGACAACA	GAAATTCGCG GCCGCTCGA CGCTCTTGAG TGAGACCCAA CAAGCTGCTT TTCACCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATTGCAAATT

- (2) INFORMATION FOR SEQ ID NO:1336:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 155 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

GTAGATTTAG	ATGTACAGAT	AGAGGTATGA	TTTTTTTAAA	AGGCACCTCA	GTATGGGTAA	60
TGTTATCTTT	CTTGTGTTTC	AGTGCACACA	CATACACACA	CACCATAGAT	GCAAAGTGTG	120
TAGAAAATGT	ATTGAAGGAT	ACCCAGGTAC	TCGAG			155

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

<ul><li>(A) LENGTH: 138 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:	
GAATTCGCGG CCGCGTCGAC ATTCATGCAA ATAAATATAT TACTAAAATG CTACCTGTTT CTTTTTCCTC TTTTTCTTCC AGTTTTAGTT TATGAGATTG GGTCTTGCTA TGCTGCCCAT GCTAGGCATG AACTCGAG	60 120 138
(2) INFORMATION FOR SEQ ID NO:1338:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 249 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:	
GAATTCGCGG CCGCGTCGAC CTAAACCGTC AATTCTTCCC ATCTTAGGTT TCTCTCCTCG GAAGCCTTCT CTTTAGAATC GAACATTTTC TCTTCTGGCT TTGTTCGGAT GGTTTCTGGT CTGTTTCTTT CTTGCTCCCT CGTGGCTTTC ACTTCTGTT TCTTTCCCAG AATGACGGTC CTCTCATTTG ACCGTGTGCT TTCCGAAGCA CCTGCTGCCA CCTTGTCTCG GCGATCCCGG TTACTCGAG	60 120 180 240 249
(2) INFORMATION FOR SEQ ID NO:1339:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 108 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:	
GAATTCGCGG CCGCGTCGAC AAAACAACAC ATTTTAAAGA TTACGTGCTT CTTGGTACAG GTTTGTGAAT GACAGTTTAT CGTCATGCTG TTAGTGTGCA TCCTCGAG	60 108
(2) INFORMATION FOR SEQ ID NO:1340:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 652 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
536	

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

			ATTCCATATT			60
			CTCCTTAGGC			120
TAAGCCTTCT	GGTAGTACCA	AGATGTATTA	TGTTCCACAA	TTAAGACAAA	TTCCTCCATC	180
TCCGGATTCC	AAATCAGATA	CCACCGTTGA	AAGCTCCCAT	TCAGGATCCA	ATGATGCCAT	240
TGCTCCAGAC	TTCCCAGCTC	AGGTGCTAGG	CACAAGAGAT	GATGACCTCT	CAGCCACTGT	300
			TAAGAGGGTA			360
AGTGGGAGAA	AAACCCTTGC	AGAATGAAAA	TGCAGATGCC	TCAGTTCAAG	TGCTAATCAC	420
			GCAAGAGATT			480
			TTTGCAGAAA			540
TGCTGCTGCT	GCAGAGCACT	CAGCTCAAGT	AGGAGACCCA	GAAATGAAGA	ACTTGCCAGA	600
CACTAAAGCC						652

## (2) INFORMATION FOR SEQ ID NO:1341:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) Lingth: 817 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

GAATTCGGCC	AAAGAGGCCT	ACGTGCCATT	TCTCTTCCAC	TATGAGAGGA	CCGATTGTAT	60
TGCACATTTG			TGCTTTTCAG			120
CCTTCCCCAA			TAGCACATGT			180
CCGATAAGAT	GAACACCGAT	GACCTAGAAA	ATAGCTCTGT	TACCTCAAAG	CAGACTCCCC	240
AACTGGTGGT	CTCTGAAGAT	CCAATGATGA	TGTCAGCAGT	ACCATCGGCA	ACATCATTAA	300
ATAAAGCATT	CTCGATTAAC	AAAGAAACCC	AGCCTGGACA	AGCTGGGCTC	ATGCAAACAG	360
AACGCCCTGG	TGTTTCCACA	CCTACTGAGT	CAGGTGTNCC	TCAGCTGAAG	AAGTATTTGG	420
TTCCAGCCAG	CCAGAGAGAA	TATCTCNTGA	AAGTGGANTT	GCCAAGGCCA	TGTTAACCAT	480
TGCTATCACT	GCGACTCCTT	CTCTGACTGT	TGATGAAAAG	GAGGAACTCC	TTACAAGCAC	540
TAACTTTCAG	CCCATTGTAG	AAGAGATCAC	AGAAACCACA	AAAGGTTTTC	TGAAGTATAT	600.
GGATAATCAA	TCATTTGCAA	CTGAAAGTCA	GGAAGGAGTT	GGTTTGGGAC	ATTCACCTTC	660
ATCCTATGTG	AATACTAAGG	AAATGCTAAC	CACCAATCCA	AAGACTGAGA	AATTTGAAGC	720
AGACACAGAC	CACAGGACAA	CTTCTTTTCC	TGGTGCTGAG	TCCACAGCAG	GCAGTGAGCC	780
TGGAAGCCTC	ACCCCTGATA	AGGAGAAGCA	CCTCGAG			817

- (2) INFORMATION FOR SEQ ID NO:1342:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 476 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

GAATTCGGCC	AAAGAGGCCT	AGCACCATGG	ACAACCCACA	GGCTCTGCCA	CTCTTCCTAC	60
TCCTGGGGAT	CCTCACCCTC	AGAGCCTCTT	CTGGACTTCA	GCAAACCAAC	TTCTCCTCTG	120
CCTTCTCTTC	AGACTCAAAG	AGCTCTTCCC	AGGGGCTGGG	TGTGGAAGTT	CCCTCCATCA	180
AACCTCCCAG	CTGGAAAGTT	CCAGATCAGT	TCCTGGATTC	AAAAGCCTCT	GCTGGAATCT	240
			GTTCCAACAT			300
ATGTTTCTGC	TGAGGGCCAA	GATTTGAGCC	CGGTTTCCCC	CTTCTCTGAA	ACCCCTGGTT	360

CTGAAGTATT TCCTGATATT TCGGATCCTC AAGTTCCTGC CAAAGACCCC AAGCCTTCCT
TCACTGTTAA GACCCCAGCT TCAAACATTT CTACTCAAGT CTCCCATCTC CTCGAG

(2) INFORMATION FOR SEQ ID NO:1343:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 726 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

GAATTCGCGG	CCGCGTCGAC	CAGGAAATGA	AGACATTGCC	TGCCATGCTT	GGAACTGGGA	60
AATTATTTTG	GGTCTTCTTC	TTAATCCCAT	ATCTGGACAT	CTGGAACATC	CATGGGAAAG	120
AATCATGTGA	TGTACAGCTT	TATATAAAGA	GACAATCTGA	ACACTCCATC	TTAGCAGGAG	180
ATCCCTTTGA	ACTAGAATGC	CCTGTGAAAT	ACTGTGCTAA	CAGGCCTCAT	GTGACTTGGT	240
				ACAAACAAGT		300
AGAAGAACAT	TTCATTTTTC	ATTCTACATT	TTGAACCAGT	GCTTCCTAAT	GACAATGGGN	360
				AAAGCCACTC		420
TATGTGACAG	GAAAGCAAAA	TGAACTCTCT	GACACAGCAG	GAAGGGAAAT	TAACCTGGTT	480
				GGCAAAATTC		540
				GTTTCAGGAT		600
				CAGGCATTGT		660
CTGAACCATT	CTGTCATTGG	ACTGAACTCA	AGACTGGCAA	GAAATGTAAA	AGAAGCACCA	720
CTCGAG						726

- (2) INFORMATION FOR SEQ ID NO:1344:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 484 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

GAATTCGGCC AAAGAGGCCT	AGGGACAGCA	ATCAAGTTCT	AATGGTGCTC	ACTTTTTAGG	60
TCACCTTCAT CACAGACTGC	TCCAAAGGCA	GAGCAATGTG	GAACGAACCA	GCACATTTAC	120
TTAAGATCAA AGTATGATAC	ATCTCTTTGA	GCGCCTCACT	TCACAATAGG	GATCCATTCA	180
TTGGCTTCCA GATGATGTTC	ACAGTTCATG	TAACACTGAT	ACTGACTTTG	TTCCTTATGT	240
TTAGACAGCT TCTCTGTCTA	TACTTCTCAG	AAACACCATC	AACCAGAACA	GAGCCACTTA	300
TTATCCACAA AAGTTGCATC	AACCAGCTTA	CCTTCTGGGA	GGGATGGATG	GTACCCAAAT	360
ACTCAAACTG AATCCTATAG	TGTGGAGCAA	CCAAACAGAA	AACAGTCCAA	GGATTCAGGA	420
AATGGTAAAA ACATTTTAAA	TCTAAATAGT	AGTTATTTTC	ATTTTGTTCT	GCTCCCACCT	480
CGAG					484

- (2) INFORMATION FOR SEQ ID NO:1345:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 125 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

GAATTCGCGG CCGCGTCGAC ATGAGTTTAA TTTTTTTTT TTTTTTTACA CTTTACATAG
AAATAGGATT ATGTGGGCTG GGCACAGGGA CTGACGCCTG TAATCCCAGC ACGTGGAGGC 120
TCGAG 125

- (2) INFORMATION FOR SEQ ID NO:1346:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 760 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

GAATTCGGCC AAAGAGGCCT	AGACCCAGCG	TACATACTGA	ATGATCTCTA	CATCTCAGAC	60
TACTGTGTGT GGATTCAGAA	AGTCAAATCC	AAAAGTTGG	CAGCTCTTGC	AGAAGCCTTA	120
AAGGAAGTCT CCCTTACAAA	GGCCCAGCTG	GGGTTAGAAC	TGGAAGAACT	AGAAGCAGCA	180
GCACTGCTTG TCCAGGAGGA	AGAAACTGCA	TTAAAAGCAG	CCCATTCAGT	TTCTGGGCAG	240
CAGACACTTT GCTCCAGCTC	TGAGGCAAGT	GATTCGGAGG	ACTCAGACAG	CAGCGTGTCA	300
TCTGGAAACG AAGACTCAGG	CTCAGATTCA	GAACAAGATG	AACTCAAAGA	TAGTCCATCT	360
GAGACAGTCA GTTCTTTGCA	AGGTCCCTTT	CTTGAAGAAA	GCAGTGCCTT	TCTTATTGTT	420
GATGGTGGAG TACGCAGAAA	CACAGCCATC	CAGGAGTCTG	ATGCCAGTCA	GGGAAAGCCA	480
CTTGCCTCTT CCTGGCCTCT	TGGAGTGTCT	GGGCCTCTGA	TAGAGGAGCT	TGGGGAACAA	540
CTGAAGACTA CAGTTCAGGT	TTCTGAACCC	AAGGGCACCA	CTGCTGTAAA	CCGCAGCAAT	600
ATTCAGGAGA GAGACGGCTG	TCAGACACCA	AATAATTGAC	TCTTAGGTGG	TTTTATTCAT	660
TGTTGAGAAA TATGGTAGAT	TGGGTTTCAT	TTACCGAATG	AGAATTCTTC	ATTTTCACTT	720
TGTAATTTTT CTTAGTATAT	AGTCAGCCCA	CACTCTCGAG			760

- (2) INFORMATION FOR SEQ ID NO:1347:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

GAATTCGCGG	CCGCGTCGAC	CATTTCGAGA	GTCCGTCTTG	TAAATGTTTG	GCACTTTGCT	60
ACTITATIGO	TTCTTTCTGG	CGACAGTTCC	AGCACTCGCC	GAGACCGGCG	GAGAAAGGCA	120
GCTGAGCCCG	GAGAAGAGCG	AAATATGGGG	ACCCGGGCTA	AAAGCAGACG	TCGTCCTTCC	180
CGCCCGCTAT	TTCTATATTC	AGGCAGTGGA	TACATCAGGG	AATAAATTCA	CATCTTCTCC	240
AGGCGAAAAG	GTCTTCCAGG	TGAAAGTCTC	AGCACCAGAG	GAGCAATTCA	CTAGAGTTGG	300
AGTCCAGGTT	TTAGACCGAA	AAGATGGGTC	CTTCATAGTA	AGATACCTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:1348:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 251 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

GAATTCGC	GG CCGCGTCGAC	TCTAGGTTTT	CTGATTTTGA	TGGTAATATG	GTATTCTGGG	60
AAATATCT	GT CCAAATTATC	CTGATCTCTG	AACTCCTGCT	GTTGAGGTCA	GTCACTTCAC	120
ACAATACC	AT GATGACAGCT	TTATCAAGCC	AGATGCTTAG	TCAGAGCTTT	CCAAGACCCA	180
GCTTTGGT	TT TATCAGCAAA	ATCCATCCTT	CCCACCCCC	ATACACACGC	CAGTTTGAGA	240
CTCCTCTC	GA G					251

- (2) INFORMATION FOR SEQ ID NO:1349:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 309 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

GAATTCGCGG CC	CGCGTCGAC	CTAAACCGTC	GATTGAATTC	TGGACCTCCT	GTGCAAGAAC	60
ATGAACCATC TO	TGGTTCTT	CCTTCTCCTG	GTGGCAGCTC	CCAGATGGGT	CCTGTCCCAG	120
GTGCAGGTGC AG	CAGTCGGG	CCCTAGACAG	GTGAAGCCTT	CGGAGACCCT	GTCCCTCAGT	180
TGTACTGTCT CT	CTCGGCGC	CATGAATGGT	CATTACTGGA	CCTGGATCCG	GCAGACCCCG	240
GGAGGGAGAC TO	GAGTGGAT	TGGATCTGTC	TATTATAATG	GAAACAGAGT	GTATCACCCC	300
TCCCTCGAG						309

- (2) INFORMATION FOR SEQ ID NO:1350:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 553 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

GAATTCGCGG	CCGCGTCGAC	AATTACTACC	ATTGTTAAGT	GTCTCTTTAA	CTAAACTCAT	60
TGTTTAAAAG	TTTTCTCCCT	CTCTGTTTCT	AAATCCAAAT	TTCTGCTCTG	GAATATATGT	120
		GAATGTTTGC				180
GGAATATTAT	GTAAATGAAA	TACCAATTAT	TTTAAAAGAG	CATTTTTGTG	TGACATAGTG	240
CTTTCACAAA	CTAAAACTGG	AATTTCTTTC	TTTAGTCTAT	CTATATCTTT	TGAAAATGTT	300
GACACAGCTA	AGAAGAAGCT	GCCTGTTCAT	ATCTTAGATG	GTCTGACCCT	CAGCTACAAG	360
		TATGAACCGT				420
ATTGGTTACT	TTCTAATTTT	GTTTTTGTTT	CATAGGTCCC	ATGGCCCGTG	GACATTGTTA	480
TAAGTTTGGA	ATGTCAAAAA	ATTTATAATC	AAGTGTTTCT	TCTCTTATTG	CAAATAAAGT	540
GGGCATCCTC						553

- (2) INFORMATION FOR SEQ ID NO:1351:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 209 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

WO 98/45437 PCT/US98/<u>0</u>6956

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

GAATTCGCGG	CCGCGTCGAC	TTTATTTCAG	TGGATTCTCT	AGGATTTTCT	ATATAAAAGA	60
TGTCATCTGA	TAGAGTAGTT	TACTTCTTCG	TTTCCAACCT	GAATGGCTTT	TATTTCATCT	120
CTTTCCTAAC	TGTCCTGGCT	AGAACCTCCT	TTACCACGTT	GAATGGAAGT	GGCAAGAATG	180
AACATCCTTG	TCTTGTTTCT	GATTTCGAG				209

- (2) INFORMATION FOR SEQ ID NO:1352:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 525 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

GAATTCGCGG	CCGCGTCGAC	AATGGCTTTT	CTTCCTTCCT	GGGTTTGTGT	ACTAGTTGGT	60
TCCTTTTCTG	CTTCCTTAGC	${\tt AGGGACTTCC}$	AATCTCTCAG	AGACAGAGCC	CCCTCTGTGG	120
AAGGAGAGTC	CTGGTCAGCT	CAGTGACTAC	AGGGTGGAGA	ACAGCATGTA	CATTATTAAT	180
CCCTGGGTAT	ACCTTGAGAG	AATGGGGATG	TATAAAATCA	TATTGAATCA	GACAGCCAGG	240
TATTTTGCAA	AATTTGCACC	AGATAATGAA	CAGAATATTT	TATGGGGGTT	GCCTCTGCAG	300
TATGGCTGGC	AATATAGGAC	AGGCAGATTA	GCTGATCCAA	CCCGAAGGAC	AAACTGTGGC	360
TATGAATCTG	GAGATCATAT	GTGCATCTCT	GTGGACAGTT	GGTGGGCTGA	TTTGAATTAT	420
TTTCTGTCTT	CATTACCCTT	TCTTGCTGCG	GTTGATTCTG	GTGTAATGGG	GATATCATCA	480
GACCAAGTCA	${\tt GGCTTTTGCC}$	CCCACCCAAG	AATGAGAGGC	TCGAG		525

- (2) INFORMATION FOR SEQ ID NO:1353:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

GAATTCGGCC	TTCATGGCCT	AGGCTCCTAA	TAATAAATAA	CCACATAATT	GTAAATGAAA	60
CACATCAAGG	ATTTGAGTTA	ATAGCCTCTG	AGCAGCATTA	ATATAGCCAT	TAGACTGGAG	120
TATTTGTTAT	CAAGAGGGCC	AGAGAACCCA	CCGCTAAAGC	CGTAGGGTGG	GAGGAACCCT	180
GGATTGCAGC	TACATGGCTT	ATGTAGGGAG	TTTGTAACAG	CCCCAAGCTG	AAACCAGCTT	240
CTACACCCAT	GACTGTTGAG	TGATTGAATT	CTAGACCTGC	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:1354:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 572 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

GAATTCGCGG	CCGCGTCGAC	CAACAAGAGC	ACTGGCCAAG	TCAGCTTCTT	CTGAGAGAGT	60
				CCTCTTACTC		120
CTTCCAACCT	TGCCATTGCA	ATAAAAAAGG	AAAAGAGGCC	TCCTCAGACA	CTCTCAAGAG	180
GATGGGGAGA	TGACATCACT	TGGGTACAAA	CTTATGAAGA	AGGTCTCTTT	TATGCTCAAA	240
AAAGTAAGAA	GCCATTAATG	GTTATTCATC	ACCTGGAGGA	TTGTCAATAC	TCTCAAGCAC	300
TAAAGAAAGT	ATTTGCCCAA	AATGAAGAAA	TACAAGAAAT	GGCTCAGAAT	AAGTTCATCA	360
TGCTAAACCT	TATGCATGAA	ACCACTGATA	AGAATTTATC	ACCTGATGGG	CAATATGTGC	420
CTAGAATCAT	GTTTGTAGAC	CCTTCTTTAA	CAGTTAGAGC	TGACATAGCT	GGAAGATACT	480
				ATTGATAGAA	AACATGAAGA	540
AAGCATTAAG	ACTTATTCAG	TCAGAACTCG	AG			572

- (2) INFORMATION FOR SEQ ID NO:1355:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 269 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

(	GAATTCGCGG	CCGCGTCGAC	TGAAAAGTAG	GTTTTTGAAG	AGATATATTC	GAAATATATT	60
,	TTTTCACTTG	AAAAAAGTAA	AAATTTTTTT	CAAAAGCAAA	TAATTCAACT	CTAAAATTAT	120
ž	ACTATTTCAA	CATTCTCATT	TATGTGAAAG	CATGTGATAA	ATTGTTGCTG	CGTCAGAGAT	180
ž	ATGAGAAACT	CCTTTGCATT	AGGTGGGCAT	TATTCATAGA	CTTCTACATG	AAAGAGAAGA	240
		ATGCACCAGG					269

- (2) INFORMATION FOR SEQ ID NO:1356:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 713 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

GAATTCGCGG	CCGCGTCGAA	CCCAGCAAAA	TGGGGATCTC	CACAGTCATC	CTTGAAATGT	60
GTCTTTTATG	GGGACAAGTT	CTATCTACAG	GTGGGTGGAT	CCCAAGGACT	ACAGACTACG	120
CTTCACTGAT	TCCCTCGGAG	GTGCCCTTGG	ATACAACTGT	AGCAGAAGGT	TCTCCATTTC	180
	GACCCTGGAG					240
	AACTGTAGCA					300
	AGGATCTGAT					360
	AGTGGAGATC					420
	TGATGCCAAC					480
CTCCAGGAAA	TGCCTGGTTT	GGCCAGGGCT	CAGGACCCAT	TGCCCTGGAT	GATGTGCGCT	540
GCTCAGGACA	CGAATCCTAC	CTGTGGAGCT	GCCCCCACAA	TGGCTGGCTC	TCCCATAACT	600
GTGGCCATGG	TGAAGATGCT	GGTGTTATCT	GCTCAGCTGC	CCAGCCTCAG	TCAACACTCA	660
GGCCAGAAAG	TTGGCCTGTC	AGGATATCAC	CACCTGTACC	CACTAGACTC	GAG	713

- (2) INFORMATION FOR SEQ ID NO:1357:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs(B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

				ATGTCAGATT		60
				GGTGAAGCTG		120
GGGGGGTGAC	ACAGCCATGC	CCTACTTAAC	TTCTTATGGA	CAGCTGAGCA	ACGGAGAGCC	180
CCACTTCCTA	CCAGATGCAA	TGTTTGGGCA	ACCAGGAGCC	CTAGGTAGCA	CTCCATTTCT	240
TGGTCAGCAT	GGTTTTAATT	TCTTTCCCAG	TGGGATTGAC	TTCTCAGCAT	GGGGAAATAA	300
				AGCAATTATG		360
TAGCTCCTTA	${\tt GGTGGAGCCA}$	TGATTGATGG	ACAGTCAGCT	TTTGCCAATG	AGACCCTCAA	420
TAAGGCTCCT	GGCATGAATA	CTATAGACCA	AGGGATGGCA	NCACTGAAGT	TGGGTAGCAC	480
AGAAGTTGCA	AGCAATGTTC	CAAAAGTTGT	AGGTTCTGCT	GTTGGTAGCG	GGTCCATTAC	540
TAGTAACATC	GTGGCTTCCA	ATAGTTTGCC	TCCAGCCACC	ATTGCTCCTC	CAAAACCAGC	600
ATCTTGGGCT	GATATTGCTA	GCAAGCCTGC	AAAACAGCAA	CCTAAACTGA	AGACCAAGAA	660
TGGCATTGCA	GGGTCAAGTC	TTCCGCCACC	CCCGATAAAG	CATAACATGG	ATATTGGAAC	720
TTGGGATAAC	AAGGGTCCCG	TTGCAAAAGC	CCCCTCACAG	GCTTTGGTTC	AGAATATAGG	780
TCAGCCAACC	CAGGGGTCTC	CTCAGCCTGT	AGGTCAGCAG	GCTAACAATA	GCCCACCAGT	840
GGCTCAGGCA	TCAGTAGGGC	AACAGACACA	GCCATTGCCT	CCACCTCCAC	CACAGCCTGC	900
	GTCCAGCAAC					925

- (2) INFORMATION FOR SEQ ID NO:1358:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 172 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

GAATTCGCGG	CCGCGTCGAC	AAATAAACCC	AGCAACTTCA	TTCATTTGCC	TTATGTTTAT	60
TGAGGGCCTG	CTAGTGCTGG	GCACTGTTCT	AGGCCCTGGG	AATTTATTAG	TGAGCAAAAC	120
AGCAAAATCT	CTGTCCTCAT	GGAGCTCACA	ATATAGTAGG	GAACGACTCG	AG	172

- (2) INFORMATION FOR SEQ ID NO:1359:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 770 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

GAATTCGGCC	AAAGAGGCCT	AAGTCAGTGA	GGTGGAGTCC	GTTTTTGAGG	TCACGCGGCT	60
AGTAATTGGA	GCCTGGTTTA	GAACCAAGTC	AGTCTCATTC	CAGAATCCAG	AACCAGTGAT	120
					TTTTTAATGC	180
					GAACACAGCA	240
CACAAATGTG	ACCGCTAGTG	GACAGCAGTG	GCAGCCCAGT	TGGATGGCAG	AGCCTGGCAT	300

GCCGACTGGG	ACAGAAGCCC	CAGCACACGG	TGTGATGATG	GCGTCTCCAG	GCTGACCTCC	360
ATGGCCTCAG	GAATCAAAGT	CCTCGGTCTC	TTTCACGCGG	GGTTCAGAAA	GAAAACTCGG	420
CTATCTTACA	TCTCCTCTCC	CCTGTTTATT	TGACTAAAGT	GAAGTTCATG	TGGCTTGAGC	480
CTCGTTTCCT	GGGGAAATCA	GCCTGGCTTA	GGATTCCATT	GTCTTCTGGG	ACTGGGAAGA	540
TGTGGAAGGC	TGACCTCACG	CCCAGCTGAA	GGTCACCTTC	CCAGACTCTG	AGCTCGGCTG	600
CCTTCTGCAT	CGCCACGGCT	GGAGGGCCTG	GCCCAGGCCG	TGGCTGCATG	CTGGCTTTCC	660
ACTGTCTCGG	TGTCCCTGCT	GCCTGTCAGT	AATGTGCCCA	GCACCTTCTG	GTGTCATGTC	720
CCCTCTTGTT	TGTGATTCTT	TTCCTGAGCT	AGTCCATTTT	CTACCTCGAG		770

- (2) INFORMATION FOR SEQ ID NO:1360:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 505 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

GAATTCGGCC	AAAGAGGCCT	ACTCAGTGGA	AACCTTTAAA	CCCTAAAATC	CAGGAAAAGA	60
AAATAAATAC	ATTATCATGG	ACCTGAGGGA	TTTTTACCTG	TTGGCTGCTC	TGATTGCCTG	120
		TAGCTCAAGA				180
		ACATACCAAA				240
		TTGTCTACAG				300
GGTGAAAGTA	TCCAGCAGCA	CTGGGGAAAT	TTTCACAACC	TCCAACAGAA	TAGACAGAGA	360
AAAACTCTGT	GCTGGCGCCT	CATATGCTGA	GGAGAATGAG	TGTTTCTTTG	AACTTGAGGT	420
GGTGATCCTC	CCCAATGATT	TCTTCAGGCT	GATCAAAATA	AAAATAATTG	TCAAGGATAC	480
CAATGATAAT	GCCCCCAATC	TCGAG				505

- (2) INFORMATION FOR SEQ ID NO:1361:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 553 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

GAATTCGGCC	AAAGAGGCCT	AAATTTGTTC	TCTCCAAACC	AGAAGACCTT	AGGTACAGAT	60
GACCCCAGGG	AGCTGGGACA	GCAGGACAGA	NAGGGGAAGG	GACAGGTCCA	TATATAGGTG	120
TGTCATTGCA	GCCACTGCAA	TGAACATAAC	ATGCAAGAAA	TGTACAGAAT	GTGGTCCAGA	180
ATTGCCCACT	GGTGTCCTGT	GCCCTGGTGG	ACCCCACAGA	GGACTGCCCC	AGGCTTTCAC	240
TTTCCTTCCC	CATGGATTGA	GCAAGCTCCC	AGGGCAGGAT	GGGTGGCCAG	GAGGGGCAGA	300
ACGCTGGCGG	GGACGGGGAA	GCCAAGTGCT	CACAGGACCA	TCCACCACAG	CTGCAGCCAC	360
ACTGCAAGAC	GGCGGGGATG	GGACACACGG	TCTAGTTCTT	AGTTCTGCCT	CCTACAGGCA	420
GCCCCTGCTG	TCACTCCAGA	ACTAATTCTC	TGTGTGCCAC	TCACTCGCGT	GTGTGACACA	480
CAACAGATAC	ACATACATAG	ACACATACGT	ACATCTCCTC	CCCCAATCTC	ACCCTCTCAC	540
CACGCCCCTC	GAG					553

- (2) INFORMATION FOR SEQ ID NO:1362:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 855 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

GAATTCGGCC AAAGAAGCCT	AGTCAACTTG	ATCCAAACCT	GTTGGTGAAG	CAGCAGACTC	60
CACCATCTCA GCAGCAGCCA	CTCCATCAGC	CAGCCATGAA	GTCTTTCCTT	GACAATGTCA	120
TGCCCCACAC TACACCTGAG	CTGCAAAAAG	GGCCATCACC	AATAAATGCT	TTCAGCAACT	180
TCCCTATAGG CTTGAACTCA	AACTTGAATG	TAAATATGGA	TATGAACAGT	ATTAAAGAGC	240
CACAGTCCAG ACTAAGGAAG	TGGACGACAG	$\mathtt{TGGACAGCAT}$	${\tt TTCTGTGAAC}$	ACATCTTTGG	300
ATCAAAACTC CAGCAAACAT	GGTGCTATTT	CAAGTGGTTT	CAGGCTGGAA	GAGTCTCCAT	360
TTGTNCCCTA TGACTTTATG	AACAGCAGTA	CTTCACCAGC	CAGTCCTCCA	GGTTCAATAG	420
GAGATGGCTG GCCACGTGCC	AAATCGCCTA	ACGGCTCTAG	CAGTGTTAAT	TGGCCACCAG	480
AATTTCGTCC CTGGTGAGCC	ATGGAAAGGT	TATCCAAACA	TTGACCCTGA	AACTGACCCT	540
TACGTCACTC CTGGCAGTGT	CATAAACAAT	CTTTCAATTA	ATACTGTGCG	GGAAGTTGAC	600
CACCTCAGGG ACAGGAACAG	TGGGTCATCC	TCATCCTTGA	ACACCACGCT	GCCTTCAACT	660
AGTGCCTGGT CATCCATTCG	TGCCTCCAAC	TACAACGTTC	CCCTCAGCAG	TACAGCACAA	720
AGCACTTCAG CCAGAAATAG	TGATTCCAAA	TTGACATGGT	CTCCTGGTTC	AGTTACAAAC	780
ACCTCTCTGG CTCATGAGCT	GTGGAAGGTC	CCTTTGCCAC	CTAAAAACAT	CACTGCTCCG	840
TCCCGCCACC TCGAG					855

- (2) INFORMATION FOR SEQ ID NO:1363:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 646 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

GAATTCGGCC	AAAGAGGCCT	ACAAAAAGTA	CATAGTAAGA	CTAAGATACC	AAGTTGTATA	60
${\tt CTAATATTTT}$	TCAGGCCTTG	${\tt GGCCTCAAAT}$	ATATATATT	ATATATATA	CTCCAGTGTG	120
AACAGCAATT	CGATGAAATG	TAAAATGTAT	CTTTTTTTTT	TTAAATCACA	CACAAGTATT	180
CATAACCACA	${\tt GGGTTCACCA}$	GAAATCTAAA	GCAAGGAGAC	ACTCACTCAT	ATAGAAATGG	240
AGTTACTCTT	CCACAGATCG	TTCTGATCAA	${\tt AGGTTTTGGA}$	ACAGAAATGA	ATTAATGATT	300
${\tt TTTTTGTATA}$	ATATCCAACA	TGTCCACTAT	CAAATACATT	TAGTATGAAA	AAACAGATGA	360
AGAAAAGGAA	CATACATTAG	GACAAAGTAT	CTGGTTAAAA	TGCTGTTCAT	TTAAATAAAG	420
CCCACTCTCC	TTACTTTAGA	GCTCCTTGGT	GAAATGGAGG	TGAGTTTGAT	GGAGTGCAGT	480
TGATGACCAC	TGAAAAACAC	GAGCCCTTTC	AACAATGTTG	CAACACTGTT	AGTTTTTGGT	540
TTAAACACAC	ACACACACTC	ACAAATGCTA	AGTGTACACT	ACCAAATTCT	GCGGTCAGCT	600
TTTCCAAGAA	CTACTGGGGA	AAGTTTCAAT	GCTGCAAATC	CTCGAG		646

- (2) INFORMATION FOR SEQ ID NO:1364:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 502 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

GAATTCGGCC TTCATGGCCT AATGGCTTAG CTGAAGGAAA TGCTCCAGAA ATTGGACTGT

GTAAACCATC AGTACAATAA TACGCTGTGT ATGTATGTGT ATATAAAATG AGAATTATGG CATAATTGGA GCATTTGCAT TAATCAACAA ACTCACATTG AGACAAAACT TAGTTTTACA GCTGTCTTGA TTAAAGCCAA GTGTTCCATG TTGCTGTGAA GAATAGCCTC TTTCAAATAC TTTGGAAAAGT AGTTACTTGG AAACTTGTAA AGGTATTACA TTTTTATATT TAAACACCTA TAGAGATCTT CAATTCCTTG AGTCTGAGCT TGTGGGTGGA ATTCTAAATT TGTATCATAA TCTGTCTTTT GTGAAACATT TTGAAAATAT GTATATATAA TATTGTATAT GCAAATTGTG TTGTTTCACT TGTAAAGGGA AAAGGCTTAT TTTTCTTTAT ATTTCTGATA ACTTGTTTTG CATATGACCG GCACTTCTCG AG	120 180 240 300 360 420 480 502
(2) INFORMATION FOR SEQ ID NO:1365:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 197 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:	
GAATTCGGCC TTCATGGCCT ACAGAAGTAC GGGAAGGCGA AGAAAAGAAT AGAGAAGATA GGGAAATTAG AAGATAAAAA CATACTTTTA GAAGAAAAAA GATAAATTTA AACCTGAAAA GTAGGAAGCA GAAGAAAAAA GACAAGCTAG GAAACAAAAA GCTAAGGGCA TCGATTGAAT TCTAGACCTG CCTCGAG	60 120 180 197
(2) INFORMATION FOR SEQ ID NO:1366:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 314 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:	
GAATTCGGCC TCATGGCCT AGGCCTGGGG TGGGACATTT TGTTTGTGAG AAGCCTGGAC AAGAGGACGA GGTGCACACC ATGTCAGTCA CGGATTTGT AACTCACAGG AGAGGGTTGG ATGTGATGG CCCGCGGTGT AGACGATGT AACGGGTGGG CTGTGATGG CACCCGCTGC TCGCAGGAGA GGGTTGGATA GGGCATGTAA ACGTGAGCCT GCAATGTAGA CGATGCGAAG TCGTGGTAAC GGGTGGGCTT GTGACGGCAC CCGCTGCTTG CAGCCTAACT CGAG	60 120 180 240 300 314
(2) INFORMATION FOR SEQ ID NO:1367:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 250 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:	
GAATTCGGCC TTCATGGCCT ACTGGTCCCA TTTTTCTATT GCAGTGGTCA TCATTTTTAT TGATGTATAA TAATATTGTA TCATAAATCT TCATAATATG TGCTTCCAAA GTTTTTTCTA	60 120

GTATCATCAA AGCTATCAGG TTATTAAAAT TGACTTCTCA TTTAGACATA CTTAGGCCAT GAAGGTCGAG	240 250
(2) INFORMATION FOR SEQ ID NO:1368:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 261 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:	
GAATTCGGCC TTCATGGCCT AGTGAGAGCA CCACACAAAG GACAGGAAAA ACACCAGCAA TACATCAGCT TTACACAGCA GGCAAGTTC CTGCTCTCTA CAAGTACAGA TGGAACTTGT CTGTGAATT AACATCCTGA CTACTTTTGT TGATCATCAC ATTTTTTCCT CATGAGAGAA ATAATAGTGT TTTATAGGCT CCTGAGAATA GGTTTACTAA AGTCATCGAG ATCTGGGTTC AAATGACACT TCATGCTCGA G	60 120 180 240 261
(2) INFORMATION FOR SEQ ID NO:1369:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 408 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:	
GAATTCGGCC TTCATGGCCT AGTTTTGTT TGTTTGTTTT GGCAAGAACA GTTAGGAACC AGATCACAGT GAGGTATAGA GTGAATGAGA GTTGAGAATG TAAAGACAAT GGATATAGAT CACTATTCCA GGAAGCTGTT TGTGAGAGGG AGGAGAAAAA TAAAACAGTT ACTGAGCAAT AGGGTGGTTG GTAAGGGGGA GGGATTTTTT TCTGAAAGAT GGGAGAAATT TTAACATACT TAAATTTGAT GGGATAAGCC ATGCACTTAT AGGCATTCAG GCAGAAAAT TTTCACAAAAT GAATGAAGAT AAATTAGGGA GAGGTTAATT GGAGATTTTA GGAGAGAGGG AATAATTGAT CATGTAAAGT CATTGATAAG GTGGGAGCAG AACTCGAG	60 120 180 240 300 360 408
(2) INFORMATION FOR SEQ ID NO:1370:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 369 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:	
GAATTCGGCC TTCATGGCCT ACTCGATTAC AGGTCTCCCG CCTGCCATGC AGAAAGTCAT GTATAAGGGA CTCGTCCCCG AGGATAAAAC ATTGAGAGAA ATAAAAGTGA CCACTGGGGC CAAGATCATG GTGGTTGGCT CCACCATCAA TGATGTTTTA GCAGTAAACA CACCCAAAGA TGCTGCGCAG CAGGATGCAA AGGCCGAAGA GAACAAGAAG GAGCCTCTCT GCAGGCAGAA ACAACACAGG AAAGTGTTGG ATAAAGGAAA ACCTGAAGAT GTGATGCCAT CTGTTAAGGG	60 120 180 240 300

GGCCCAGGAG CGCCTGCCAA CGGTACCGCT GTCCGGCATG TACAATAAAT CTGGAGGAAA 360 AGTCTCGAG 369

- (2) INFORMATION FOR SEQ ID NO:1371:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 443 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

GAATTCGGCC	AAAGAGGCCT	ATTTTTTTTT	TTTTTAACTG	ATAGATGGTG	CAGCATGTCT	60
ACATGGTTGT	TTGTTGCTAA	ACTTTATATA	ATGTGTGGTT	TCAATTCAGC	TTGAAAAATA	120
ATCTCACTAC	ATGTAGCAGT	ACATTATATG	TACATTATAT	GTAATGTTAG	TATTTCTGCT	180
TTGAATCCTT	GATATTGCAA	TGGAATTCCT	ACTTTATTAA	ATGTATTTGA	TATGCTAGTT	240
ATTGTGTGCG	ATTTAAACTT	TTTTTGCTTT	CTCCCTNTTT	TTGGTTGTGC	GCTTTCTTTT	300
ACAACAAGCC	TCTAGAAACA	GATAGTTTCT	GAGAATTACT	GAGCTATGTT	TGTAATGCAG	360
ATGTACTTAG	GGAGTATGTA	AAATAATCAT	TTTAACAAAA	GAAATAGATA	TTTAAAATTT	420
AATACTAACT	ATGGGATCTC	GAG				443

- (2) INFORMATION FOR SEQ ID NO:1372:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 770 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

GAATTCGGCC	AAAGAGGCCT	ACTTCCGGCT	GGAGCTGCTG	GGCGCGGGAC	CTGGGGCGGT	60
TAATTTGGAG	TGGCCCCTGG	AGTCAGTTTC	CTACACCATC	CGAGGCCCCA	CCCAGCACGA	120
GCTACAGCCT	CCACCAGGAG	GGCCTGGAAC	CCTCAGCCTG	CACTTCCTCA	ACCCTCAGGA	180
AGCTCAGCGG	TGGGCAGTCC	TAGTCCGAGG	TGCCACCGTG	GAAGGACAGA	ATGGCAGCAA	240
GAGCAACTCA	CCACCAGCCT	TGGGCCCAGA	AGCATGCCCT	GTCTCCCTGC	CCAGTCCCCC	300
GGAAGCCTCC	ACACTCAAGG	GCCCTCCACC	TGAGGCAGAT	CTTCCTAGGA	GCCCTGGAAA	360
CTTGACGGAG	AGAGAAGAGC	TGGCAGGGAG	CCTGGCCCGG	GCTATTGCAG	GTGGAGACGA	420
GAAGGGGGCA	GCCCAAGTGG	CAGCCGTCCT	GGCCCAGCAT	CGTGTGGCCC	TGAGTGTTCA	480
GCTTCAGGAG	GCCTGCTTCC	CACCTGGCCC	CATCAGGCTG	CAGGTCACAC	TTGAAGACGC	540
TGCCTCTGCC	GCATCCGCCG	CGTCCTCTGC	ACACGTTGCC	CTGCAGGTCC	ACCCCCACTG	600
CACTGTTGCA	GCTCTCCAGG	AGCAGGTGTT	CTCAGAGCTC	GGTTTCCCGC	CAGCCGTGCA	660
ACGCTGGGTC	ATCGGACGGT	GCCTGTGTGT	GCCTGAGCGC	AGCCTTGCCT	CTTACGGGGT	720
TCGGCAGGAT	GGGGACCCTG	CTTTCCTCTA	CTTGCTGTCA	GCTCCTCGAG		770

- (2) INFORMATION FOR SEQ ID NO:1373:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 597 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

GAATTCGGCC	AAAGAGGCCT	AGTCTCTTTG	AAGATCTCTA	GGAACTTGCT	TTATGAATCT	60
TCATGCTCCT	GTGTTGGATG	CATATACATT	TAGGATAGTT	AGGTGTTCTT	TTTGAATTGA	120
AACTTTTACC	ATTATGTAAT	GCCCTTGTTT	GTCTTTTAAA	ATTTTTGTTG	GTTTAATATC	180
TGTTTTGTCT	AAAATTAGAA	TTTCAGCCTC	TGCTTTTTTT	CTGTTTTCCA	TTTGCTTAAT	240
AAATTTTTCT	TCATTCCCTT	ATTTTTAGCC	TATGGGTGTC	ATTGGATGTG	AGATTCATCT	300
CTTGAACACT	GTACTACTGG	TTCTTGCTTT	TTTACTCAGC	TTGTCACTCT	GTGTCTTTCA	360
ATTGGGCATT	CAAGGCTAGT	GTTGATATGT	GTGAATTTGT	TTCTGTCATC	ATGTTATTAG	420
TTGTTTATTA	TGCTGACTTG	TTTGTGTGGT	TTCNTTATAG	TGTTACTGGT	CTGTGCACTT	480
AAGTGTGTTT	TTTTAGTAGC	AATATTTTCT	TTTCATATGT	AGTGCTTTAT	GCGAGGTATT	540
TTGCAAGGAT	TTTCTGAATN	NTCNGAATTT	TTATGTGGGC	TAAACTAGGG	GCTCGAG	597

### (2) INFORMATION FOR SEQ ID NO:1374:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 459 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

GAATTCGGCC AAAGAGGCCT AGCCTCCCAG TGTGAGCCAC CGCACCCAGC CTGGATTGTT	60
GAATTCAATG CTTGGGTCAC CTCCAGATTC ATTTTCACAG TCTTTCATGT TTTGGTCATA	120
TGACATTGTA TTTTGCTGCC ATATGACTGA TCTTTTTTTG TTAAATGTGA GATACTTGTT	180
AAAAAATGTT TAGCAATGAA TTGAGGCCTA GTAGCATGTT ATCTTGCTGC AGAAGAGATG	240
GGAGTCTACT TCTGGGGGAT GGTCAGGGGT CCTCCATACA GGCTGCAATT GAAGTCGTCG	300
GTGCAGGCTC AGTCCCTACA AAGGCCAGGG TATTTCCTGT CCACCTTTAT TCTGATGCAT	360
GACTCTTCTG GGTCTCAACC AGAGCCAGTG GACTTCAGTA TGGGTCGCTT TCATTGGCAG	420
ACCCTCAATC CACTTGTTTT CCATCTAATC CCACTCGAG	459

### (2) INFORMATION FOR SEQ ID NO:1375:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 531 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

GAATTCGGCC	AAAGAGGCCT	AATGGATCTC	ATGTGCAAGA	AAATGAAGCA	CCTGTGGTTC	60
TTCCTCCTGC	TGGTGGCGGC	TCCCAGATGG	GTCCTGTCCC	AGCTGCAGCT	GCGGGAGTCG	120
GGCCCAGGAC	TGGTGAAGCC	TTCGGAGACC	CTGTCCCTCA	CCTGCTCTGT	CTCTGGTGGC	180
TCCATCAGCA	GCAATAGTTA	CTCCTGGGGC	TGGATCCGCC	AGCCCCCAGG	GAAGGGGCTG	240
GAATGCATTG	GGAGCATCTC	TTACAGTGGG	AGCACCTACC	TCACCCCGTC	CCTCAAGAGT	300
CGAGTCACCG	TTTCCGTAGA	CCCGTCCAAG	AACCAGTTAT	CCCTGAGGCT	GAGCTCTGTG	360
ACCGCCGCAG	ACACGGCTGT	GTATTATTGT	GCGGGGGGT	CTCCGGGCGA	TTATTCCTAT	420
GAGAATAGTG	ATTACCCCGA	CCCCCGTAC	TATTTAGACT	CCTGGGGCCG	GGGAACCCTG	480
GTCACCGTCT	CCTCAGCTTC	CACCAAGGGC	CCATCCGTCT	TCCCCCTCGA	G	531

- (2) INFORMATION FOR SEQ ID NO:1376:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 661 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376: GAATTCGGCC AAAGAGGCCT AATGACTCAG AAGAAAGAAG TTACTTTACC ATTTTTTTT 60 ACACCATTTA AACTGCTTTC TGATTCCAAA CAGTTCAACA TTTTAAGAAA AGCAAGATCT 120 TATATAAAAC ACAGAAAGTT TGATGAAGTG GTCTCCCTTT GCAAGGAGCT AATTCATCTT 180 GCATTGAAAG GATTGTCCTA TTATCACACA TATGACAGAT TCTTTTTGGG CGTCAATGTT 240 GTTATTGGTT TTGTGGGATG GATATCTTAT GCCTCTTTGT TGATCATCAA GTCTCATTCC 300 AACCTTATAA AAGGTGTTAG TAAAGAAGTG AAGAAACCAA GCCATCTCCT GCCTTGTAGT 360 TTTGTAGCTA TTGGCATTTT AGTAGCATTT TTTCTGCTGA TTCAAGCCTG TCCCTGGACA 420 TATTATGTAT ATGGTTTGTT GCCACTGCCA ATATGGTATG CGGTTCTAAG AGAATTTCAA 480 GTTATTCAGG ACCTTGTTGT ATCAGTGTTG ACCTATCCTC TGAGCCATTT TGTTGGGTAC 540 CTGTTAGCCT TTACCCTGGG AATTGAAGTA TTAGTTCTCA GTTTTTTCTA CCGCTATATG 600 CTTACCGCTG GACTTACTGC CTTTGCAGCT TGGCCATTTC TCACTCGGCT GTGGACTCGA 660 661 (2) INFORMATION FOR SEQ ID NO:1377: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377: GAATTCGCGG CCGCGTCGAC AAAAAAGGTA AAGATGTTGC TGTATGCAAA ATGGACCCAA 60 GTTATGTTTA TTCAAGTTGC CTGTAGAAAC TTAGTGCTCT ATAGCCACAA ACTCGAG (2) INFORMATION FOR SEQ ID NO:1378: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378: GAATTCGCGG CCGCGTCGAC CTTAAATTTA AAACTGGCCT GGTTTGCCTT TTTTATCAAG คก AGAGCTTAAC AGATAAAAAA TGAAATTAGT CTATTTTCTA CTTGCCAGCA GTCTCGAG 118 (2) INFORMATION FOR SEQ ID NO:1379: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 229 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1379:	
AGATTTGACT TTGTGGTATC	CCGCGTCGAC ATTTTATATA ATATTTTAAA TAAGTTTGTG TACAAAACAA GCATTTGAT TGTGACCCCG TTGCATGAAG TCAGGTGTGG AGTTTTCCAC ATGTTGCTGC TGCTCAAGAA GTTTCTGATT TTGGAACATT TTGGATTTTG TTGGGGATAC CTAATGTGAG AGAGCTAGG CCACTCGAG	60 120 180 229
(2) INFORMA	ATION FOR SEQ ID NO:1380:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 140 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1380:	
CTTTCTATCT	CCGCGTCGAC GTTGGGGACA TGGTGGGTCT GAGAAAAGTG TTGCCCGCAA GGCATTCCCT GCGGAGGAAA TAGAATGCGC GCTCTCCGAC AGCATTTCCT CGAACTCGAG	60 120 140
(2) INFORMA	ATION FOR SEQ ID NO:1381:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 99 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1381:	
	CCGCGTCGAC TCTCAGAAGA GGTTTGTTTA ACTTCTATAA ATACAACCAC GGCATCTCCT TGAGAAAAGG CTTCTCGAG	60 99
(2) INFORMA	ATION FOR SEQ ID NO:1382:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 442 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1382:	
GGAAATGACA TTCCAAACAG AATGTATTCC	AAAGAGGCCT AGTTTAAGTG CTGTGGAGTA GTATATTTCA CTGACTGGTT GAGATGGACT GGCCCCAGA TTCCTGCTGT GTTAGAGAAT TCCCAGGATG GCCCACCAGG AAGATCTCAG TGACCTTTAT CAAGAGGGTT GTGGGAAGAA TTTTTGAGAG GAACCAAACA ACTGCAGGTG CTGAGGTTTC TGGGAATCTC ACACAAATCC TGGCCATGAT TCTCACCATT ACTCTGCTCT GGGCTCTGTA	60 120 180 240 300

360

TTATGATAGA AGGGAGCCTG GGACAGACCA AATGATGTCC TTGAAGAATG ACAACTCTCA

GCACCTGTCA CACATCCATG	A TGTCCCTCAG TAGAACTGTT GAAACCAAGC CTGTCAAGAA TCTTTGAACA G GCAAACCTCG AG	420 442
(2) INFORM	MATION FOR SEQ ID NO:1383:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 501 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	) MOLECULE TYPE: CDNA	
(xi)	) SEQUENCE DESCRIPTION: SEQ ID NO:1383:	
GAACTCACCA CAGTGTGAGG	AAAGAGGCCT ATTCAGGTGT TTTCATTTGG TGATCAGGAC TGAACAGAGA TGGAGTTTGG GCTGAGCTGG CTTTTTCTTG TGGCTATTTT AAAAGGTGTC TGCAGCTGTT GGAGTCTGGG GGAGGTTTAA TACAGCCTGG GGGGTCCCTG GTGCAGCCTC CGGGTTCATC TTTAGCAACT ATGCCGTGAG TTGGGTCCGC	60 120 180 240
CAGGCTCCAG	GGAAGGGGCT GGAGTGGGTC TCAAGTATAA GTGACATTGG TGACACCAGA	300
TACTACGGAG	ACTCCGTGAG GGGCCGATTC ACCATCTCCA GAGACAATTC CAAGAACATG	360
AGGGATTCCT	ACATGAACAG CCTGAGAGCC GAGGATACGG CCGTGTATTA TTGTGCGGCA ATCATACTCG TGGCTATTAC TGGTACTACT TTGACTTCTG GGGCCAGGGA	420
TCCTTAGTCA	GCGATCTCGA G	480
		501
(2) INFORM	ATION FOR SEQ ID NO:1384:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 634 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1384:	
GAATTCGGCC	AAAGAGGCCT ACTTCAATAT TCTGTTACGG GTTTTTTTAG TCTTTTTTTC	60
TCTTTGCTTT	CCTGTGTTGG AATTTTCTAT TTCTATATAC TCAAGTTCAG AGATTCTTTC	120
CTTTTCCATA	TCCTGTCTAC TAGTGAGCCC ATCCAAGGCA TTGTTCATTT CTGTTACAGT	180
GTTTTGATCT	TTAGTATTTC TTTTTCATTC TTCATTACAC TTTCTCTCTG CTAACATTGC	240
CCATAAGTGC	TTATATGCTG TATACTTTAT CTGTTGATCA TATTTGTTTT AAATTCCTAA	300
TCTGATAATT	CAACATCTCT GACATGTCTG GTTCTGGTTC TGATACTTGT TGTCAAACTG	360
ATACTTCCAC	TCTTTTAGAG TGGCTTTTAA TTTTCTTTTT GTTTTTTTTTT	420
CTCCTAGAC	ATGACGTACT AGATAAAAGC AACTACTGTA AATAGACCTT TAGGAATGTG GTGAGAGGAA GAAAAGCATT CTGTAGTCCT GTTAGGTTTC AGTCTTTTAA	480
CCCATTTATG	CTTAGTGTTC TATTACTGGA ACGCTAGGCA TGTGGAAGTT ATTTATATCC	540 600
TACTGCTAAA	GGTTATCACC AAGCTGTACT CGAG	634
(2) INFORMA	ATION FOR SEQ ID NO:1385:	
131	SEQUENCE CHARACTERISTICS:	
(1)	(A) LENGTH: 700 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

SAATTCGGCC AAAGAGGCCT ACTCAAGTTC AAGGAAAATG AAGACAAAAA GTGATATGAT	60
GGAAGAAAAC ATAGATACAA GTGCCCAAGC AGTTGCTGAA ACCAAGCAAG AAGCAGTTGT	120
IGAAGAAGAC TACAATGAAA ATGCTAAAAA TGGAGAAGCC AAAATTACAG AGGCACCAGC	180
TTCTGAAAAA GAAATTGTGG AAGTAAAAGA AGAAAATATT GAAGATGCCA CAGAAAAGGG	240
AGGAGAAAAG AAAGAAGCAG TGGCAGCAGA AGTAAAAAAT GAAGAAGAAG ATCAGAAAGA	300
AGATGAAGAA GATCAAAACG AAGAGAAAGG GGAAGCTGGA AAAGAAGACA AAGATGAAAA	360
AGGGGAAGAA GATGGAAAAG AGGATAAAAA TGGAAATGAG AAAGGAGAAG ATGCAAAAGA	420
BAAAGAAGAT GGAAAAAAAG GTGAAGACGG AAAAGGAAAT GGAGAAGATG GAAAAGAGAA	480
AGGAGAAGAT GAAAAAGAGG AAGAAGACAG AAAAGAAACA GGAGATGGAA AAGAGAATGA	540
AGATGGAAAA GAGAAGGGAG ATAAAAAAGA GGGGAAAGAT GTAAAAGTCA AAGAAGATGA	600
AAAAGAGAGA GAAGATGGAA AAGAAGATGA AGGTGGAAAT GAGGAAGAAG CTGGAAAAGA	660
SAAAGAAGAT TTAAAAGAAG AGGAAGAAGG AAAGCTCGAG	700
(2) INFORMATION FOR SEQ ID NO:1386:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 127 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:	
GAATTCGCGG CCGCGTCGAC CTTTAGTGTG TCTTTTCATT CTCTAAAAAG TGTCCTTTGC	60
AGAGAAAAA AAAATTTTAA TTTTGATGAA ATCCAACTTA TCAATTTTTC TTCTGTGGCC	120
CCTCGAG	127
/-\	
(2) INFORMATION FOR SEQ ID NO:1387:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 128 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:	
(XI) SEQUENCE DESCRIPTION. SEQ ID NO.1367:	
GAATTCGCGG CCGCGTCGAC CTCTGTTCAG TCGTTTTGCT GAATATTTAT TAGCATTCCA	60
CCACTTTGTG TTTAATTAAT AGAAGTTGAG TTCAAACAAT GTTTTTAAAA TTCACACAAA	120
TACTCGAG	128
•	
(2) INFORMATION FOR SEQ ID NO:1388:	
(i) CECHENCE CUNDACTEDICTICS.	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 816 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(C) STRANDEDNESS: GOUDIE (D) TOPOLOGY: linear	
(U) TUPOLOGI: Tinear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:	

GAATTCGGCC AAAGAGGCCT AGTTTCTTTT GCTCTACATC TTCACCAGTA TTTGGTGTTA

TCAGTGTTCT	GAATTTTGTC	CATTCTGATA	GGTGTGTAGA	GGTATCTTAT	AATTTTAATT	120
TGTGTTTCTC	TGATGCCATA	TGATGTGTGG	GACATCTTTT	CATATGCTGA	ATTGCCATCT	180
GTATATCTTT	GGTGAGGTGT	CTGTTAAGGT	TGTTGGCCAA	TTTTTTAATT	GGGTTGTTTG	240
TTTTCTTGTG	GAATTTTAAG	AGTTCCTTAC	ACTGTCTCTG	TCTGTCTTGT	CTGTCTGTCT	300
GTCTGTCTGT	NGAGACAGAG	CCTCGCTCTG	TCACCCAGGT	TGCAGTACAG	TGGCACAGTC	360
TTGGCTCCCT	GCAACCTCTG	CCACCTGGGT	TCAAGTGATT	CTCCTGCGTC	AGCCTCCCGA	420
GTAGCTGGGT	TTATACCCGT	GCACCACCAC	ACCTGGCTAA	TTTTTGTATT	TTTAGTAGAC	480
ACGGGGTTTC	ACTANGTTAG	CCAGGCTGGT	CTCGACCTCC	TGACCTCAGG	TGATCCACCC	540
ACCTTGGCCT	CCCAAAGTGC	TGGGANGNGA	GCCACCACAC	CCAGCCTCCT	TACACATTTT	600
AGTTAATAGT	TCTTTATCAG	ATGTGTCTTA	TGTAAATATT	TCCTCCCTAT	CTGTGGCTTG	660
TCTTTTCATA	CTCTTGACAT	TGTCTTTTGC	AAAAGACAAC	AATTTTTAAG	AAACAAGTAG	720
ACAATTTTAA	TGAAGTCTGG	CTTATCAGTT	CTTTTCTTCA	TGGTTGGTAC	CTTTGGTGCC	780
GTATCTAAAA	GTCATCACCA	AACCCAAGAA	CTCGAG			816

- (2) INFORMATION FOR SEQ ID NO:1389:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 163 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

GAATTCGCGG	CCGCGTCGAC	CTAAACCGTC	GATTGAATTC	TAGACGAACT	ATATGTTTAA	60
GCAAAAACAA	AAATAAAAT	CCTCAAAAAA	AGTAATATCA	GAGTTTTAAT	TTCAACCAGC	120
TGGCACAACA	ATGAAAGTGT	CAGACTTTCT	GAAAGTACTC	GAG		163

- (2) INFORMATION FOR SEQ ID NO:1390:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

GAATTCGGCC	TTCATGGCCT	AAAACCCTCA	AAAATAAATT	AGAATCCAGC	ACTGCTACAA	60
TATATTATCT	AAAATGTCTA	ATTCTCAAAA	ATATGAGTGA	TGCAAAGAAA	CAGGAAACAG	120
TGAAACACAG	AGGAAAAAAC	AGTGACTAGA	AACTGACTTA	AGAGTAAGCC	CAGATGTATT	180
TGGGAGCCAG	AGCCTTCAAA	GTAGCTATTA	AATATGTTCG	AAAAAATTAA	GGGAAAATAT	240
GACAATGACT	CAAAAATAAG	GACTCTAAAT	ATAGAAATGG	GAGCTG		286

- (2) INFORMATION FOR SEQ ID NO:1391:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 392 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

GAATTCGGCC TTCATGGCCT GTGACAGGTG CTCACTGCTG					60 120
GATCTGCTTT CTGACGGCAG					180
TCTTTTCCA CTGAGAGTGC					240
CATAATGTCT CATCTGTTTT					300
CAGTACAACT GCCACCTATA					360
TCCCATTCTG TGTAGTTATG					392
(2) INFORMATION FOR S	EQ ID NO:139	92:			
(i) SEQUENCE C					
	TH: 286 bas	-			
	: nucleic a				
, -,	INDEDNESS: d				
(D) TOPO	LOGY: linea	r			
(ii) MOLECULE	TYPE: cDNA				
(xi) SEQUENCE I	DESCRIPTION:	SEQ ID NO:	1392:		
GAATTCGGCC TTCATGGCCT	3 CM 3 3 MCMMM	aaaaaa amm	mmmaca maa a	G	60
CTGAAGGGCC TICATGGCCT					120
CCTTCCACAG TACCAAAGCG					180
AGAATGCCAA AGTATCTTTG					240
GTCGTGTGTG CTCAGGCAAC				IGACGAGGGI	286
GICGIGIGIG CICAGGCAAC	1000000011	CIICCIIIIG	CICGAG		255
(2) INFORMATION FOR S	EQ ID NO:139	93:			
(i) SEQUENCE C					
	TH: 320 bas	-			
*	: nucleic a				
	NDEDNESS: d				
(D) TOPC	LOGY: linea	r			
(ii) MOLECULE	TYPE: cDNA				
(xi) SEQUENCE	DESCRIPTION:	SEQ ID NO:	1393:		
GAATTCGGCC TTCATGGCCT	_ <u>አር</u> ፕርአርጥጥርጥ	СУУДСТВОС	GTTTTAGGAA	TTTTTTATTC	60
CTGCAGAGAG TTGGGGAGCT					120
TCAAGGTCAA CACAACGCCA					180
ACTGTGTGAT GGCCAAGTCC					240
CTCAAGAAAG GGGGGGCAAA					300
CGCAAGACTG AGGTCTCGAG		9100000111	CCCPMIIN	1100101101	320
(2) INFORMATION FOR S	EQ ID NO:13	94:			
(i) SEQUENCE C	HARACTERIST:	ICS:			
(A) LENC	STH: 450 bas	e pairs			
	E: nucleic a	-			
	ANDEDNESS: d				
* * *	DLOGY: linea				
(ii) MOLECULE	TYPE: cDNA				
(xi) SEQUENCE	DESCRIPTION	: SEQ ID NO	:1394:		
. ,					
GAATTCGGCC TTCATGGCCT	AACGCCATCT	ACGACCTGAT	CGAGCGCATC	GAGGATTTGG	-60
CCCTCCACAA CCACATCCCC					

-	GCTGAGCCGC TCCGTACCGG AGCTTAAAGT GGGCATAGTG G		180
	GTCAGCCCTG GTGCACCGCT ATCTGACGGG GACCTATGTC C		240
	GGGGCGGTTT AAGAAGGAGA TTGTGGTGGA TGGCCAGAGT T TGAAGGAGGC CCCCCTGAGC TCCAGTTTGC TGCCTGGGTG G		300 360
	CAGCCTGGAG GATGAAATCA GTTTCCAGAC GGTGTACAAC TA		420
	CTTCCGCAAC ACCCCTCGAG		450
GICICIGCAG	CITCOGCINE MECCATOMA		430
(2) INFORMA	ATION FOR SEQ ID NO:1395:		
(i)	SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 276 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: double		
	(D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1395:		
GAATTCGGCC	TTCATGGCCT ACCGTCATTC ATTGCAGGGA CCATCAAACC C	CAGACAATC	60
CTATTTTGGT	GGGAAATCTA GCAGATAGAG AAGCCAAACA AGTAGCCCTA C	AACCTGTAC	120
AAGGCCAGTT	TCTGTGCCTG TCCTCGTTCT CTCCTCTTTA CTCTCCAGAA G	AAAAGGAGG	180
	CCAAAACCTT CAAAAACAAG GACCATGGTA TGTCAAGGAA G		240
TTCTTCCTCA	CTCTCAAACA ATCTCTATCC TTCGAG		276
(2) INFORM	ATION FOR SEQ ID NO:1396:		
(i)	SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 241 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: double		
	(D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1396:		
GAATTCGGCC	TTCATGGCCT AGGGGGGGGG GGGCGGGGGG GGTCTCAGAA A	TCAGGAGTA	60
	AACTAAATAG TTTAAAATCT CATCCAACTT CCACCTAACT T		120
	ACTCTGTATA TCCTGTATAA AACATTCTAA CTGATGCCCA C		180
	GTTTTGCTAG TATACAGTAT GGCCACTTAC TGCCATTCCC A		240
G			241
(a) TMEODM	ATION FOR SEQ ID NO:1397:		
(2) INFORP	ATION FOR BEG ID NO. 1357.		
(i)	SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 314 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: double		
	(D) TOPOLOGY: linear		
(ii)	) MOLECULE TYPE: cDNA		
(xi)	) SEQUENCE DESCRIPTION: SEQ ID NO:1397;		
			۲۵
	TTCATGGCCT AGAAAATGAA GAAGAAGATC ATCAAGGACC A		60
	GGGGGCATGC TGCTGATCGA CCTGTGTATC CTGATCTGCT C		120 180
	: CGAAGGACAG TGGAGAAGTA CAGCATGGAG CCGGACCCAG ( : CGCCCTCTCC TGGAGCACTG TGAGAACACC CATATGACCA 1		240
TATCTCCATC	, COCCETETE TOGAGLACIO TGAGAACACE CATATGACCA I	1016661166	2.20

CCGCAACTCT CGAG	314
(2) INFORMATION FOR SEQ ID NO:1398:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 342 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:	
GAATTCGGCC TTCATGGCCT AGTGCACACC AAGAACCAAG TTTCAGCTTG GTTACTGTGT TGAAGACACC TTTGCTATAT TTCAAGTCAT TCCTTCTTTT CTCAATTTTT TTTAATTGAC AAAAATTTTA TATATCGTGT ACAACATCAA TCCATCTTGG CATCTGTATT TGTCAGGGTT GTCTTAGAGG GACAGAACTA ATAGGATATA TATAAGGGGG AGTTTATTAA GTATTAACTT ATATAATCAC AGGGTCCCAC AACAGGCTGT CTGCAAGTTG AAGAGCAAGG AGAGCCAGTC AGAGTGCCGA AACTGAAGAA CCTGGAGTCC GATGTTCTCG AG	60 120 180 240 300 342
(2) INFORMATION FOR SEQ ID NO:1399:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 614 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:	
GAATTCGGCC TTCATGGCCT AGGGCCATGT TGGTTAGAAT GGTGCCATAT TTTCTGGGAT AGCACCATGC TGGCTGGGAT GGTGCCATGT TGGCTGGGAT GGCACCTGCC TCAGCCTCCC AAATAGCTGG GATTACAGGC ATCTGCCACC ATGCCTGGCT AATCTTTTGC ATTTTAGTA GAGAAGGGGT TTCGTCATGT TGTCAGGCTG GTCTCTCACT CCTGAACTCA GGTGATCCGC CTGCCTCGGC CGCCCAAAGT GCTGGAATTA CAGGCATGAG CCGCCACGCC TGGCCTTTTA CTTGAGTTTT AATAGGATCG CTCTTGCTGC TATTGAGGAT AGTACATATG GGGTAATGAT GCAAGCAGAG ACCTACTGTA GTACTCTTCA GGAGAGAATG GTGGCTTGCA CAAGGATGGA AGCAATGAAG GTGGTCAGTT TCTATATTTA TTAGGAAACA CCTAGGATGA TATCTTAATA GACCAAAATG TGAAATGTAA GAAAAATAGA GATGTCAAGA TGACACAAAG ATTTTTGGCT TTGACAACTG AAAGAATAGT TACTATCAAC TGTGATTGGT AACAATGCAC ATGGATCTCT CGAG	60 120 180 240 300 360 420 480 540 600
AGCACCATGC TGGCTGGGAT GGTGCCATGT TGGCTGGGAT GGCACCTGCC TCAGCCTCCC AAATAGCTGG GATTACAGGC ATCTGCCACC ATGCCTGGCT AATCTTTTGC ATTTTAGTA GAGAAGGGGT TTCGTCATGT TGTCAGGCTT GTCTCTCACT CCTGAACTCA GGTGATCCGC CTGCCTCGGC CGCCCAAAGT GCTGGAATTA CAGGCATGAG CCGCCACGCC TGGCCTTTTA CTTGAGTTTT AATAGGATCG CTCTTGCTGC TATTGAGGAT AGTACATATG GGGTAATGAT GCAAGCAGAG ACCTACTGTA GTACTCTTCA GGAGAGAATG GTGGCTTGCA CAAGGATGGA AGCAATGAAG GTGGTGAAAA GTGGTCAGTT TCTATATTTA TTAGGAAACA CCTAGGATGA TATCTTAATA GACCAAAATG TGAAATGTAA GAAAAATAGA GATGCCACAAAGG ATTTTTGGCT TTGACAACTG AAAGAATAGT TACTATCAAC TGTGATTGGT AACAATGCAC	120 180 240 300 360 420 480 540
AGCACCATGC TGGCTGGGAT GGTGCCATGT TGGCTGGGAT GGCACCTGCC TCAGCCTCCC AAATAGCTGG GATTACAGGC ATCTGCCACC ATGCCTGGCT AATCTTTTGC ATTTTAGTA GAGAAGGGGT TTCGTCATGT TGTCAGGCTG GTCTCTCACT CCTGAACTCA GGTGATCCGC CTGCCTCGGC CGCCCAAAGT GCTGGAATTA CAGGCATGAG CCGCCACGCC TGGCCTTTTA CTTGAGTTTT AATAGGATCG CTCTTGTCTTCA TATTGAGGAT AGTACATATG GGGTAATGAT GCAAGCAGGA CCCTACTGTA GTACTCTTCA GGAGAATG GTGGCTTGC CAAGGATGAA AGCAATGAAG GTGGTGAAAA GTGGTCAGTT TCTATATTTA TTAGGAAACA CCTAGGATGA TATCTTAATA GACCAAAATG TGAAATGTAA GAAAAAATAGA GATGCACAAAG ATTTTTGGCT TTGACAACTG AAAGAATAGT TACTATCAAC TGTGATTGGT AACAATGCAC ATGGATCTCT CGAG	120 180 240 300 360 420 480 540
AGCACCATGC TGGCTGGGAT GGTGCCATGT TGGCTGGGAT GGCACCTGCC TCAGCCTCCC AAATAGCTGG GATTACAGGC ATCTGCCACC ATGCCTGGCT AATCTTTTGC ATTTTTAGTA GAGAAGGGGT TTCGTCATGT TGTCAGGCTG GTCTCTCACT CCTGAACTCA GGTGATCCGC CTGCCTCGGC CGCCAAAAT GCTGGAATTA CAGGCATGAG CCGCCACGCC TGGCCTTTTA CTTGAGTTTT AATAGGATCG CTCTTGTCT TATTGAGGAT AGTACATATG GGGTAATGAT GCAAGCAGGA ACCTACTGTA GTACTCTTCA GGAGAATG GTGGCTTGCA CAAGGATGGA AGCAATGAAG GTGGTGAAAA GTGGTCAGTT TCTATATTTA TTAGGAAACA CCTAGGATGA TATCTTAATA GACCAAAATG TGAAATGTAA GAAAAATAGA GATGTCAAGA TGACACAAAG ATTTTTGGCT TTGACAACTG AAAGAATAGT TACTATCAAC TGTGATTGGT AACAATGCAC ATGGATCTCT CGAG  (2) INFORMATION FOR SEQ ID NO:1400:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 244 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180 240 300 360 420 480 540

60

GAATTCGGCC TTCATGGCCT AGTTCTATTT AAAAAATAAA CAACTAGACA ATTAACTAGT

TGTATTAAAG	ATCACAATTG AATTTTTTTT TAA TAATACATTG TAGTAGTAGG ATT CTACTGTTTA GTGGAAAACT CTG	ATATACT CCTTGGCTGA	GAATTCCAAG TATGAAACCT	120 180 240 244
(2) INFORMA	TION FOR SEQ ID NO:1401:			
(i) :	(A) LENGTH: 325 base pa (B) TYPE: nucleic acid (C) STRANDEDNESS: doubl (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO:1401:		
AAGAAGCCAC AAGCACTTAA TCACATAATT TCAAATTGTC	TTCATGGCCT AAAACAAACA AAA AGAAATGTTT AAAAACTTCA TCG ACAGAAGCAG AGGCTAATTC AGT ACTTTCGTAA TAGCTCAGAT TAG CTATTGTGAC TCTTCTAAAA ATG AACGGGAAAC TCGAG	ACTTAGC CTGAGTCATA CTCACAT GAGGAAGTAG AATGGCT ACCCCATTCT	ACGGTTAAGA CTGTCAGATG CTAGACAAAA AATGACACAC	60 120 180 240 300 325
(2) INFORMA	TION FOR SEQ ID NO:1402:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 364 base particles: nucleic acid  (C) STRANDEDNESS: doub.  (D) TOPOLOGY: linear		. ·	
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SE	Q ID NO:1402:		
TAGTCCCTTT TTCCTTTAGC GTTCAAAAGT TACATCAGCA	TTCATGGCCT AAAAGAAAAG AGA GTTCTAGTAG GAAAAAAGGT GCC CTACTTCCTG CAGCTTCCAA TTT CTGTTCTAGT CAATAGCAGG AGA AGAGAAATGT CACGTGATAC TCA ATGTCAATAA ACCCACTTTG GCT	CTAGAGGT AGTATATAGA PATCCAAG GAAATGTCTA AAGTCCAC GTTATTGGGC AGGCCGCG CTTTCTCTTC	GTAAATATTG CAACAATTTT TGATTTTGCT CATCACACCA	60 120 180 240 300 360 364
(2) INFORM	ATION FOR SEQ ID NO:1403:			
(i)·	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base p  (B) TYPE: nucleic acid  (C) STRANDEDNESS: doub  (D) TOPOLOGY: linear	airs		
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SI	EQ ID NO:1403:		
TAAGATTGTT	TTCATGGCCT AGTTAGGGAC TA TATTATACAG CAGGGTACAA TG TAAAAATTAT CGCTAGGCTT TA	GTAGTGCT AATGCCAACA	GGGCACCATG	60 120 180

	GGAAATGATC TGCTTCTAAT ACTAAGCAGT TCTTTAACAT TTTTAAATAT ACCTGCCTCG AG	240 262
(2) INFORMA	ATION FOR SEQ ID NO:1404:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 396 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1404:	
TGTCCTCTTT CTGTGTATTT CTTCTCTTCC TAATTCTGTT CGGCTCTGGC	TTCATGGCCT AGCAATTTGC TTCAGTTTCC TTATGTTTGC CTTTCTATC TCCATTTTAT TCCTACTCT TCTCAGTCCA CTTACAGTTA TATTTCCTAT TATAATATTT GTGCTTTAAT ACTTTTACAAA TATCCTTTAT CCTGTCATAT TTTAAAGTGT TTTATTTCCT AGCCTTCTACAAT AGAGTCCGTT CCCAAGCTTC TGTCCTCCA TCCTCTCCAC ACACCCCCGA CTCGAG  CTCGAG  CTCGAG  CTTATTTCCTA TTATTCCTA TATAGGAAT ACAAATCTTT TACCCTTGTA TCCTCTCCAC ACACCCCCGA CTCGAG	60 120 180 240 300 360 396
(2) INFORMA	ATION FOR SEQ ID NO:1405:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 444 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1405:	
ACATACACTG CATGCGTGCA AACAGGTTAG AGGGTCATTG GTTGTTGGCC ATGCCTTGGG	TTCATGGCCT AGACCAAAAT GTCTGCCCAG ATAAAGGATA CATTGTGCAT GGGAGAGGCA GACAAAAAAA CAATGTAGTT TGAGTGTGT TGCGTGCTTG TGCAGGCATG TGCATATATA ATGCTAAAAC ATGATAAGTA CTATTAAAAA GGTGATTGAA ACTACTAGGG TATGAATAAG AGTGGGTTGC AATTTAAAGT TGGTTGGCCT TATTGAGGTC ACATTGGAGT CAAGACTTGG AAGAAGAAAG ACACAGCTAT TGAGGGAAAA ATGTTCCAGA TAGAAGAAAC AGTCAGGGCA ATGGAATCAT GCATAGAGTA TTCACAGAAT AGCAAGGAAG CTCTAGTTCT GACTGAGACT CGAG	60 120 180 240 300 360 420 444
(2) INFORM	ATION FOR SEQ ID NO:1406:	
(i) _.	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 363 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1406:	
	TTCATGGCCT ACCTAGAAGG TAGTAATGAT AAGCATTTAA TTAGAAGTAG TGCAGTGCAA TGCAGTAAGT ATTTACCGAG TGATTCATAT GAGTAAGGAT	60 120
	CTATAAGAGC TGCAAAGTTT ATTAAGATAC ATCCCTGTCC TGGAAACACT	180

GCCAGCTTCG ATGAGAATAC AACAATGTTA GATATATTCG TTTTGGAAGA TACCTTTCCC CCAGTTATTT TCATTTCACA GCTTCTCCAG CCTCCTTCAG CTTCTGTTCT CCCTCTTTGC TTTTCTGTCT CAATTTTCCT GCCCAGCCCT AAATTCACAG AGTAAATCCA CCAGAACCTC GAG	240 300 360 363
(2) INFORMATION FOR SEQ ID NO:1407:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 229 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:	
GAATTCGGCC TTCATGGCCT AGGCTTCAGG GATAACCACG TTCAGGTGGG TTAGACACAC CTCCTGTGGG AGGGTGATTG CAATTAGCTA TCATAAGGCA GGAGACACAA CAGCAACTTA AATTATCCAC AAGCAGAATC ATGAGCTGTT TGCAAAGGGA GTTTCCATCG CAAGACAGTT TCACTGTATT TAAGCGAGAT CCTGCCCTCG TACACGATCA CCGCTCGAG	60 120 180 229
(2) INFORMATION FOR SEQ ID NO:1408:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 512 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:	
GAATTCGGCC TCATGGCT AGGCTTCTAG AACAAGAATG TAGGCAGGCT CCCAAATGGA GAGGTAAACA TGACCGCGTT GTTTGAAACT ACTTCATTAA TTTGTAAACT AGAACCAAAA AGCTCTGGCC CTCCCACTTC TCTTAGCTGA CCCTCCTCCC CACTTACGGA TAAACAGACT TTAACTTCCC TAACCCAGAA ACACTTCCAC CAAAAATGTA TGGTTATACC TTATCCTAAA AAGGCACCAT GCAGGCATTT AAGACTGAAC CAGTGAACTC TAAAATAGTA GTAGTAGAAA ATATCACTAA TCAAAACTTC CAGCATCAGA TGGTACAAAA CCCCAAGAGG ACTGGTGACA TGTACCCCGG GATGGCAACC CCAGCTTCTG GCAACCCCAC AGCCCAGCGG GAGCTTCAGC TCTGGTCAGG TGCACGGCTG CCAAAGTCTG CACACCTTGG GGACAAGGAA AGGAGACACT TGCTTCATTG TGCTATTCAT GACCCAGTCG AG	60 120 180 240 300 360 420 480 512
(2) INFORMATION FOR SEQ ID NO:1409:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:	
GAATTCGGCC TTCATGGCCT AATGGATTAT ATTTCTATAA CAGTTAGAGT ACTATTCCAT TTATCTCTTT CATTTTGAGT AAAGTTTGGT AGTTTAGGGA GGAATTGATC AATTTCATCT AAATTGAAAG ATTCAGGTAC ATAAAGTTGT TGTTATATTA CTTATTATTC TTTTAATGTC	60 120 180
560	

TTTTTGTGCC AGCATGCTCG AG

(2) INFORMATION FOR SEQ ID NO:1410:

TGTGGGGTCT AGTGATGTCT CCTCTTTCAG TTCTGATATT GGTAATTTGT GTCTTCTCTC 240

262

	•	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 441 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(b) Astonosti Iliani	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1410:	
,,		
GAATTCGGCC	TTCATGGCCT AGGGAGGTGG TTTCTCTATC ATTGCATGAG GTAAGAGTCT	60
GGCCCTGGAT	GCTAAGGCTG CAGTTTTCTA CAGAAAGGAG TCATCTCTGT GAGGCAGCAT	120
CAGCCTCCAA	GACACAGTGI GCTGACCTGG TTTTGTATAA AGATGAAAAC AGCTGTTCTC	180
	GGCCGGCCAC AGAGAGAGCG GCGGGCTCAG CCTTCACAGG ATTGTCCTTC	240
	TAGGGGGTTT TAATCATCGC AGAAAGGAAG TGGGGGTGAA GGTCAGGAAA	300
	CGAATTCACC CCTCAGGCCT CAGCTAGAGG AAGCTAAGAG AAGAAATGAG	360
	TGTTAAGAAA AAGGCAAAGC TGGAGAGAAT GCAGAGGATT CTGGTTCCTG	420
GAGAGAACCT	TCAGACTCGA G	441
(2) INFORM	ATION FOR SEQ ID NO:1411:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 479 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1411:	
GAATTCGGCC	TTCATGGCCT AATTCATTGT CTGGTCCTTT ACAAAAGACA TATGCTGGCT	60
CCTGCTCTCT	GTGGATGATA GGTCTACAAA GATGTGATTC AACTCATATA TGTCTCCAAA	120
TTATATATT	AATTCATATA CTGTTTTGTC TTACATTAAT CTAGCATTGT CTTTTGGCTT	180
GCTACTGCAG	TAAGTTACCT TCTAATTCAT CATTAGGTCA ACTTTATCAA CTCACCTAAG	240
TCCAAAAGTA	AATGTAGGTT TCTCCTGGGT TCTTTTGCCT CTTAAGTTTT GCCATCCCCA	300
AATAAGCACA	ACAGAGACCT GCACCAAGAG ACCTTACTTT TAGACTGTAA GCACCAAAGT	360
	GAGAGAGTGA GCCAGGCTCA GTCTTATGAC TGGCAATACA AGTTGAGGGT	420
AGGAGCTTTG	GACAGAACAC TAGCTATGTA TAGTGTTGTC TAGGTGAGTG CTTCTCGAG	479
(2) INFORM	ATION FOR SEQ ID NO:1412:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 497 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1412:	
		_
	TTCATGGCCT AGCCGATTTA TAAATATGTA TATATAACCT TTCCCTTTTT	60
GAGAGATCTC	TTAGTAATAG TCAAAGCCAT ACCCTATTCC TTAGTGAGAA AGCCAGTTTG	120
	561	

AAACGAATGT	AGCAATAGAT	GTAAAAACAT	TTAAAGGCGT	TTTAATGTGG	CTTTTTAATG	180
AGCTGGCTTA	TGCCTGTAGT	CCCAGCACAT	TGGGCAGCTG	AGCTGGGAGG	ATCGCTTGAG	240
CCCGGGAGTT	CAAGACTAGC	CAGGGCAACA	TAGTGAGACC	CCATCTCTAT	TTAAAAAAAA	300
ATGTTTTŢĀĀ	AGATAAGGAA	CAGACTTAAA	GTGATGATTG	ATTGCTCATA	GAACGTTCAT	360
TTTGGGCTCC	AGAACTAGGA	ATGATGTAGA	ATTTATTGTT	GTGTCATTGT	CTCATTAAAT	420
GCTGTAGTTT	CCTATGTCCT	TGCCTACCTT	CTTTCCTCAG	AGCCTCGCAT	CTGACCCTCA	480
GAGAGTAGCA	GCTCGAG				,	497

- (2) INFORMATION FOR SEQ ID NO:1413:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 439 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

GAATTCGGCC	TTCATGGCCT	ACAGGAACAA	AAAATGCTAT	GCTATTATCT	CAAAAATGCA	60
TACTCCTTCC	TACTTAAGAA	TAATAAATTT	ATATATTATG	ATATGGTAAA	ATTCACAACT	120
AATTGTATTT	TTCCCTAGAA	TGTTTAAAGC	ATTATCTAAT	ACCAGCTTCA	GTGTCTATAT	180
TACTGTAACT	TCATGAAAGA	CTACTAACAA	TACTGGCTAT	CATTTATTAA	TATTAAGTAG	240
TACTTGCCAG	ATGCCGTTAG	AGGTGCTTTA	AATGCATTCT	CATTTAGTCT	TCGTGTGTAC	300
TACCGTTATC	TTCACTTTTT	AGATAAGGAG	ACTAAAGTAT	AACTAGAGCT	AAGAAACATG	360
AGAAAGACGA	CCTAGCTACT	GCCTATTTTG	TAATTCCCAT	GGACTAAGCT	TGGAGAAGTA	420
AGAACTATTA	CTACTCGAG					439

- (2) INFORMATION FOR SEQ ID NO:1414:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 243 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

GAATTCGGCC	TTCATGGCCT	AGCCACTTCA	AGACGGCAAG	TTATTTTAGC	TCCTGTCTAA	60
ATAAGTTAGT	GGGCTCCAGT	CCTTAAACCA	CTATTTTCTT	TATTAATTCC	TCAAGTACAG	120
ACTTTTGTAT	GTAACCAGTC	TTTTTAAACC	TGTGTATAAT	GACTCATTAA	TGAGTTGTAA	180
AATAAATGTA	GTGAGTTATG	ACCAATATAA	AAAAATAGAA	AAGGCCAGGC	ACAGTCGCTC	240
GAG						243

- (2) INFORMATION FOR SEQ ID NO:1415:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 276 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

CTGTATCAGT CAGTATTTGT AAAGGTGCTC	TTCATGGCCT AGTCTTCCAA GACAGGAATC AGCAACCTTT TTTTGTTTTT AATTCATTCT GTATATTTTA AAAAGTTTTA ACCTCTTCTT CCTAGCCCTC TTATAAATTA AAACGTTTCC CAAAGTGTTT TCTGTGAAAC AATAGTTCTA TAAGAAAAGC TAAGTACATG GCAAAATCCA AAGTATATGT TTTATTCATT AATTTTTTTT GTTTTTCCT CTCGAG	60 120 180 240 276
(2) INFORM	ATION FOR SEQ ID NO:1416:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 341 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	•
(ii)	MOLECULE TYPE: cDNA	
·( <b>xi</b> )	SEQUENCE DESCRIPTION: SEQ ID NO:1416:	
GATGTGTACA CTCAACTTAG ACAAACCTCA CAGATCTCAC	TTCATGGCCT AGAGAGCAGG TTTTAGCTTG CATCCAGCTG TTTCTTGAGT GCTTACCCC AAAGAGGCAA CTGAATTTCA GCTGCTCTAA TACCCACACC GTTTAGTCAT AATAAAAAAC AGAATGGATT TGTTAGTTCC ATTGATTGCC CCTTCTGTGT GGCAGAGATG TGCTTTAGTT CTTCATTGGA ATGTTACTTT AAACCTCAAA CCTAGGGCAC CACCAATGAC AAAGAGAATG CTAAATAGAT CCAGGTCTTC AAGCTTTCCA CTCCCCTCGA G	60 120 180 240 300 341
(2) INFORM	ATION FOR SEQ ID NO:1417:	
	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 455 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1417:	
CTATTAAAA ATTATTATTA CTCCATTATT TACCTGCCAT TTGCTACCTG AGGATTGCTA GCTACCTTAT	AAAGAGGCCT AGCCATTATT ATTAAAAAGT AGGATTGCTA CCCGCCATTA GTAGGATTGC TACCCGCCAT TATTATTAAA AAGTAGGATT GGTACCCGCC AAAAGTAGGA TTGCTACCCA ACATTATTAT TAAAAAGTAG GATTGCTACC ATTAAAAAGT AGGATTGCTA CCCTCCATTA TTATTAAAAA GTAGGATTGC TATTATTAAA AAGTAGGATT GCTACCTGCC ATTATTATTA AAAAGTAGGA CCATTATTAT TAAAAAGTAG GATTGCTACC CGCCATTATT ATTAAAAAGT CCCGCCATTA TTATTAAAAA GTAGGACTGC TACCCGCCGT TATTTGCACA GAAAGTAGTT TCACGCTGTC TCGAG	60 120 180 240 300 360 420 455
(Z) INFORMA	ATION FOR SEQ ID NO:1418:	
	SEQUENCE CHARACTERISTICS: (A) LENGTH, 573 base pairs	

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

GAATACCTAG CTTCCATGAT TTATGATAGA TATCCTTTAT TGGACCAATT CGTGTCTGTA

60

ACCAGCCTCC	TGTTTCTACT	GCCATCCCCT	CCTCATGCAC	AGATGCCTCC	TCCCTTGGCT	120
CCTGCTCTGA	TCCCTGTACC	CAGCTTGTCC	CCTGCAAGCA	TGTTCCCCTC	CCTTGCCCAG	180
GCTCTGACAC	CCCACACATG	TGTGGATCCC	CTCCCCTGTC	CCAGCTCTGA	TACCCCTTGC	240
ATGTGTGGCT	GCCCCTCACC	TGGGTGTCCT	CTTCCCTGTC	CCAGCTCTGA	CAÇCCACGCA	300
TGTGGGGCTG	CCCCGTGCCT	AGGTGTCCCC	TCCTCTGCTC	AGGCTCTGTC	CTCCTGCGGT	360
TGGCTTTCCC	ATTCTGGATG	CACCTCACAC	ACAGCCTTGT	CATCTTTGGA	TGAATTTGGC	420
CTCCCCCATC	CACTGCTGGT	GCAGATGCTT	CCTTACGGGG	CCTTGTCTGA	TGGCTTTAGG	480
GCTGAATCAT	GCAGGAAGGA	AGGAGAAGGA	CAAGAAGAAA	AGGGAAGGCT	GGGAAGGGAA	540
GCGGGTGGTA	AAATTGGTTC	ACAAGCCCTC	GAG			573

- (2) INFORMATION FOR SEQ ID NO:1419:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 188 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

GAATTCGGCC AAAGAGGCCT	ATTTTAAAAA	AAACTATTTA	TAATTTTTAAT	TTATTTTTGG	60
TTGTTTTTTG CACAATGAAG	TTTCAGCTTC	TCAACCTTCT	CCCCTACCCA	GGGCTGTGGA	120
CCCAGACTGG CCTTGAGCCA	CAGTCCCTCT	TTCCCTCCTC	ACCCTCTTCC	CCCTCCGGGC	180
ACCTCGAG					188

- (2) INFORMATION FOR SEQ ID NO:1420:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 572 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

GAATTCGGCC	AAAGAGGCCT	ACGAGGAAAG	ATCTAATTAT	CATGGACCTG	CGACAGTTTC	60
TTATGTGCCT	GTCCCTGTGC	ACAGCCTTTG	CCTTGAGCAA	ACCCACAGAA	AAGAAGGACC	120
GTGTACATCA	TGAGCCTCAG	CTCAGTGACA	AGGTTCACAA	TGATGCTCAG	AGTTTTGATT	180
ATGACCATGA	TGCCTTCTTG	GGTGCTGAAG	AAGCAAAGAC	CTTTGATCAG	CTGACACCAG	240
AAGAGAGCAA	GGAAAGGCTT	GGAAAGATTG	TAAGTAAAAT	AGATGGCGAC	AAGGACGGGT	300
TTGTCACTGT	GGATGAGCTC	AAAGACTGGA	TTAAATTTGC	ACAAAAGCGC	TGGATTTACG	360
AGGATGTAGA	GCGACAGTGG	AAGGGGCATG	ACCTCAATGA	GGACGGCCTC	GTTTCCTGGG	420
AGGAGTATAA	AAATGCCACC	TACGGCTACG	TTTTAGATGA	TCCAGATCCT	GATGATGGAT	480
TTAACTATAA	ACAGATGATG	GTTAGAGATG	AGCGGAGGTT	TAAAATGGCA	GACAAGGATG	540
GAGACCTCAT	TGCCACCAAG	GAGGGTCTCG	AG			572

- (2) INFORMATION FOR SEQ ID NO:1421:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 498 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

GCAAGACGGC	TACTGAGGCA	GGAGAATCGC	TTGAACCCAG	GAAGCGGAGG	TTGCAATGTG	60
CCAAGATCGT	GCCACTGCAC	ACTCTAGCCT	GGGCAACAGA	GCAAGACTGT	GTCTCAAAAA	120
AAAAAAATCT	TNGACNAAAC	ATAGTTGTTN	ACATACTTCT	TTAATCCCAG	AGTTAGTTTT	180
AAAAANNACA	TGATTGCTGT	TTTTGCATAT	TATCTCAGCG	GTCTAAAATT	AACCTAGCCA	240
TGTGCAGGAA	TGGGTAAAGT	CCCCTTAAAC	AAAAATGGGG	TTAGTTANGT	TAGTTCTTTT	300
			TTAGCCTGAC			360
AGCCGNGATC	AGCGGTCCTG	ACGGGGGTCA	GAGTCAGACC	AGGGGTCTTT	TACCCAAGTG	420
GGGAAGATTG	GGAAAGGCCT	AGGATCAGAG	AGGGAAATGG	GTCCCTGGTT	GCCCATGGAC	480
CTAATGGGGT	CTCTCGAG					498

#### (2) INFORMATION FOR SEQ ID NO:1422:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 827 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

GAATTCGCGG	CCGCGTCGAC	GAGGAAACCA	GCCAAGGACT	AACTACGACC	ATGAGATTGG	60
CAGTGATTTG	CTTTTGCCTG	TTTGGCATTG	CCTCCTCCCT	CCCGGTGAAA	GTGACTGATT	120
CTGGCAGCTC	AGAGGAGAAG	CTTTACAGCC	TGCACCCAGA	TCCTATAGCC	ACATGGCTGG	180
TGCCTGACCC	ATCTCAGAAG	CAGAATCTCC	TTGCGCCACA	GAATGCTGTG	TCCTCTGAAG	240
AAAAGGATGA	CTTTAAGCAA	GAAACTCTTC	CAAGCAATTC	CAATGAAAGC	CATGACCACA	300
TGGACGACGA	TGATGACGAT	GATGATGACG	ATGGAGACCA	TGCAGAGAGC	GAGGATTCTG	360
TGGACTCGGA	TGAATCTGAC	GAATCTCACC	ATTCGGATGA	GTCTGATGAG	ACCGTCACTG	420
CTAGTACACA	AGCAGACACT	TTCACTCCAA	TCGTCCCTAC	AGTCGATGTC	CCCAACGGCC	480
GAGGTGATAG	CTTGGCTTAT	GGACTGAGGT	CAAAGTCTAG	GAGTTTCCAG	GTTTCTGATG	540
AACAGTATCC	TGATGCCACA	GATGAGGACC	TCACCTCTCA	CATGAAGAGC	GGTGAGTCTA	600
AGGAGTCCCT	CGATGTCATC	CCTGTTGCCC	AGCTTCTGAG	CATGCCCTCT	GATCAGGACA	660
ACAACGGAAA	GGGCAGCCAT	GAGTCAAGTC	AGCTGGATGA	ACCAAGTCTG	GAAACACACA	720
GACTTGAGCA	TTCCAAAGAG	AGCCAGGAGA	GTGCCGATCA	GTCGGATGTG	ATCGATAGTC	780
AAGCAAGTTC	CAAAGCCAGC	CTGGAACATC	AGAGCCACGG	CCTCGAG		827

- (2) INFORMATION FOR SEQ ID NO:1423:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 348 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

GAATTCGCGG	CCGCGTCGAC	GGGAGAGGAA	GGGTTGGGCA	GGATGGAATA	TTAAATTGTA	60
ACATGATAAA	CATGCAAGAC	TGTTATCCAA	TCTAGATAAT	TTATATACAT	TTTGATGACT	120
TAGGAAAACA	AAGCAATCAT	TTGTGACAAG	CCTAAAAAGC	TTGACATATT	TAACATACTT	180
AGGAACTTTT	TTTGTGCGGT	GGGAATTCTC	TAATTGTATC	ATGTGGGCCT	TTTGAAAGTA	240
ACAAACAGAA	GGCCAGTCTG	TTGCAAGTTT	GCTGCTGAAC	ATCACATTCC	ACCCTAAGAA	300
AACACAAGGT	GGATTGCATC	GAGGGTGGAT	ACCTTACCTT	AGCACAGA		348

(2) INFORMATION FOR SEQ ID NO:1424:

(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid

(i) SEQUENCE CHARACTERISTICS:

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:	
GAATTCGCGG CCGCGTCGAC TTGGAGAATG TGGCCTCTGA TCACTAACCA GGGTTTTCTC TTTACACTGG CTTGTTTACT TATTTCTTCA CCAAAGCCAG GGAACGTCCC TTTAGCTACT GCAGCATTTC TAACAGATGC GACAAATCAC AG  12	20
(2) INFORMATION FOR SEQ ID NO:1425:	٠
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 206 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:	
GAATTCGCGG CCGCGTCGAC CTAAACCGTC GATTGAATTA GACCTGCCTC GAGATGCGCC ACTTTCTGCT CACCCACCTT AGAGCCTTTG CATATGCAGT TGCTTCCTCA GAGTATTGCC ATCCCCAGCA CGACCCCCAG CTCATTCTTC AGGCCACTAA CGTAAATGTT ACTTTCTCAA AAACACCCCTC TCCATCCCGG CACCCA	2 O
(2) INFORMATION FOR SEQ ID NO:1426:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 353 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:	
GAATTCGCGG CCGCGTCGAC GTGGGTACTT CATCCTCCTC ATCACTGGTT GGCACTGAGA GCTTCTTAAG ACGCTCCATG AGCTCTTTCT CTTCTCCATC ATCACTGCACA TCCTTCTTCC GCCTGCCTTT TCGGGTATCT CGCTTTTTT TTTGCTGCTG TTGCTGTTGC TGCTGCTGCT GCTCCTTCTC CTTGAGCACT TTCTCTTCTT CCCCAGCCTG TTTATCTTCT ACTGCCAGCT CTTCAAAGAA CGTTTTTTG ATCTTCTNGT CCTTCTTCCC TTTCTTCACC ACTTTGTCTG ATGGGCTCGT GCTCTCCCG TCCCCGATCC ACTCGGGCTC CGGCGGACTC GAG	8 C 4 C 0 C
(2) INFORMATION FOR SEQ ID NO:1427:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 343 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
566	

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

GAATTCGCGG	CCGCGTCGAC	AGATATTTGG	TTATCTTGAC	TAAAATTTTT	AACATATTTC	60
TACAGGATTT	TGAGTCTGAG	AAGAGAAAGG	TAATATGCAA	${\tt GACACTTCGA}$	TTTGTTGCAC	120
ATTATTATGG	AGCATCATTA	ATGGTTTGTA	CATTTCTTGT	CCTTTGGGCT	TGAATGGACA	180
GTACCAAATT	TGGGGAAATC	AGCAACTTGA	TGCACAGCTA	CGAGGAATAA	ATGCTTTTGC	240
TAATGCACAT	GGTCCCGTTG	CTTTCCCACT	GCTGAAGACC	TCTCCTTACA	GAGTGTTTGA	300
TAATGCATCT	GTTGAACATG	CACTGCTAGA	TGGTCCTCTC	GAG		343

- (2) INFORMATION FOR SEQ ID NO:1428:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 542 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

GAATTCGCGG	CCGCGTCGAC	GAGGGGAAGA	TGTCACGCAA	GATAGAAGGC	TTTTTGTTAT	60
TACTTCTCTT	TGGCTATGAA	GCCACATTGG	GATTATCGTC	TACCGAGGAT	GAAGGCGAGG	120
ACCCCTGGTA	CCAAAAAGCA	TGCAAGTGCG	ATTGCCAAGG	AGGACCCAAT	GCTCTGTGGT	180
CTGCAGGTGC	CACCTCCTTG	GACTGTATAC	CAGAATGCCC	ATATCACAAG	CCTCTGGGTT	240
TCGAGTCAGG	GGAGGTCACA	CCGGACCAGA	TCACCTGCTC	TAACCCGGAG	CAGTATGTGG	300
GCTGGTATTC	TTCGTGGACT	GCAAACAAGG	CCCGGCTCAA	CAGTCAAGGC	TTTGGGTGTG	360
CCTGGCTCTC	CAAGTTCCAG	GACAGTAGCC	AGTGGTTACA	GATAGATCTG	AAGGAGATCA	420
AAGTGATTTC	AGGGATCCTC	ACCCAGGGGC	GCTGTGACAT	CGATGAGTGG	ATGACCAAGT	480
ACAGCGTGCA	GTACAGGACC	GATGAGCGCC	TGAACTGGAT	TTACTACAAG	GACACTCTCG	540
AG						542

- (2) INFORMATION FOR SEQ ID NO:1429:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 465 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

GAATTCGCGG	CCGCGTCGAC	TTAAGAGTCT	GCTTCGGAGA	CCGTAAGGAT	ATTGATGACC	60
ATGAGATCCC	TGCTCAGAAC	CCCCTTCCTG	TGTGGCCTGC	TCTGGGCCTT	TTGTGCCCCA	120
GGCGCCAGGG	CTGAGGAGCC	TGCAGCCAGC	TTCTCCCAAC	CCGGCAGCAT	GGGCCTGGAT	180
AAGAACACAG	TGCACGACCA	AGAGCATATC	ATGGAGCATC	TAGAAGGTGT	CATCAACAAA	240
CCAGAGGCGG	AGATGTCGCC	ACAAGAATTG	CAGCTCCATT	ACTTCAAAAT	GCATGATTAT	300
GATGGCAATA	ATTTGCTTGA	TGGCTTAGAA	CTCTCCACAG	CCATCACTCA	TGTCCATAAG	360
GAGGAAGGGA	GTGAACAGGC	ACCACTAATG	AGTGAAGATG	AACTGATTAA	CATAATAGAT	420
GGTGTTTTGA	GAGATGATGA	CAAGAACAAT	GATGGCATAC	TCGAG		465

- (2) INFORMATION FOR SEQ ID NO:1430:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 373 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

GAATTCGCGG	CCGCGTCGAC	GCTGTTCATG	AGGAGACTTA	ACCACAATTC	AAAGTGTAGC	60
AGTTGTGTAT	TTTAGCATTA	TAATATTTGA	TTGAGGCCCT	GAGGTGTTAA	TATCTCAATC	120
TCAGAGTTAG	ATGTTCATGT	CCTTTTTGAA	TTTTTTAAAC	ATTTTTCATA	ATTTTTTTTT	180
TAAGTTAGGG	AGCACATTGA	GTGAAGTTCT	CTGTGTAGAA	CAATACCTTC	TGCTCTGCTT	240
CTCCCAGCTT	TCACTGAGGG	CTGGAAAAGG	ACAGGCCTGT	CCAGCTGTAC	TGTCCCACTG	300
TGTATGGGGA	AGCTCAGGCT	CTGGTGGAAG	CAGGGGGCAT	GGATGTCAAA	CAACTGATGT	360
GCAAACACTC	GAG					373

- (2) INFORMATION FOR SEQ ID NO:1431:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 632 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

GAATTCGGCC TTCATGGCCT	ACTACTGATG	AGAACATTAT	CTGCATATGC	CAAAAAATTT	60
TAAGCAAATG AAAGCTACCA	ATTTAAAGTT	ACGGAATCTA	CCATTTTAAA	GTTAATTGCT	120
TGTCAAGCTA TAACCACAAA	AATAATGAAT	TGATGAGAAA	TACAATGAAG	AGGCAATGTC	180
CATCTCAAAA TACTGCTTTT	ACAAAAGCAG	AATAAAAGCG	AAAAGAAATG	AAAATGTTAC	240
ACTACATTAA TCCTGGAATA	AAAGAAGCCG	AAATAAATGA	GAGATGAGTT	GGGATCAAGT	300
GGATTGAGGA GGCTGTGCTG	TGTGCCAATG	TTTCGTTTGC	CTCAGACAGG	TATCTCTTCG	360
TTATCAGAAG AGTTGCTTCA	TTTCATCTGG	GAGCAGAAAA	CAGCAGGCAG	CTGTTAACAG	420
ATAAGTTTAA CTTGCATCTG	CAGTATTGCA	TGTTAGGGAT	AAGTGCTTAT	TTTTAAGAGC	480
TGTGGAGTTC TTAAATATCA	ACCATGGCAC	TTTCTCCTGA	CCCCTTCCCT	AGGGGATTTC	540
AGGATTGAGA AATTTTTCCA	TCGAGCCTTT	TTAAAATTGT	AGGACTTGTT	CCTGTGGGCT	600
TCAGTGATGG GATAGTACAC	TTTTCACTCG	AG			632

- (2) INFORMATION FOR SEQ ID NO:1432:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 298 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

GAATTCGGCC	TTCATGGCCT	ACTAATTTCC	AAGAGCTAAA	CTTTATACCG	CCTGCAATAT	60
TTCCATTTAC	TACCAGTTTT	TTTCTGACCT	AGTCAGATAT	AAGAAGCCCC	CTTACTGGAT	120
ACAAGACAGT	TAATTATCAG	ATCCAGTCTG	ATCCTAGATC	CAGTCTGATC	CTAGACCCAG	180
TCCAGTTTCT	GTTGTGACTT	CCAAACCCAG	TTTGGATCAG	AAATTTGCTC	AAAGAAACTA	240
GGAGAGCTCA	AAACACAAAT	ATGTGGAGCT	TCTGAATCTG	AGAGAGAACG	AACTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:1433:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

GCGTGGTTTC	ACCTTGTTGG	CCAGGCTAGT	CTTGAACTCC	TGACCTCAGG	TGATCCACCC	60
ACCTCGGCCT	TCCAAAGTGC	TGGGATTACA	GGCATGAGCC	ACCGCATCTG	ACTGGTGCAC	120
TTTACTTTGA	CCTGTCATAA	ATCCCTTGGT	TTGTTATTAC	TAGTTTTTAC	TTTAGACAGC	180
AATTATCTTT	CAAGGAAAAA	TTTAAAAGGA	AAAAATGTCT	TATATTTACC	CTCATGTTTA	240
CCATTCCCAG	TGCTCTTTAT	TTCTTTATGT	CAATCCGGAT	TTCAATTTGT	TATCATACTG	300
TTTCTGCCTG	AATAACAGTT	TAACAGCAAC	TCGAG			335

- (2) INFORMATION FOR CEQ ID NO:1434:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

GAATTCGGCC	TTCATGGCCT	AATGCTCTGT	GTCACTGTCT	CCCGGTGCTC	AGCACAGACA	60
AGTTCAAGAC	AGATTTTTAT	GATCAATGCA	ACGACGTGGG	GCTCATGGCC	TACCTCGGCA	120
CCATCACCAA	AACGTGCAAC	ACCATGAACC	AGTTTGTGAA	CAAGTTCAAT	GTCCTCTACG	180
ACCGACAAGG	CATCGGCAGG	AGAATGCGCG	GGCTCTTTTT	CTGATGAGGG	TACTTGAAGG	240
GCTGATGGAC	AGGGGTCAGG	CAACTATCCC	AAAGGGGAGG	GCACTACACT	TCCTTGAGAG	300
AAACCACTGT	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1435:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 383 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

GAATTCTAGA CCTCCCACCC	TGTAGAACAT	TCTCCTCACT	TAGGAGATAG	TCATATTTTC	60
AGGCTGCCTT TGAAACTGTG	GGTACACAAA	CAGCAGAGCG	ATCTATTTCA	GCAGTTGAAG	120
TTGTATTTGA GCCATTATTT	CTTCCACTCT	CTTTTTGGTT	GAGTTTCTAG	GAAGGAAAGG	180
GCTGAACTCC ATGACTGCTC	ATATTACAGT	GCTAAGTCCT	CACAGCCATC	CACTGTTTAT	240
ACACAAGAAG AAACTAGGCC	CACCAAGAGT	AAGCGCCTGC	CTGAGGTCCG	TGAGTGAGTA	300
AGGGCCAAAG GTGAGGTTGG	GATCTGGCCC	TTTCTCTTTT	CTGGCCACCA	CAGGGCACTA	360
CCTCCCATAC CCACACACTC	GAG				383

- (2) INFORMATION FOR SEQ ID NO:1436:
  - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 303 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

GGAGAACTGC	TAAGGTCCAC	AACGTCGACA	ATTGAAAGCT	TTGCTGCACA	AGAAAAACAA	60
ATGGAAGTTT	${\tt GTGAAGTATG}$	TGGAGCCTTT	TTAATAGTAG	GAGATGCCCA	GTCCCGGGTA	120
GATGACCATT	TGATGGGAAA	ACAACACATG	GGCTATGCCA	AAATTAAAGC	TACTGTAGAA	180
GAATTAAAAG	AAAAGTTAAG	GAAAAGAACC	GAAGAACCTG	ATCGTGATGA	GCGTCTAAAA	240
AAGGAGAAGC	AAGAAAGAGA	AGAAAGAGAA	AAAGAACGGG	AGAGAGAAAG	GAAAGAACTC	300
GAG						303

- (2) INFORMATION FOR SEQ ID NO:1437:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 228 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

GAATTCGGCC	TTCATGGCCT	AGACTTTTAC	ACATTTTTAT	TAGCTACCTG	GAATTATTTT	60
TGTAACACGT	TAAGTGTAAA	TAAACAAATA	ATGCTTTGCT	TTTTGTTTTC	TGGAATTATT	120
GTTGTATTTC	TTTGCCAAAT	GCATATATCT	TCAGGTCTTT	TTTTTTATAAC	CATATGCATA	180
CCAAGGCACC	ATTCCATTGA	CTTTCCAACT	TCTGTCCCAA	CCCTCGAG		228

- (2) INFORMATION FOR SEQ ID NO:1438:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 498 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

GTGAATTCCA GTCCCCACCC	AGAAACCCGC	AGCATGATTG	TCTGCCTCCT	TTTCATGATG	60
ATTTTATTGG CAAAGGAAGT	TCAACTGGTA	GACCAAACAG	ATTCACCTTT	ACTTAGTCTC	120
CTTGGACAGA CAAGCTCACT	TTCATGGCAT	CTTGTGGATA	TTGTGTCGTA	CCAGAGTGTG	180
CTAAGTTATT TCAGCAGCCA	TTACCCGCCG	TCCATCATCC	TGGCAAAAGA	ATCTTATGCT	240
GAATTAATCA TGAAGCTCCT	AAAAGTGTCT	GCGGGCCTTT	CTATTCCTAC	TGACAGCCAG	300
AAGCATCTTG ATGCAGTTCC	AAAATGCCAA	GCTTTTACTC	ATCAGATGGT	TCAATTCCTC	360
AGCACCCTGG AACAAAATGG	AAAAATCACC	TTAGCAGTCC	TAGAACAGGA	AATGTCTAAG	420
CTCTTAGACG ATATCATTGT	CTTTAACCCG	CCCGACATGG	ACAGCCAGAC	CCGCCACATG	480
GCCCTCAGCG GTCTCGAG					49B

- (2) INFORMATION FOR SEQ ID NO:1439:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 314 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

GAATTCGGCC	TTCATGGCCT	AGCAGGGAGA	GGGGTTCTGT	GCTCCTGAGA	TTAGTTCAGA	60
TGGTCTAACC	ATTGTTCTAT	ATGTGCATTT	TAGTTAATAT	TGTGTATTAA	AGGATAAGTC	120
TTAATGCTCA	AAGTATGTTA	AAAATAGATG	TAGTAAATCA	GTCCCTTTGT	GAATGTCCTT	180
TTGTTAGTTT	TTAGGAAGGC	CTGTCCTCTG	GGAGTGACCT	TTATTAGTCC	ACCCCTTGGA	240
GCTAGACATC	CTGTACTTAG	TCACGGGGAT	GGTGGAAGAG	GGAGAAGAGG	AAGGGTGAAG	300
GGAAGTGGCT						314

- (2) INFORMATION FOR SEQ ID NO:1440:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 424 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

CCAGCCGTCT	GCAGCTCCGG	CCGCCACTTG	CGCCTCTCCA	GCCTCCGCAG	GCCCAACCGC	60
					AGCTGTCGGT	120
					TCTACCAGTA	180
	GAGGTGAAGC					240
CCTCAAGTCC	CCTTCTGACC	TGTCCCCAGA	GAGCCCTATG	CTCTCCTCCC	CACCCAAGAA	300
GAAGGACACC	TCCCTGGAGG	AGCTGCAAAA	GCGGCTGGAG	GCAGCCGAGG	AGCGGAGGAA	360
GACGCAGGAG	GCGCAGGTGC	TGAAGCAGCT	GGCGGAGCGG	CGCGAGCACG	AGCGCGGGCT	420
CGAG						424

- (2) INFORMATION FOR SEQ ID NO:1441:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 346 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

GAATTCGGCC	TTCATGGCCT	ATAGGCCATG	AAGGCCGGCC	TTCATGGCCT	AGTCAGGCTT	60
AAGTTTAATA	AATAGCAAAT	TGCATACAGA	TATTTACAAT	GATCGAAAGA	CAAACAGAGG	120
TCCTATCCGT	GCAGTCCCAA	CAATAAAGAC	AGGCATTGGC	ATANAGTGTT	TATAAATTCT	180
TGGGTACAGC	TGTTCTGAAA	GTAAAGTTCA	CTTTCAATCC	TAAAAAAAGT	CCGCTATTCC	240
TCCCTGGCTG	CTCTGGACTG	TCCTCATCCT	CTTTAGCTGC	TGTTGCGCCT	TCCGCCACCG	300
ACGAGCTAAA	CTCAGGCTGC	AACAACAGCA	GCGGCAGCAT	CTCGAG		346

- (2) INFORMATION FOR SEQ ID NO:1442:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 591 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

GAATTCGGCC	TTCATGGCCT	AGGCTTCCCT	GTTCCCTCAG	CCCCAGTCGA	GAGGAAAGAG	60
AATCGGGCCA	CTGCCAGAAA	GAGAGTCAAG	CAAACCTGGA	AGGGCAAATC	TGAGAGTGGG	120
AAGGCCAAAG	GCCGAGGCCC	AGATTTAGTA	TTCACTAGCA	GCGCCTTCGG	GTAGCAGGAT	180
GATTCCTTTT	CCTGCCTGTC	TGCTGCTGGC	TCTCTTCCCT	AAGGTACAGG	TTGGCAGGAC	240
CACCTCCGCC	TACTTCTCCA	CCATCCCTAG	CATGCCAGCC	CGTTCCCAGA	TCAACCTGCC	300
AGTGGAGTCA	${\tt GGCAGTGCAC}$	TCCTGGAGCC	AAGAGGGAAG	GGCAGGGTAG	AGAGGGTATG	360
TCCAGTAGCC	TGGAGCTCCA	TGGTGGCTTC	ATGCCTCCCT	TCTCCCAGCT	CAGGTGGCCC	420
TGAGGGCTCC	CTCGGAACAG	TGCCTCAAAT	CCTGACCCAA	GGGCCAGCAT	GGGGAAGAGA	480
TGGTTGCAGG	CAAAATGCAC	TTTATAGAGA	TTTTCTATTG	CTGGGAAGGT	GTGTTTCTCC	540
CACAATTTGT	TTGTGAATAT	TCACTTGTTT	TATAAATGTC	TGACCTGTCC	G	591

- (2) INFORMATION FOR SEQ ID NO:1443:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 526 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

GAATTCGGCC	TTCATGGCCT	AGATTGAATT	ACCTGCCTCG	AGCTCCTGTC	CTTAGGTGAT	60
CTGCCCGCCT	TGGCCTCCCA	AAGTGCTGGG	ATTATAGGAG	TGAGCCACCT	GGCCCAGCTA	120
GCTTTTAAAG	TTCTGCCAGC	ATAGCCCCGG	${\tt GATGGGGTGG}$	GGGTAGACAG	GGCCTTAGGA	180
CTTTCATTTT	TAAAATGCTC	ACTCCACAGT	GAAGAAACAG	GTGATGACTA	TCCTGAATAT	240
TTGGGAAGCT	GTGTCCTAGA	ATTTTTGGCC	TCAGTTCCAG	AACCCACAGC	TTCTTTACAA	300
CATGCTTCAA	GCCTGGGACT	GAGCTGCCAG	TAAATAAACC	CCTAGTAACC	TTAATATGGG	360
TTAATAAGAT	TAGGTGCCCG	CTCTGCACGC	TCCCCTGCCC	CTCCTCGTCC	GGGCACCTGT	420
TATGCTAGGC	CAGCATGTTT	GCAGCTTAGC	CAGGGAAAAT	CGTGGACCAA	GACAGGGCTT	480
TTCATCCACG	ACTGGCTAAA	AAGATGGCTC	TCAATAATAT	CTCGAG		526

- (2) INFORMATION FOR SEQ ID NO:1444:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 279 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

GATTGAATTC	TAGACCTACC	TCTCTTTTTT	TGTGGTCTCT	CCTTCATTCT	CTGTTCATTT	60
CTCCGTGAGA	TTTTCTGATT	AGTAGTTACC	TTCAGCATGC	CAGTTGACTT	GCAAACCTAC	120
AATCCAACCT	TTCTTCTACT	TTGTCATCTG	ACAACAGCCT	GGTTTGTAGC	TGATTCCAGG	180
ACTTCTTCAC	TTGGGTGGCC	ACTCTCATTA	CCACAGAGTT	CACTAGTCAT	GGTGAACACA	240
CCAGTCTTTT	ACACCTCCCT	CACTCCCAAA	CCACTCGAG			279

(2) INFORMATION FOR SEQ ID NO:1445:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 644 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

GAATTCGGTC	TTCATGGCCT	AGGGGAAGAA	AGGCACCTTT	CTCACAGGGT	GGTGAGAGAG	60
AGGAAGGGGG	ACGGGGAAAG	CCCTTTATAA	AAGCATCAGA	TCGGCTGGGC	ACAGTGGCTC	120
ACGCGTGTAA	TCCCAGCACT	TTGGGAGGCC	GAGGCGGGTG	GATCGCGGGG	TCGGGGGTTT	180
GAGGCCGGCC	TGGCCAATAT	GGTGAGACCC	CGTCTCTGCT	GAAGATACAA	AAATTGGCTG	240
GGCATGGTGG	CGGGCACCTG	TGGTCCCGGC	TGCTTGGGAG	GCTGAGGCGG	GAGAATCGCT	300
TGAGCCCGGG	AGGCAGAGGT	TGCAGTGAGC	TGAGATCGCG	CTACTGCACT	CCAGCCTGGG	360
CAACAGAGCG	AGACTCCATC	TCAAAAATAA	AAGAAAGGCA	TAAATATTAC	ATTACCCTCT	420
GAATACTGTG	GTTGTATACT	TGAGTTTTTA	TGTGTGTATA	TATATGTGTA	TAGGAGAGTA	480
TAAAATAAAA	GAAATTAGGA	TTTTGCAAGT	TATAATCATA	TAAAATTGAT	TACCCTAAAT	540
ATATCATTAG	GATATTATGT	TATTTACATC	TCTTATGCTA	ATTCTAATTT	TCTTTTATTG	600
TAGTATAGTA	GAATTGAGAT	TTGNNAATGG	AATTGGTCCT	CGAG		644

- (2) INFORMATION FOR SEQ ID NO:1446:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 756 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

${\tt GAATTCGGCC}$	TTCATGGCCT	ACCTCACCCG	GCCCGGACAC	GGACAGGATT	GACAGATTGA	60
TAGCTCTTTC	TCGATTCCGT	GGGTGGTGGT	GCATGGCCGT	TCTTAGTTGG	TGGAGCGATT	120
TGTCTGGTTA	ATTCCGATAA	CGAACGAGAC	TCTGGCATGC	TAACTAGTTA	CGCGACCCCC	180
${\tt GAGCGGTCGG}$	CGTCCCCCAA	CTTCTTAGAG	GGACAAGTGG	CGTTCAGCCA	CCCGAGATTG	240
AGCAATAACA	GGTCTGTGAT	GCCCTTAGAT	GTCCGGGGCT	GCACGCGCGC	TACACTGACT	300
GGCTCAGCGT	GTGCCTACCC	TACGCCGGCA	GGCGCGGGTA	ACCCGTTGAA	CCCCATTCGT	360
${\tt GATGGGGATC}$	GGGGACTGCA	ATTATTCCCC	ATGAACGAGG	AATTCCCAGT	AAGTGCGGGT	420
CATAAGCTTG	CGTTGATTAA	GTCCCTGCCC	TTTGTACACA	CCAACCCGTC	ACTGACTTTT	480
ACCGCAGCTG	GAACTGTGCT	CCAGGGCCTT	TCCATCTTTT	CCCCCACACT	CCCTTTGACC	540
CTGTGTTGCC	CTCAGAGGCC	AAATTCTTGG	GCTCAGGGAC	TGGCTTTCGG	CCTATTGGTG	600
${\tt GTGGAGCTGG}$	GGTTCTGGCA	AGGAATTTCA	GGCAGCGCTT	GGAGGCAATG	TTCCCCGAGA	660
GCAGTTCACG	GTGGTGATGT	TGACTTATGA	GCGGGAGGAA	GTGCTTATGA	ACTCTTTAGA	720
GAGGCTGAAT	GGCCTCCCTT	ACCTGGAACT	CTCGAG			756

- (2) INFORMATION FOR SEQ ID NO:1447:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 359 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

GAATTCGGCC TCATGGCCT ACCTGCCTCG AGGTCACTGG GATCATCTGA ACAGAAGTGC ACAGGCTACT TGTACAGAGA AAAAATTAAT ACTCAAAGGA AATCTTCATT TTTTAGATTG ACTTTGGGAA TTTGAATTTT CATCAGTGCA AATATAAATT TCTCTATCCT GCTCTGAGGC TAATTGGTAC CATATTTCC CTTTGTGTCT TGTGACTCTG CCACATCCCA TCTCATCCTG GCCTCTGAGT CAAGAACCCA GTGAACTGAC TTTCTAGTTC TAGAAGTTCC GCTGCAAGGC CAGGAAAGGT TGAGAAAGGT ATTGTGGAAG AAGCAAAGGT AGACCCCCAT TCACTCGAG	60 120 180 240 300 359
(2) INFORMATION FOR SEQ ID NO:1448:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 146 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:	
GAATTCGGCC TTCATGGCCT AGGGAAAATA AGTTAATTCT AAATCAAATC	60 120 146
(2) INFORMATION FOR SEQ ID NO:1449:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 308 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:	
GAATTCGGCC TTCATGGCCT ACTTTCAAA AGCAGCTTTG CTCTACTGAT TTGGGTAAAA GCTTAGTTGC AGTTGGNTTG GGAGGAAATG GGAGCAGAAA ATTTGAGAGA GTGAGTGTAG ACAACTCTTT CAAGGAATTT CGCTATAAAT GGGAGTAGAG ATCTGAAGAC TGAATAATTA GCAAACTGAA AAGTGGGAAG ACGTAATTCT CTTATTATTT CATTTTTCTT AGTGAAATTAA GAGGTGAAGT TCTCTGAGTA ATAGGAGGGT CAAACAGGNG TTAGAAGTTC ACAAAGAAAG GTCTCGAG	60 120 180 240 300 308
(2) INFORMATION FOR SEQ ID NO:1450:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 545 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:	
GAATTCGGCC AAAGAGGCCT AGCATGTTGT GGCTGTTCCA ATCGCTCCTG TTTGTCTTCT GCTTTGGCCC AGGGAATGTA GTTCACAAA GCAGCTTAAC CCCATTGATG GTGAACGGGA TTCTGGGGGA GTCAGTAACT CTTCCCCTGG AGTTTCCTGC AGGAGAGAAG GTCAACTTCA TCACTTGGCT TTTCAATGAA ACATCTCTTG CCTTCATAGT ACCCCATGAA ACCAAAAGTC CAGAAAATCCA CGTGACTAAT CCGAAACAGG GAAAGCGACT GAACTTCACC CAGTCCTACT	60 120 180 240 300

CAAAGACCTC TACAAGTTAC	CAGCAACCTG AAGATGGAAG ACACAGGCTC TTACAGAGCC CAGATATC TGCAAAGCTG TCCAGTTACA CTCTGAGGAT ATTAAGACAA CTGAGGAA CAATCACAGT CAGCTATTTC AGAATATGAC CTGTGAGCTC CATCTGAC GGATGCAGAT GACAATGTCT CATTCAGATG GGAGGCCTTG GGAAACAC	CA 420
(2) INFORMA	ATION FOR SEQ ID NO:1451:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 331 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1451:	
GACTGAAGGG CCTCGTTTTT CCACCAAGAG CTTGATGGAC	AAAGAAGCCT ACAGTAAGCA GATGAACTTG CTTGCTGTTC TCGAAGTG, AACGAAAACT GGGGTGGGTT TTTGCGCTTC AAAAAAGGGGA AGCGATGT; GGACTGATAA TAATGACCTT GGTAATGGCT TCTTACATCC TTTCTGGGC CTTCTGATCT CATCACCTTT CCATTACGGA GGCTTCCCCA GCAACCCC, AGCGAAAACC CAAGTGACAC AAAGGAGCAT CACCACCAAT CCTCTGTAC TACATGAAGG GAACCCTCGA G	AG 120 GC 180 AG 240
(2) INFORMA	ATION FOR SEQ ID NO:1452:	
(i) :	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 263 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1452:	·w
TCTTTGGAAC CCTTAGTCCT TGCACGAAAA	AAAGAGGGAA GGGAAAATTT CAAGTCAGAT AGAATTCTAT ATATACCA CTTCAGCCCT CAAGATTCCA ACATCATGAC CTCAGTTTCA ACACAGTTC CATGTCACTG CTTTTGGTGC TGCCTGTTGT GGAAGCAGTA GAAGCGTAC AGAAATGGAC AGATGTGACT TTGAAAGGCC TACTGAGTCA AACCTCACC TGCAGCACTC GAG	GT 120 FA 180
(2) INFORMA	TION FOR SEQ ID NO:1453:	
(i) s	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 558 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1453:	
TTTGTTTATT 'GCATACCTGG'	AAAGAGGCCT AATTTAAAG CCCTGCTAAC TTCAATGTCT AGGTCACCC TTTATGGTCT TTTTTCATCC TGATTTTTGG TCATTTGGTC CCGTCTTA: TAATATTTTA TTGAATCCTT AGTACTGTAC ATGAAAAATT GTAGAGGCC CTTTCTCTGA AGAGGAGTCA CCCTTTCCTT CACTAGACAG TTATGTTGC	rG 120 CC 180

GGTTATATAC	CTTACTCCAA	TCAAAGATTG	AGCTGAGTCA	GAACTCTAAG	GGAGTTAAGT	300
				TGATATTCAC		360
				CACATCAAGG		420
				CAGCTTTAGA		480
TGTCTTACAG	GGAAAAGTAG	CTGTGTAACA	AGCTCATGTC	TCTGCCTCTC	TTCCACTGAT	540
ATCTTAGCCC	CGCAGGAG					558

- (2) INFORMATION FOR SEQ ID NO:1454:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 328 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

GAATTCGGCC AAAGA	GGCCT ACCTAAACC	G TCGATTGAAT	TCTAGAAATA	CAATGATTTT	60
AAAAAAGATT TCCAA	AGGCT TTTTCTTTT	r TTCTTTTTC	TNGAGACAGG	GTCTCACTCT	120
GTCGCCCAGG CTGGA	GTGCA GTGACACAA	r cregecteae	GGCAAGCTCC	GCACTGCCCC	180
CTCAGGTTCA CGCCA	TTCCT CCGCCTCAG	CTCCCGAGCA	GCCGGGACCA	CAGGCACGCG	240
CCACCACGCC CAGCC	AACTT TTACATTTT	r AGTAGAGACG	GGGCTTCACC	ATGTTGGCCA	300
GGATGGTCTC GGTCT	CTTCT GCCTCGAG				328

- (2) INFORMATION FOR SEQ ID NO:1455:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

GAATTCGGCC	AAAGAGGCCT	ACTTGATGTC	TGTGACCCAC	ACNTATTCGC	ACACTCCCTC	60
CCCTTTTGAA	AATCCCTAAT	AAAAACTTGC	TGGTTTTTGC	GGCTAGTGGG	GCATCATGGA	120
ACCTACTGAC	ATGTGATGTC	TCCCCCGGAT	GCCCGGCTTT	AAAATTTCTC	TCTTTTGTAC	180
TCTGTCCCTT	AATTTCTCAA	GCTGGCCGAT	GCTTAGGGAA	AATAGAAAAG	AACCTAGGTG	240
AATATTGGGG	CAGGCTCCCT	GATGAAATGA	TATATATTCT	TAAAATAAAC	TTTTCATCTT	300
TGCATATACG	TTTATATGCC	GAGTTTTCTC	CAACCTTGTC	TTACAGCACT	TTGTATACTA	360
CATTCTAGCC	ATACTAAACT	CTTGCAGTTC	CTGAGACATG	TGCTGTATCC	TATTTCTTCT	420
GGTCCTTTTC	TCATTGATTA	ACTACCTGGA	GCATACTTTT	AATTCAGTGT	CAGCGCTCGA	480
G .						481

- (2) INFORMATION FOR SEQ ID NO:1456:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

GAATTCGGCC AAAGAGGCCT ACTTCACCTT CAAGTCCCCT TTCTCAAGAA TCCTCTGTTC TTTGCCCTCT AAAGTCTTGG TACATCTAGG ACCCAGGCAT CTTGCTTTCC AGCCACAAAG AGACAGATGA AGATGCAGAA AGGAAATGTT CTCCTTATGT TTGGTCTACT ATTGCATTTA GAAGCTGCAA CAAATTCCAA TGAGACTAGC ACCTCTGCCA ACACTGGATC CAGTGTGATC TCCAGTGGAG CCAGCACAGC CACCAACTCT GGGTCCAGTG TGACCTCCAG TGGGGTCAGC ACAGCCACCA TCTCAGGGTC CAGCGTGACC TCCAATGGGG TCAGCATAGT CACCAACTCT GAGTTCCATA CAACCTCCAG TGGGATCAGC ACG	60 120 180 240 300 360 393
(2) INFORMATION FOR SEQ ID NO:1457:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 266 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:	
GAATTCGGCC AAAGAGGCCT AGTGTGTGT TGTGTGTGTT TTATCTCCTT CAACTCTGAC CACCTGGAAG TCAGCCTAAT CTCTGCCCTC GTGTTGATCT TTAATTCAAC ATTTAATTAC CTATCTTGGT ATCCATATGA ATTTGATTGT TTTTTTTGGCT TTTTTTTGAAC TCATAAAAGG TATCCAAGTT CCTGGAGGGC ATAGTGCCCA TCTCCTCCCA TCCACCAGTG GACATTCTTT TCCAAAAGAC ACATGG	60 120 180 240 266
(2) INFORMATION FOR SEQ ID NO:1458:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:	
GAATTCGGCC AAAGAGGCCT AGGTTGTAGT TACTTTCAGA GTAGATACAG GGTTTTAGAT CATTACAGTT TAAGTTTTCT GACCAATTAA AAAAACATAG AGAACAAAAG CATATTTGAC CAAGCAACAA GCTTATAAATT AATTTTTATT AGTTGATTGA TTAATGATGT ATTGCCTTTT GCCCATATAT ACCCTGTGTA TCTATACTTG GAAGTGTTTA AGGTTGCCAT TGGTTGAAAA CATAAGTGTC TCTGGCCATC AAAGTGATCT TGTTTACAGC AGTGCTCTCG AG	60 120 180 240 292
(2) INFORMATION FOR SEQ ID NO:1459:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 289 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:	

60

GAATTCGGCC AAAGAGGCCT AGTTTTATGA GAGGGTTTCC ATTAAGAAGT TAATTGAAAT

GAGGCCTCTT TTACGCTGTA GTCCTGCAAA TGCTGTGTTT TATTCCCCCT CCCCTGCTCA

240

GCACTCACCC ACGACTGACA CATGGGGTAC ACACACACA ATACTCGAG	289
(2) INFORMATION FOR SEQ ID NO:1460:	•
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:	
GAATTCGGCC AAAGAGGCCT ACACCTGCGT TGGAACATCT GATCCAGTGA TACCTAGGTGCCT TAATTAATAA AGCCAAAATA TCTTTCCACT AGCAAACTAA TCTTTTACTCTC CCATTTTTAA TTAATCTTTC CTATTTCATT TCACCCTCTC ATCTATTGGAT TATCTCAGGT ATCTAATCCA ATTCACTACT GTTTAATGAA TGACCAGTCTGC AATTCCTAAG GTTTTGTTTC TTTGCTTTTT TCTTTTGTAG TCTTGCTACACTC AAGCAGGTCT AGAATTCGAG	GTATTCAC 120 CTCTTTCC 180 TAATTGCA 240
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 383 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:	
GAATTCGGCC AAAGAGGCCT AGGGACAGTG ATTATAGGAC TCCACACATG CATAGCATTACT GACTTTAAAT TTTTTGAGCC TATCTAAAGG CCAGATGCTA TCCACACATC ACCAAAACCA GCTGCAAAGA TAGAAGCGGA ACAACTGGTT TGCATTACACA AACGAGTTGG GAAATAGGTA AAATAATAAC ATGGGGTAGA GGTGTTTCTCC AGGCCAAAAC CAGCAGCTGA TTTGGATACC ATCAAGATAC CTCATCAGCC AGATGCCAAG GAAGAGATTT TGGGAGGAAC CCGAGGACCC CATTTTTACCTAT TCCCCAACTC GAG	AGCAGCTG 120 GTGGAGAG 180 TTATGCTT 240 GAAAACTT 300
(2) INFORMATION FOR SEQ ID NO:1462:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 375 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:	
GAATTCGGCC AAAGAGGCCT ACGATGACGT CACCGTCACC ACCGGCGTGA AG TGGTGAGGGC TTCTGGACTG GATGGAGGAC CTGAAGACAT GAGGTGGAGG CA AGAGAAGATT CTCACCATCG CTGATTCACA CAAAAGCATT TCTCCAAGTG GT ACATGATTTC CCAAAGTGTT AGAGCTGAAG TGTGTTTCCT TGTGTATATA TA CCTTTATCCC TTCATCTGTG GATAGACAGG TGCAACCGTG TGGTTCCCCA CG	CAGGTAGA 120 TGCAGATG 180 CTGTGGTT 240
578	

TCATTGTGGT TTTCTGTCTG AAGAGTATCC CAGTATGTAC CTGTGGAGCA GCTTCTTAT CCCTTCTTAC TCGAG	360 375
(2) INFORMATION FOR SEQ ID NO:1463:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 174 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:	
GAATTTGGGC GGAGACACAA ATTCAAATCA TATCAACCTG GTAAAGAATT TGGATTTTAT TTTGAGTGTG TTAGTGAGTA TTGCATGGCT TTGAGCAGAG AAAGGATGAT TTATATGTTT AAAAGAGTGC TTTGCCTCTT ATATGTGGAA GAGATTGTAG GAGGAGGACT CGAG	60 120 174
(2) INFORMATION FOR SEQ ID NO:1464:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 122 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:	
GAATTCGGCC AAAGAGGCCT AGTTGCGGTT TAAATTTCCA AATGTATGGC ATTTGCTTGT TTTTTAAGTT GATTTCTAGT TTTATCACAT TGTGGTCAGA GAATGCTGAG AAAGAGCTCG AG	60 120 122
(2) INFORMATION FOR SEQ ID NO:1465:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 315 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:	
GAATTCGGCC AAAGAGGCCT ACTTGAGCTT TTTTCATGTG TATATATTTA TGCTTCTTTT CTAAAAAAAA TTGAGATGGA AATTCACATA ACAGAATTAA CTAAAGCATA CATTTCATTG GTATTTACTA CATTCACAAT GTTGTGCAAT CATTACCTCT CTCCAGITCT AAACATTTCA TCACCCCAAA AGGAACCCCT AAGCGGTCAC TCCCCACTCC ACTGTCTCCC ACAGCCCCTG GCAACCAGCA GTCTGCTTTG TGTCTCAATG GATTTACCTA CTCTTGATAG CTCTACAAAT GGAACAATAC TCGAG	60 120 180 240 300 315
(2) INFORMATION FOR SEQ ID NO:1466:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 175 base pairs  (B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

GAATTCGGCC	AAAGAGGCCT	AGGTAAGAGA	AACGACCAAT	TCTACCAGTT	ATTCTACAAT	60
GTGGGTTTTC	ACTGCTCTGT	TCACATGCCT	TATTCAGACT	TCTTGTGGTG	GTCAATTGCT	120
AGATGGTCTG	TTGGAATTAT	CTGCTGTCAT	ACATCCAAAA	AGGTCTCACA	GAGAG	175

- (2) INFORMATION FOR SEQ ID NO:1467:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 350 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

GAATTCGGCC	AAAGAGGCCT	AGAAGGACAC	CTCCATCCAT	TCCACGCAGT	TGCTCAAAGC	60
AGAAATTTTC	AGTGCAAGTC	TTGATGCTGC	GCCGTCCCCC	ACTCCCTACA	TCAGAACGCA	120
TCCCTCATCT	GGACTCCAGC	GGTGGCTTCT	TGATGCTGCG	CGGTCCCCCA	CTCCCTACAT	180
CAGAATGCAT	CCCGCATCCA	GACTCCAGCG	GTGGTGCTCT	ACCTGCACGC	TGTTGCCAAG	240
TCCAAGCTAC	CATACTCCTG	CCTGAGCTAT	GACAACAGCC	TCCTCACTGA	TCTCCCCTTT	300
$\mathtt{CTTCCCTTTG}$	CCTCCTCCAG	CTCATTTTTC	ACAGTGTAGA	ATGACTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:1468:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 419 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

GAATTCGGCC AAAGAGGC	CT ACTATACTAA	AATTCTGTGC	AAAAAGATGC	TTGAAATTAT	60
TGTAGAGACT GAATCTTI	GC TGCTTGTTAT	AAATATTGCA	GGGCATAAAC	CTTCCATTCA	120
TAGGTTCATC AGCTTTTA	TG ATTGGGAGTG	ACAGGGAGGC	AGCATTGCAG	TCCTTAGTCC	180
TAGGTGTGGT CTAGAATI	TA CCCTGTATTT	AAGTCACTTT	GGAATAGAAG	TTTTTTTTCT	240
CGGACAGGAT ACACTATA	TA TTTTTAAATC	TCCTCCCATA	GTCGTAGTGC	AGAGATATAA	300
ATAGAAGTAC AGGTAAGA	GA TGTCTTCTGC	CTTTCAAACC	CTTCCTAAGT	TTGTGTGCTG	360
CTTTAACTTT ATTCACAT	AG AGCAGTCTGT	TTTATTACTC	AGGATATGGG	CCACTCGAG	419

- (2) INFORMATION FOR SEQ ID NO:1469:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 612 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

GAATTCGGCC	AAAGAGCGAT	GGGGACAAAG	GCGCAAGTCG	AGAGGAAACT	GTTGTGCCTC	60
TTCATATTGG	CGATCCTGTT	GTGCTCCCTG	GCATTGGGCA	GTGTTACAGT	GCÁCTCTTCT	120
GAACCTGAAG	TCAGAATTCC	TGAGAATAAT	CCTGTGAAGT	TGTCCTGTGC	CTACTCGGGC	180
TTTTCTTCTC	CCCGTGTGGA	${\tt GTGGAAGTTT}$	GACCAAGGAG	ACACCACCAG	ACTCGTTTGC	240
TATAATAACA	AGATCACAGC	TTCCTATGAG	GACCGGGTGA	CCTTCTTGCC	AACTGGTATC	300
ACCTTCAAGT	CCGTGACACG	GGAAGACACT	${\tt GGGACATACA}$	CTTGTATGGT	CTCTGAGGAA	360
GGCGGCAACA	GCTATGGGGA	GGTCAAGGTC	AAGCTCATCG	TGCTTGTGCC	TCCATCCAAG	420
CCTACAGTTA	ACATCCCCTC	CTCTGCCACC	ATTGGGAACC	${\tt GGGCAGTGCT}$	GACATGCTCA	480
GAACAAGATG	GTTCCCCACC	TTCTGAATAC	ACCTGGTTCA	AAGATGGGAT	AGTGATGCCT	540
ACGAATCCCA	AAAGCACCCG	TGCCTTCAGC	AACTCTTCCT	ATGTCCTGAA	TCCCACAACA	600
GGCGCACTCG	AG					612

- (2) INFORMATION FOR SEQ ID NO:1470:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 220 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

GAAAAGCCAA	GACTTTAACT	TTCATTACAT	ATCTAATAGT	TGATATCACC	AGTTACCATT	60
TTGAATTTTG	TATAGTACTA	GGTTAGAACA	TTGCTTAATC	CTTTTAAAAA	AAATGCATTT	120
ACGTAGAACT	CGAGCAGGAT	GTTTGGCCCC	GATGTTTTTT	CTTCATACTC	TTCTGTCGCC	180
TCCTCCCATT	TCTGCACAGT	TCTCACCCAC	TACTCTCGAG			220

- (2) INFORMATION FOR SEQ ID NO:1471:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 349 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

GAATTCGGCC	AAAGAGGCCT	AGGGCATCAT	GCAGACACAT	CTGTTAAAGC	AGGAAAAAA	60
AAACCATGTG	GAAGATTAAG	CTAGGCAGAG	TGCCTGAAAA	GCCCTCTGCA	ATAAGTTGAG	120
CTGGAAAAAC	CTCCATATCT	AAAGATGCTT	TAATCATCTC	AAGAACACCA	ACAACATTTT	180
CTATTATAAT	ATAACTATGA	TAGATGTGAA	TCTACCTCTT	GGATTAAGGC	ATTAATTTA	240
TAGCTATCAA	ATTTTCACAG	ACACCATTTT	CACTACTCTG	AGTTGCATCT	CTAACAAGCT	300
TCTTTAGCCT	CTGCCTACAG	ATTTCAGTGA	CAAAGCCATT	CAGCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:1472:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 310 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

GAATTCGGCC	AAAGAGGCCT	ACAACAAACC	ATTCTTCAGC	ACCTTTGCAA	AAACATCTAT	60
GTTTGTTTTG	TACCTTTTGG	GCTTTATTAT	TTGGAAGCCA	TGGAGACAAC	AGTGTACAAG	120
AGGACTTCGC	GGAAAGCATG	CTGCTTTTTT	TGCAGATGCT	GAAGGTTACT	TTGCTGCTTG	180
CACAACAGAT	ACAACTATGA	ATAGTTCTTT	GAGTGAACCT	CTGTATGTGC	CTGTGAAATT	240
CCATGATCTT	CCAAGTGAAA	AACCTGAGAG	CACAAACATT	GATACTGAAA	AAACCCCCGC	300
GGTACTCGAG						310

- (2) INFORMATION FOR SEQ ID NO:1473:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 297 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

GAATTCGGCC	TTCATGGCCT	ACAACTTTAA	GATTAGCTAC	TTTGAATAAT	CTCAGTAGGT	60
TCTGGGGCAC	AGGAGCTGCC	CCTCTTGGTC	TGAGATTTGG	CCATGGGGTG	ATTAGGACAG	120
GTATAGTGGC	ACAGAGTGTA	AAAACCCCAT	AATGGTGTGG	ATTCTGGATT	GCTTAGTTTG	180
CATTTGACAA	GTGCATGCCT	GGGAGGAGGA	CTCCTCTTAG	TAAAGAGGAT	GGGAGGCAAG	240
AAGAGAGGCC	AGAGGCCAAG	ACAAGGTAAC	TTAGGCATAG	CATCAGGTTG	TCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:1474:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 510 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

GAATTCGGCC	TTCATGGCCT	AAAAAAGTAT	GCAACACTCA	GTTTATTTAA	TACTTACAAG	60
GGGAAATCAT	TAGAAACACA	GAAAACCACA	GTTGCAGCTC	GACATGGATT	ACAGAGTCTT	120
GGAAAAGTCG	GTATTTCACG	GCGTATGCCT	CCACCTGCTA	ACCTCCCAAG	TCTTAAAGCA	180
GAAAACAAAG	GCAATGATCC	TAATGTAAAC	ATTGTACCTA	AAGATGGCAC	AGGGTGGGCA	240
TCAAAACAAG	AGTAACATGA	AGAAGAAAA	ACACCAGAAG	TGCCACCAGC	ACAGCCAAAA	300
CCTGGGGTTG	CAGCTCCCCC	AGAAGTAGCA	CCTGCTCCCA	AATCATGGGC	CAGTAACAAG	360
CAAGGTGGGC	AAGGAGATGG	AATCCAAGTG	AATAGTCAGT	TTCAGCAAGA	ATTTCCCAGC	420
CTGCAGGCAG	CTGGGGATCA	GGAAAAAAAA	GAAAAGGAAA	CAAATGATGA	CAACTATGGA	480
CCTGGACCCA	GTTTACGTCC	ACCACTCGAG				510

- (2) INFORMATION FOR SEQ ID NO:1475:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 400 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

GAATTCGGCC	TTCATGGCCT	AATCCATTCA	TTTGATGGAC	ATTTTCTAAG	TACCTGTGAG	60
CCAGGTGCTG	CCATTTCAAA	GTCTCTTCTT	ACCACGCTCC	TCAGTGGCTA	GACATTTTCA	120
CGTGGCCAGA	AAGTCCCGAC	TCTTGCTGGG	CGTCCCTGGA	CAAGTTGCCT	TCCTCCTCTG	180
AGCTTGGCGC	TCCCCATCTG	TATAGTGGAG	${\tt ACCCTTGGCC}$	CCCCTCTGTA	CGGAAGGGCC	240
GATGCGAAGC	TGCAGTTAAA	AAAGGCTCAC	ATGCTCCTAG	CCTTGTGCAG	TCAGGAGGGG	300
AGACCAGGAC	AGTTGGAAAT	TATGATTGCA	AATGGCTTTG	CATTTTAGAT	CATTCGTGTG	360
TGTGGATCAG	AGAAACGCAC	AAGTTCCCTG	GCATCTCGAG			400

## (2) INFORMATION FOR SEQ ID NO:1476:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 465 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:

GAATTCGGCC TTCATGGCCT	ACCACATTTT	GTCAGCAGAG	AGCCTTTTAA	ACTTGGATTC	60
CAACTTCCTG TTGTCTAAAC	GGAACCCTCC	GAACGTAGGA	CTTATAGGGG	AAGCTGCTGT	120
GCATGTCAAA AAAACTACTA	ATCAGAATGA	GCTTTGTCAT	CCAGAGCCAG	AACTGCTGCA	180
GAAATTTTTA TAATTTTGCA	ACTTCTTTTT	TTACAAGGAA	CTTTTGTGCT	ACTACACATC	240
AGGACTTTTG AAGCATCCAA	TAAATCCATT	TAATAAGTAT	GAGCATGTGT	CTGAGTGGAC	300
AAGAAAGTGA AACCATCCAT	GCTACATTGG	ATAATTTTTC	CTCCCCCAGA	CTGGACAGGG	360
AATCTCAGCT TTCAAAACAG	AGTAACCTGG	CTCCACTTAC	AAAGCTGCAC	AGGCATTAAA	420
GATCGTGCTG CCTTTGTTAG	GCAGATTTGG	AGGGGAGAGC	TCGAG		465

- (2) INFORMATION FOR SEQ ID NO:1477:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 377 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:

GAATTCGGCC	AAAGAGGCCT	ACATGTAGCT	ATCCTAAGAC	GTATTTTATT	TTGAGCCACT	60
TTCTCAGAGG	GAATTGGGTG	GGTGTGGTCG	TAAGAACACC	TAGAAAATAG	GGGTGAAACC	120
TTTATGGGGC	CAGGGGAGCC	ATGGCAGAGG	GTGGAGTGGG	GGATAGAAGC	CTTCAGACTC	180
CTCCGCCCCA	GCCACTCTGC	ACCTGGGGCC	TTTCAGCTGT	TAAAATGAAA	AGCCAATTAT	240
CTTCTGTAAA	TGAGGGAAAA	AAAGAAGGAA	TAAAAGTGTC	TATTATGTAT	GCTGATATGC	300
ATAACACTTC	AAATAAAAGG	ATATATAAGC	ACTTGACAAA	TTGAGGGAGA	AGGAGGGGAG	360
AGTGCTGGGC	GCTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:1478:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 280 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

GAATTCGGCC AAAGAGGCCT	AGAGATTCAG	TTTATTCTAT	ACTCAGACTT	TGGTATCCCC	60
TTAGATGCCC ATGTCAAAAA	TGAGAAAGTT	GGTGACATGG	TATGGCATTT	TATTGCTTTT	120
TGTTTGTTTT CCATTGCTAC	TTTCACTCAA	ATTCCAAGGA	AATCACAGAA	GAAGGGCTTT	180
TGGTGACCTA AAAGTAGAAA	TGAAAGCAAC	AAAATGCATT	CTGTCCAGCA	GTACACTGAA	240
GACAAAAAT GTAGTTGAAA	AGTCTCAGGG	AGCGCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:1479:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 491 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

GAATTCGGCC	AAAGAGGCCT	AATTTGCTTT	GCCCAGTAGT	TGGAAAGTGA	ACTCGACTCG	60
TGATGGTTCT	CCTGTCACTT	TGGTTGATAG	CAGCCGCTCT	GGTAGAGGTT	AGGACTTCAG	120
CTGATGGACA	AGCTGGTAAT	GAAGAAATGG	TGCAAATAGA	TTTACCAATA	AAGAGATATA	180
GAGAGTATGA	GCTGGTGACT	CCAGTCAGCA	CAAATCTAGA	AGGACGCTAT	CTCTCCCATA	240
CTCTTTCTGC	GAGTCACAAA	AAGAGGTCAG	CGAGGGACGT	GTCTTCCAAC	CCTGAGCAGT	300
TGTTCTTTAA	CATCACGGCA	TTTGGAAAAG	ATTTTCATCT	GCGACTAAAG	CCCAACACTC	360
AACTAGTAGC	TCCTGGGGCT	GTTGTGGAGT	GGCATGAGAC	ATCTCTGGTG	CCTGGGAATA	420
TAACCGATCC	CATTAACAAC	CATCAACCAG	GAAGTGCTAC	GTATAGAATC	CGGAAAACAG	480
AGCCACTCGA	G					491

- (2) INFORMATION FOR SEQ ID NO:1480:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 523 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

GAATTCGGCC	AAAGAGGCCT	AATTCATTCA	GTCGTCATGA	GTTGAGTGCT	TACTACATGC	60
AAGGCACTCT	GCTAGTTATA	TTCTAATAAT	GCAGAGATAA	TTAGACATGG	TTCCCGCCCT	120
CAAGAAGCTC	ACAAAAGTAT	TCAGGAAATA	ATGCAGACTA	GTGATTTTGC	ATTAAAATTA	180
TTTTTGAAGG	AAGCAGACAC	AGCAGTATTT	ACCTGTAGGT	GGAGCAAGTA	ATAAGCCATG	240
CTGTGCAATA	TATACATAAA	GCTTCTGCTT	CTCATGGGAA	TTTAGTTACA	GTGCTTGGAA	300
TGAGAAGGGG	AAGGAAAGAA	TTAACAAATG	CCAAGATTTC	TGGAGCAGAT	TGTACAGCTG	360
TGACTTTGGA	AAACAGAAAG	TAAGACCCTC	AGAAAACCAA	TGAAGTCTAA	GAGAAATAAA	420
ATTTAGTGGA	CAGGTATGAA	AAGTGTAATT	GCGCCTAACT	ACCAGATGGA	GACCTTCAGA	480
ATGGGCTATC	CTTAGAGTCT	AGTACATCAA	GAGACCCCTC	GAG		523

- (2) INFORMATION FOR SEQ ID NO:1481:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 104 base pairs
    - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:
GAATTCGGCC AAAGAGGCCT AAAAAAAAAA AAAAAAGAAG ATATAAGCTA CTAGTATCAA 6 AAATGAAAGA GGGGCTGTTT CTACTGATCC TGCAGACACT CGAG 10
(2) INFORMATION FOR SEQ ID NO:1482:
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 337 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TC:OLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:
GAATTCGGCC AAAGAGGCCT AAACTGAACT AAGAGATGCA CCTGAGAAAA CCTTGGCTTG CATGGGTTTG GCAATGCATC AGGTGTTAAC TAAGGACCTT GAAAGGCATG CAGCTGAGTT 120 ACAAGCCCAG GAAGGATTGT CTAATGATGG AGAACAATG GTAAATGTGC CACATATTCA 180 TGCAAGGTGA GGAATTGAT GTATTAAAGT ATTACTTAGA ATGGGACATT GAAGGCCATT TAAGAATGA NACGCTCATT TTATAAAAAT GAGGAAATCA GTAAAAAGGA CATGAGTTCC 300 TTGCCATCTC ATTGATCATC ACACTGAACA ACTCGAG 330
(2) INFORMATION FOR SEQ ID NO:1483:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 168 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:
CGATTGAATT CTAGACCTGC CTCGAGAGGG CGCTGTTGAA TACCCAGTAT GATGGTCCTT AGCCTTCTTA GACCTTCCT GTACCACTAC CTCTATGCCT TTTGCCAAGT CCAAGTGTTC ACCAGAAATG GAACTGATGC CAGAAAGACT ACAGCAACAA TACTCGAG 16
(2) INFORMATION FOR SEQ ID NO:1484:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 478 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:
GAATTCGGCC AAAGAGGCCT AGCAACCGCG CCTGGCTGCC TTTTCATTTT TAAAAACGTC 60
585

AGTGTCGCTC	CCACACAACA	TGCAAACCCT	CCTGCCGAGC	TGCGACCTTC	GCCTGTCACG	120
GAACCTGGTG	CTGAGTGTGG	TGAGAGTGAA	TCCTGCAGCA	CGTGGCGCAC	TGTCGGCCTC	180
TTTCATGTTT	AGCTTTTGAT	TGTGCTTATT	GTCCATTTGT	ATTTCTTCTT	CTAAGTGTCT	240
GTTCAAGACT	TTTCCGTCTT	GGCTGGAGGT	GGGAGGTGCC	TGCTCCTGTG	TTTTCTGGCA	300
TCTTTCTCTG	CTGTCTTTGT	GTGTCTGCAC	TCAGGGAGTT	TCCCTGGGGT	GTGTGCCTAG	360
AGAGGTGCTG	GTTGTACATT	TCAACGTAGG	GACAGATTCC	CAGCGTGTCT	TTAAAGGAGC	420
TGTGCCGCTG	TGTGCTCACT	TGACTCGCCG	GCGTTCTTGT	TTCTCCAGGC	CTCTCGAG	478

- (2) INFORMATION FOR SEQ ID NO:1485:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 307 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

GAATTCGGCC	AAAGAGGCCT	ACACACTGCA	AGAACAGAGC	CAAGAACCTA	CCATGTACCC	60
TTTACTTGGA	TTTATCATTA	CTGTTTTGCA	CATTTGCTTT	ATCATTCTTG	TTATATTTAC	120
ATATAGTTCC	TTCCCCTTGG	ATTATTTGAG	AACAAACTGC	AGAACTCACA	CCTCTTTCCC	180
CGAAGAACTA	GGCATTAGCA	CATTACAAGA	ATACGATGAT	AGAGATCAGA	AGTTAAATGC	240
TGATGAGATA	TTCCTGTCTA	ATCCACGAAC	CTTATTTCAT	TGTCATCAGT	TGTCCCAACA	300
GCTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:1486:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 579 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

GAATTCGGCC	AAAGATTGCT	GTCCTTCAAC	GTGTTCATTA	TGAAGTTATT	AGTAATACTT	60
TTGTTTTCTG	GACTTATAAC	${\tt TGGTTTTAGA}$	AGTGACTCTT	CCTCTAGTTT	GCCACCTAAG	120
TTACTACTAG	TATCCTTTGA	TGGCTTCAGA	GCTGATTATC	TGAAGAACTA	TGAATTTCCT	180
CATCTCCAGA	ATTTTATCAA	AGAAGGTGTT	TTGGTAGAGC	ATGTTAAAAA	TGTTTTTATC	240
ACAAAAACAT	TTCCAAACCA	CTACAGTATT	GTGACAGGCT	TGTATGAAGA	AAGCCATGGC	300
ATTGTGGCTA	ATTCCATGTA	TGATGCAGTC	ACAAAGAAAC	ACTTTTCTGA	CTCTAATGAC	360
AAGGATCCTT	TTTGGTGGAA	TGAGGCAGTA	CCTATTTGGG	TGACCAATCA	GCTTCAGGAA	420
AACAGATCAA	GTGCTGCTGC	TATGTGGCCT	GGTACTGATG	TACCCATTCA	GGATACCATC	480
TCTTCCTATT	TTATGAATTA	CAACTCCTCA	GTGTCATTTG	AGGAAAGACT	TTATAATAAA	540
ACTATGTGGC	TAAACAATTC	GAACCCACCA	GTCCTCGAG			579

- (2) INFORMATION FOR SEQ ID NO:1487:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (5) 10102001. 121100
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

GAATTCGGCC	AAAGAGGCCT	AGATTGAATT	CTAGACCTGC	CTCGAGAGTC	ACCCTTAGTT	60
TGCCATTGTG	CCAGCTAGTG	ATATTGCTGA	TGTTTTTGT	GGGTGTTCTT	TTAGCAAAAC	120
GTGAATGAAT	GCATGTTTAC	AGGGATGCTC	TGGACTGGAG	GATGGTGAAA	TCCATCGTGG	180
TTGTCCCTCT	CCCTGAATGT	CCTTTTGTAG	CCAGGGCATC	TTTCCAATAT	GAATTATTAA	240
GCCTTAACTT	ACATTTTTGC	ATAACTTATA	ACTCTCCATT	ATATATTTGG	TTACATTTCT	300
TAGATGTTTT	CAACATTCTT	TATTAAAGTT	ATTTTATCAG	CATCCGCTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:1488:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 422 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

GAATTCGGCC	AAAGAGGCCT	ACAAATGGGC	AGAAGTGAAA	CAGTCTTGTG	AGATACCTGT	60
TTTTTAAAAC	TCCATTTTAG	AAAAGGAATT	AACTAGGACT	TTATATCTCT	TCGTTCAATA	120
TAATTTTAAA	GAAGAATTGT	TGAAAAGTAG	ATATGTTTTG	CCATTTGCTG	AGAATATTTT	180
GTACGTTAGC	TTGTCTCTTA	CAAAAACTAA	ATGTGTTCCT	ACTTCTGATA	ATGTATGTCA	240
ATTTAAAATT	TGGAATGGCC	AAGATAAGTT	GCTCTGCATC	TGTCCTTCAT	ATGGCTCCTG	300
AGCACAGCTC	AGTGACTGGC	CCTTGCAGTG	CTTCTACCGT	TGTAATGGGT	AAAACCAGGG	360
GAAACTGCCT	TGCTCTTGAG	CTTGAGCAGG	TTAATCAAAA	GGATAGAGCT	TCCACTCTCG	420
AG						422

- (2) INFORMATION FOR SEQ ID NO:1489:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 293 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

GAATTCGGCC	AAAGAGGCCT	AGAGAAAGAG	AGAAAGAAAG	GAGGGAAGGA	AAGGAAGGAA	60
GGAAGGAAAG	AAGGAAAGAA	GGAAAGAGAG	GAGACTGAAG	GGCCAAGGAG	GGCATACAAT	120
GGAAGATGAG	AGCTGTGCTC	CCGGGAGGCT	TGTACTCATC	AAGAAAGAAA	GGAGAAAGAG	180
GGGGAAGAAA	AGAAAAAAAA	AGAATAAAGA	AAGGAGAGAT	GAAGGAATAA	AGGAAAAAA	240
GTAGAAAGGA	AAGAAGGAGA	AGGGAGAGAA	GAAAGTAGGA	AGGAGAACTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:1490:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 250 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

GAATTCGGCC	AAAGAGGCCT	AGTGCAACTA	CAGATAAGTA	AACTTCGACT	GGGTTTAGTA	60
ACACCTGTCT	TTAATATTTG	TCAGTGTACC	TACATTGATA	ACATTGACCT	TTGGAAAAAT	120
TGGACTTGTA	TTGTGTTATT	TCTCTAGCAT	ATTAGTCCTA	AAAAAGTGTG	AGTAATAGGA	180
GATGGAGAGG	TGTTTGTGGA	TTGTCATTCT	GTGGTTCCTA	CAGCATTCAA	GTTGCGTCCG	240
TACGCTCGAG						250

- (2) INFORMATION FOR SEQ ID NO:1491:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 435 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

GAATTCGGCC	TTCATGGCCT	AATTCTTAGA	AATAAAGCCA	CTATCATGCA	GGTTATTTAC	60
AAGTAAAAAC	ATGGAGTCAG	CCCAGTAGAG	AAACGTTCAA	ATAGTGTGGC	TCCTGCTCTG	120
CCACGTTCTG	TTTATGACTT	TGGATATTTT	ATTTATCCTT	TCTGGGGTAG	TTTTTCAACT	180
TTAAGGTCCT	AATAAACTTT	TAGATTTTAT	GACCTGTCCT	CTTTAGCCCT	GTAAGATTTA	240
AATATTATAA	AGAACCTGAT	TTCAAAGACA	CTGGTAAACT	TGGACAACTA	AACAAGTCCA	300
AGTATGGTAC	TTATTTGTGT	GTGTGCATAT	ATTAACCTTA	TGCATATGCT	GTTTTCACAC	360
CTATTTAAAC	TGTTTTTGAA	AAACGTATAT	ATCAGTTTTT	GGAAAACAGA	AGAAGATTTT	420
AAACGGCTAC	TCGAG					435

- (2) INFORMATION FOR SEQ ID NO:1492:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 360 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

GCGATTGAAT	ACATGTTCAA	TAAGGACAAT	GGACAGGCAC	CTTTTACCAT	CACTCCTGTG	60
TTTTCAGATT	TTCCAGTCCA	TGGGATGGAG	CCCATGAACA	ATGCCACCAA	AGGCTGTGAC	120
GAGTCTGTGG	ATGAGGTCAC	AGCACCATGT	AGCTGCCAAG	ACTGCTCTAT	TGTCTGTGGC	180
CCCAAGCCCC	AGCCCCCACC	TCCTCCTGCT	CCCTGGACGA	TCCTTGGCTT	GGACGCCATG	240
TATGTCATCA	TGTGGATCAC	CTACATGGCG	TTTTTGCTTG	TGTTTTTTGG	AGCATTTTTT	300
GCAGTGTGGT	GCTACAGAAA	ACGGTATTTT	GTCTCCGAGT	ACACTCCCAT	CGATCTCGAG	360

- (2) INFORMATION FOR SEQ ID NO:1493:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 271 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

ACTTTCTGTA ATAGAGATCC CATGGTATTA	TTCATGGCCT AAGCAGACAA TATAGTAGTA GTCCCTAAAC AAACAACAAA AAATCCTAGT AAGAGAAAAT AAGCCATTTT TCACCATTGT AGAAGCCCTT TTCAGTCTGG TTGCAGTATT GCTGTATGCC CACAGCTCGA G	AATCTTAAAC GGACCCAAAT	TTTTACATTA AAATCATAGA	60 120 180 240 271
(2) INFORMA	ATION FOR SEQ ID NO:1494:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 310 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO	:1494:		
CCCCAGGGTC AAAGTTAGAT GTTTCTCCAA	TTCATGGCCT AATGGGTCAG AAATTTGGGC TCTCACAAGG CTGCAATCAA AGGGCTGACT TGGGGAAGGA TCTGCTTCCA AGCTCACTCA GGTCGTTGGA CTAAGGGTCT CAGTTCCTCA TCTTGCCATG TGGGCCTCCC CAGCATAACT	AGGACTTGGA GTAGTTACTG CTGACAGTTG	ATCTCATTTG GCAGGATTAG GCCTGAGGCT	60 120 180 240 300 310
(2) INFORMA	ATION FOR SEQ ID NO:1495:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 138 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO	:1495:		
	AAAGAGGCCT ACGTCGATTG AATTCTAGAC GATTGTCTGC CCTTCCTCTT CCTCTTCTCT CCCTCGAG			60 120 138
(2) INFORMA	ATION FOR SEQ ID NO:1496:			
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 102 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO	:1496:		
	AAAGAGGCCT ACAAAATTGT TCCTTTTACCCTAGTGCCCTT TTTTTTTCTC TTTTTTAGCCC		TTCTGAAATG	60 102
(2) INFORM	ATION FOR SEQ ID NO:1497:			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

GAATTCGGCC	AAAGAGGCCT	ATTTGTTTCT	TTGTACTGCC	TAACTTTAGA	AAGACCTGNA	60
ANCGGTANCA	TGAAAACATT	TTTAGAGAGA	ATTACCAGGC	ATTTTTGGTA	GAATGAGTGT	120
TTAATGGAAC	AGTCCAGAGA	ACTCATCAAA	${\tt GATGTTTATT}$	AAAACGCGCA	GACCTGCTCC	180
AATTAAGGGC	CCAGTCAGTG	GTGTTAACAG	TGAAGGGACT	GTTCCAGAGG	CGTGCTGCAC	240
GGGACGCCCA	CCCCAAATAC	AAATGGTTTG	${\tt CCAGTAGCTC}$	ACAAATGAAC	CCCATTGCCT	300
TGCACTTAAG	CTTCCTGAAG	CACATACATA	TCCTGCTTTG	TGCTTTCCGC	CCTATAGTAA	360
ACGCAAACCA	ATGGAGATGT	GAAGCAATCT	AATAGCAACA	AGGCAAACCT	CTACTTCCTC	420
TAAAGAGGAT	TGCATCCTCT	TGCTATCTTT	GCCGATGCTC	TCCTACAGAC	CCATCCGCTC	480
GAG						483

- (2) INFORMATION FOR SEQ ID NO:1498:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 144 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

GAATTCGGCC	AAAGAGGCCT	AAAATTTCAA	TAGGCTATAG	AGTTTTCCAT	GAGAGTGTGT	60
GTGTGTGTGT	GTGTGTGTGT	GTGTAAAGAA	$\mathtt{CTCTTACATT}$	TCAGTGAGAA	AATATTTTCA	120
TTGAAAGGAA	ACACAGAACT	CGAG				144

- (2) INFORMATION FOR SEQ ID NO:1499:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 418 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

GAATTCGGCC	AAAGAGGCCT	AAAATAACTG	TCCAATTAAC	TGAACACTGA	GGTAGCTGGG	60
TACAGACTTT	AGCGGCTACA	TTTGACAAAC	ATTGCAATTA	CAAGCAGCAA	CACAAACCAA	120
CCTTGGGATG	GGGATAGAAA	TCTTTTCNTT	CTTCNTTCTT	GGGGGTTTGA	GACAGAGTCT	180
CGCTCTGTCA	CCCAGGCCGG	AGTGCAGTGG	CGCAATCTCC	GCTCACTGCA	AACTCCACCT	240
CCTGGGTTCA	AGTGATCCTC	CTGCCTCAGC	CTCCCAAGTA	GCTTGGATTA	TGGGTGCCCA	300
CCACCATGCC	TGGCTAATTT	TTGTATGTTT	GATAGAAACG	GTGTTTCACC	CTGTTGACCA	360
GGCTGGCCTT	GAGCTCCTGA	CTTCAGGTGA	TCCACCTGCC	TCAGCCCCCC	GACTCGAG	418

- (2) INFORMATION FOR SEQ ID NO:1500:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 337 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

GAATTCGGCC	AAAGAGGCCT	ACAAAGACCA	AGGTATCACA	TTCTGCCATT	AGCTGCTACC	60
TCTCCCTTCC	CCATTTTCAG	ACAGATTGAG	CCCACTTTTT	GTGTCCTCCT	CTGCTCTTAA	120
GCTGTTTCTC	ATCGTGGGTG	CTCAGCAACT	TGTCTGCTCT	CACTCTAGTT	TCTATTTGCT	180
TCCCTGAAAT	TAGCCTTTAA	CTATGCCCAG	ACAAGCCAGA	GCCTTGCCTA	AACTTCTAAT	240
TCCTCTGTGC	TTCTTAGTGT	ATCCTTTCTG	CCTGCTTGCC	TGCCTGCCTT	CCTGCCTGCT	300
TGCCTGCCTT	ACTGACCCTT	TGCCCCACGC	TCTCGAG			337

- (2) INFORMATION FOR SEQ ID NO:1501:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 105 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

GAATTCGGCC AAAGAGGCCT AAACCGTCGA TTGAATTCTA GACCAGCCTC ATCTCCTGTT 60 CCTCTCTCCC TCCCAACTAT GTTGGCCTCC CTGCTGCTC TCGAG 105

- (2) INFORMATION FOR SEQ ID NO:1502:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 701 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

GAATTCGGCC	AAAGAGGCCT	ACTGTGAACC	TAAAACTCCT	ATAAAGAAAA	GTAAAGTCTT	60
AAAAACAAAC	AAATACACAG	CAACAATCTT	ATTTTCCCCA	GCCTGTCTTA	TGTTAGGGTG	120
CAGATGTGAT	TTCTGTGTGG	CTAATCAGAT	GCCCTTGTGT	GAGAGACTGA	TTTGAACAGA	180
GGCAGGGGCA	TCCATCTTTC	TAGTGTCAGT	CACAGCAGAA	GCAGTGAGGT	CCTGGTGTCT	240
GTCGCTGCAG	TGGTGGCTTT	TGATACAGGA	GTTCCCTGAT	GGCAGTAGCT	TCTTTGTGGG	300
TTCAGTTCTG	TTGTGTGGTT	CTGCAAGTTC	AGCTTAGAGT	CTGTTTCTTC	AGCTGTTTCA	360
ATGACCCTCT	GAGCTGTCTA	CCATGAAAAA	TTCTATCCTG	CTTACACTAA	TTAGAGCCAA	420
TCCTGTTATT	TACAAATGAA	TATCCTGACC	AGTAATGAAG	GTCTAGACTT	AACTGTAATA	480
TTTTATGACT	TAAATTGTTG	GCATATGTGA	AAACTTTTTG	TTTATTCTAA	ACTTTTTTGT	540
TGTTGTTGTA	AAATAAAACA	TTTATGAAAA	GCGCACCAAA	AAGGATAACA	AATGAGAGTA	600
ATGCAACATA	CAGGCACCAG	CAACTCAGGC	CAGGGAGATG	ATATATGAGC	ATCCCCAATC	660
TCCCCTTTAC	ACTCCCTCAA	ATAACTCAAT	CAAGACTCGA	G		701

- (2) INFORMATION FOR SEQ ID NO:1503:
  - (i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 257 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEO ID NO:1503: GAATTCGGCC TTCATGGCCT AGGAACTAGG TGACTTTGGG GCTCATCTCA CAAGTTTCCT 60 TACACTTAGG GATCAGTCTT TTGCTTCCTG TTGTCCTCTG CCTGAAAGTA GTTGCCAAGT 120 TGTACTGTTT TATATATCCA CCACAGCATG AGTTAAACCA AAGTCTGGAT CAGCAGACTG 1.80 CCAGATTTTT TTTTAACAAA TTTATTAATC AATACATTTT GTCCATGTCT ACAGTTGTTT 240 ATGGGGGAGA ACTCGAG 257 (2) INFORMATION FOR SEQ ID NO:1504: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 277 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504: GAATTCGCCC TTCATGCCT AGGGGACCTT GGGAGAATGT AATCCCTGCC CCTAGTCTCA 60 GTTTCTGCAT CCACGGAAGA GGGGTGAAGA TGGTCCCTAC CCCTCCAGAA TGTTCTTTTT 120 TTTTTTTT AAAAAAAAA AAAAAAAA AAAGTACGTT ATGTTTTCAG ÁTAAGAACAC TTCTTCATGG ATGACTTGAA ATAATTGCCA TGGTCCCTAA GTTTTCCTCT CTGTAGATGA 240 ATGATATAGC TCAGTATCTA AGCAGTGGAT CCTCGAG 277 (2) INFORMATION FOR SEQ ID NO:1505: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 341 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505: GAATTCGGCC TTCATGGCCT AGACCTGCCT CGAGCCTCCC AAGCTGCTGG TATTACAGGC GTGAACCACT GCACCTGGCC TAATACGATA TTCTTACAAT TTAAAAAATG AAAGCAGAGG 120 AATGGTGGCA GGGAAGCTGA CATTTTAAGA GTTCACTTCC TTGTAGTTAT CACAGTTAAT 180 TCTTACTGTT AGAATAAGTG GTAACTTGCC AAGGTCACAT TGCTAGATGT CAGAGCAGAA 240 300 GTTAGTGTTT ATTGAACACC TATTGTGTTC TGGCCCTCGA G 341 (2) INFORMATION FOR SEQ ID NO:1506: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 270 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

GAATTCGGCC	TTCATGGCCT	AGGCATTTTG	TCTCTAGAAT	TACCCACCCG	TTCCTGCGCT	60
CTACGGTTCT	CCATGCCCCC	TCCAGTTTGG	GGGTCTAAAC	CGAACAGGAG	AGGTGCAGGG	120
GACCAGGAGG	TGTCCTGGCA	CAAAGGTTCG	GGGGTCTCCC	TGGCAAGGGG	TCCCAGGGCC	180
TGGAGCCCGA	GGCCCAGCCA	AAAGCACACA	GCATCAAAAC	ATGTTTTTAG	TGGGAAGCTC	240
CAGGCCCTGC	CCCTCCCCGG	GGGCCTCGAG				270

- (2) INFORMATION FOR SEQ ID NO:1507:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 462 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

GAATTCGGCC	TTCATGGCCT	AGAGCAGGAA	GATTGTGTGA	GTGCTGGGGT	TTGGGGGTGC	60
CCAAGTTGGG	AACCAGTGGA	GGGAGAGAGA	GGTAGGAGGT	AGATGGATGG	AGATCAAAGG	120
CCAGGCCTGT	GGCCAAGGGG	GCTGCTAACC	CTTCAACCCT	GTGTTAGCCT	GTACACTCAC	180
CAGGCCAGGC	TCAGCAGGCG	GGCTGTTCAC	CTCCTGGCAG	CAAATGGTCC	AGAATGTGCC	240
CTCGCTGCAG	CCCAGCTGGC	TCCAGAAGGG	GGACCACAGA	GGCTGGAGCT	ATGCATGCAC	300
AGTGCTTTCT	CCCAACCTTG	CTTCTGAGAA	AAGTGTCCCT	GCGAGGGCCC	TGGAGGAGGG	360
AGCTAGGGAC	CAGCAGAAGG	GCCTAGGTTT	CTGTAGCATC	ATTTTTAGCC	CTGGCTGAAT	420
CTGGGAAGCA	CCTGGTGGCT	TTAACATTCC	CGTTAGCTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:1508:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 694 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

GAATTCGGCC	TTCATGGCCT	AGTCACAATC	CACTTAAAGA	AGTTTGGTTA	TATTTCAGTG	60
AAAATTTTCT	TCCAGAGTAG	GTTTTTTTC	GTGGGTTGGG	GGGTAACTTT	ACTACAATTA	120
GTAAGTATGG	TGCAGAATTT	CATGCAAATG	AGGAGTGCCA	GCAGTGTGAT	AATTTAAACA	180
TATTTAAACA	AAAACAAAAA	AAATGAATGC	ACAAACTTGC	TGCTGCTTAG	ATCACTGCAG	240
CTTCTAGGAC	CCGGTTTCTT	TTACTGATTT	AAAAACAAAA	САААААААА	TAAAAAAGTT	300
GTGCCTGAAA	TGAATCTTGT	TTTTTTTTAT	AAGTAGCCGC	CTGGTTACTG	TGTCCTGTAA	360
AATACAGACA	CTTGACCCTT	GGTGTAGCTT	CTGTTCAACT	TTATATCACG	GGAATGGATG	420
GGTCTGATTT	CTTGGCCCTC	TTCTTGAATT	GGCCATATAC	AGGGTCCCTG	GCCAGTGGAC	480
TGAAGGCTTT	GTCTAAGATG	ACAAGGGTCA	GCTCAGGGGA	TGTGGGGGAG	GGCGGTTTTA	540
TCTTCCCCCT	TGTCGTTTGA	GGTTTTGATC	TCTGGGTAAA	GAGGCCGTTT	ATCTTTGTAA	600
ACACGAAACA	TTTTTGCTTT	CTCAAGTTTT	CTGTTAATGG	CGAAAGAATG	GAAGCGAATA	660
AAGTTTTACT	${\tt GATTTTTGAG}$	ACACTAGACT	CGAG			694

- (2) INFORMATION FOR SEQ ID NO:1509:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:

GAATTCGGCC	TTCATGGCCT	AATGAGGTTC	TATCTAGAGG	TGATGGGAGA	CAGTGACAGA	60
TCATCAGGCA	TTAGATTCTC	ATAAGGACTG	CGCAACCTAG	ATCCCTTGAA	TGAACAGTTC	120
ACAATAGGGT	TCACTCTCCA	ATGAGAATCT	AATGCTGCCG	CTGATCTGAC	AGGTGCCAGA	180
GCTCAGGCGG	TAATACGAGA	GGCTGGAGAT	ACAGATAAAG	CTTCAGTTGC	TTGCCCGCCA	240
CTTACCTCCT	CTTGTGCGGC	CCAGTTCCTA	ACAGGCCACA	GACCGCTACC	AGTCCATGGC	300
CTGGAAGTTG	GGGACCCCTC	TACTGGGATA	TTTATAATTG	CATATGTGGT	TACCTAATAT	360
TTCCATGATA	CAACACTGGT	CTAGATTCTA	GGCCATTCTC	CTTCAAAAAG	AACCCTGCTT	420
CCTTACAGTT	TTACTGTTTA	GCAGCAATGT	TTTCTACCCC	TTCTTAAAAT	TTTCAGCCAC	480
CACACTCGAG						490

- (2) INFORMATION FOR SEQ ID NO:1510:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 313 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

GAATTCGGCC	TTCATGGCCT	ACTCTCTCAT	TCCTACCCTC	CTCCCCTCCA	CTCACGCTCC	60
TCCCAATCCC	CAAGGTCCTC	TCATTCCCAC	CTTCCTCCCT	TCCTCTCCTC	ACGCTCCTCC	120
CTATCCCCGA	GCTCCTCTCT	CATCCCTACC	CTCCTCCCCT	CCACTCACGC	TCCTCCCAAT	180
CCCCAAGGTC	CTCTCATTCC	CACCTTCCTC	CCTTCCTCTC	CTCACGCTCC	TCCCTATCCC	240
CGAGCTCCTC	TCTCACTCCC	TCCCTCCTCT	CATGCTCCTC	CCCCCTCTCC	TCATGCTCCT	300
CCCCATCCTC	GAG					313

- (2) INFORMATION FOR SEQ ID NO:1511:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 354 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:

GCCGGGTGGG	CCGGAGGTGG	CGCGGCCGCA	CGGCTTTGTT	CCGGAAAGCC	CTTAGGTGGA	60
GAGCGATGTG	GGGCGCGCA	GGGGGATCGC	GTAGAGGAAC	CTTCGCGCAC	CGCCTCTCCG	120
GGTCTGGGAA	TCTGCTGAAC	TCCTTGCCTC	TCTTGGGGTC	CCTCGAACGC	CCCAGCTAAG	180
AAGGGCGGG	GCCTTGCCAG	GGCGCGAGCA	ACATGACGTT	CAAGGTCTTC	CTGTGGCTTC	240
TGTAAAGAAA	TGTTCACGTG	GGAGCCTGTC	CACATGGGCT	GTACTAAGGA	TCTGGCACGA	300
GGAAGAAATA	TCACTGCAGA	ACCTGAAGCC	CTCCGTTGGA	AGGGTCACCT	CGAG	354

(2) INFORMATION FOR SEQ ID NO:1512:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 407 base pairs

  - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

GAATTCGGCC AAAGAGGCCT	AGAGCAGCTT	GGCTAAAAGT	AAGGGTGTCG	TGCTGATGGC	60
CCTGTGCGCA CTGACCCGCG	CTCTGCGCTC	TCTGAACCTG	GCGCCCCGA	CCGTCGCCGC	120
CCCTGCCCG AGTCTGTTCC					180
CTCTGCCTTG ATGTTGCTCC	CCTGCCGCCC	AGTTCTTACT	TCTGTGGCCC	TTAATGCCAA	240
CTTTGTGTCC TGGAAGAGTC					300
TGGGGGCCGA GACCACACAC	GTGGGAACAA	GGACAGGGGG	ATTTAAGCAG	TCAAAAGGAA	360
AAACATGTTA AGACCCTAGA	CTTGTATATT	GACACACAGA	ACTCGAG		407

- (2) INFORMATION FOR SEQ ID NO:1513:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 422 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

${\tt GAATTCGGCC}$	AAAGAGGCCT	ACATTCATAC	AATTACAGAA	TTCAAATATT	GCAAAAGGAT	60
GTGTGTCTTT	CTCCCCGAGC	TCCCCTGTTC	CCCTTCATTG	AAAACCACCA	CGGTGCCATC	120
TCTTGTGTAT	GCAGGGCTAT	GCACCTGCAG	GCACGTGTGT	ATGCACTCCC	CGCTTGTGTT	180
TACACAAGCT	GTGGGGTGTT	ACGCATGCCT	GCTTTTTTCA	CTTAATAATA	CAGCTTGGAG	240
AGATTTTTGT	ATCACATTAT	AAATCCCACT	CGCTCTTTTT	GATGGCCACA	TAATAACTAC	300
${\tt TGCATAATAT}$	GGATACGCCT	TATTTGATTT	AACTAGTTCC	CTAATGATGG	ACTTTTAAGT	360
TGTTTCCTTT	TTTTTTTTTT	TTTGCTACTG	CAAACGATGC	TATCTAGGCC	TCTTTGGCCG	420
AA						422

- (2) INFORMATION FOR SEQ ID NO:1514:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 485 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

GAATTCGGCC	AAAGAGGCCT	ATGGAAATTC	AAGACCTGAT	GTTTGAGGAG	ATGAGGGAAA	60
CTCTTAAAAA	TGACCTAAAA	GCAGTTTTAG	GAGGAAAAGC	TACAATACCT	GAGGTAAAGA	120
ATTCAGAGAA	CTCCAGTAGT	AGGACAGAGT	TTCAGCAAAT	AATCAATTTA	GCATTACAAA	180
AAACAGGGAT	GGTAGGGAAA	ATAGAAGGAG	AAAACTCTAA	AATAGGTGAT	GATAATGAAA	240
ATTTAACCTT	TAAATTAGAA	GTAAATGAGC	TGAGTGGTAA	ATTAGACAAC	ACTAACGAAT	300
ACAATAGTAA	TGATGGTAAG	AAATTACCCC	AGGGTGAATC	ACGAAGTTAC	GAAGTCATGG	360
GAAGTATGGA	AGAAACCTTA	TGCAATATAG	ATGACAGAGA	TGGAAATCGC	AATGTCCATT	420
TAGAATTTAC	AGAAAGAGAG	AGTAGGAAGG	ATGGAGAGGA	TGAATTTGTC	AAAGAAAAAC	480

485

TCGAG

(2) INFORMATION FOR SEQ ID NO:1515:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 400 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:	
GAATTCGGCC AAAGAGGCCT AGGCACAGAA GGGTGGTGAG TGTGATCAAA TCTAGTCTCA CTCCCACTTT TTAGTCTCAC TCCTACTTTT GTCCACCACC CAGGCACGGA GAGAAAGGAA TGTTTAGCAC AAGACACAGC GGAGCTCGG ATTGGCTAAA CTCCCATAGT ATTTATGGTG GCCGCCGGC GGGGCCCCAG CCCAGCTTGC AGGCCACCTC TAGCTTTCTT CCTACCCCAT TCCCGGCTTC CCTCCTCCTC CCCTGCAGCC TGGTTAGGTG GATACCTGCC CTGACATGTG AGGCAAGCTA AGGCCTGGAG GGTCAGATGG GAGACCAGGT CCCAAGGGAG CAAGACCTCG CGAAGCGCAG CAGCCCCGGC CCTAGGCCTC TTTGGCCGAA	60 120 180 240 300 360 400
(2) INFORMATION FOR SEQ ID NO:1516:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 145 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:	
GAATTCGCGG CCGCGTCGAC GTCGACGCGG CCGCGAATTC GGCCAAAGAG GCCTACCCAT GTCAATCAAG ATGGGTGATT ATGAAATGCC AGACTTCTAA AATAAATGTT TTGGAATTCA ATGGGTAAAT AAATGCTGGC TCGAG	60 120 145
(2) INFORMATION FOR SEQ ID NO:1517:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 277 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:	
GCTGGACCTC CTGTGCAAGA ACATGAAACA GCTGTGGTTC TTCCTTCTCC TGGTGGCAGC TCCCAGATCG GTTCTGTCCC AGGTGCAGCT GCGGGAGTCG GGCCCAGGAC TGGTGAAGCC TTCGGAGACC CTGTCCCTCA CCTGCACTGT CTCTGGTACT TCCGTCAGAA GTGTTAGTTA CGACTGGAGT TGGCTCCGGC AGTCCCCGGG GAAGGGACTG GAGTGGCTTG GAGAGATTGA TTACAGGGGG AGAGGCAATT ACAACCCGTC CCTCGAG	60 120 180 240 277
(2) INFORMATION FOR SEQ ID NO:1518:	
(i) SEQUENCE CHARACTERISTICS:	

- (A) LENGTH: 161 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

GAATTCGGCC A	AAAGAGGCCT	ACTCATGCAC	CTAATTGGAT	CCTATCTTTG	TGTTGTTAGC	60
TGGTTATTAT G	CAGACTTTA	TTATGTGGTT	GTTTTATAGT	GTCCATAACC	TATGTACTTA	120
AGTTTGTTTT T	TGTGGTGGCG	CTTCCAATTA	$\tt GGGCTCTCGA$	G		161

- (2) INFORMATION FOR SEQ ID NO:1519:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 561 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

GAATTCGGCC	TTCATGGCCT	AATATAAAAC	AATGTTTTTC	AAGGCATTAT	ATAATAGGCT	60
AAGGACAGTG	ACCTCCAAGA	GACAGCAAAC	AAGGTAATAC	CTGTGACTGC	TCCAGCTTAC	120
TGCCTTGAGA	GAATTAATAG	TAGGTTTGTG	GTACAGGGAG	GGAGAATCCA	GTCAGAGCCC	180
AGCGGACTTG	CTGAATTAAG	GAAATGGAGC	TGAGAGTCCA	GAGAGACCAA	CATGGCTAAA	240
GTTGTCATGA	CAGAGCACTC	AGAACTAGAG	AGCTGCACAG	CAACATAACC	TAAGAGCTCT	300
GAAGATAATC	TCCCTCAAAT	ACTCAGCTGA	GTACTGATCA	ACATATATGT	GTGAGGAAGC	360
TATCTGAGGC	TGACAAAGAA	CTGCCTGAAG	AGATTAGAGG	GAACAGTACT	TGGCACTCAC	420
ACAGAATTGG	AAACTGTACC	TGTTCCCACC	AGCCAAACTG	GAAAAACCTC	AGGATTCATG	480
GGGTACTCAG	AAAGGACTTG	CATCAGGTAT	GGGGAATAAT	TAGCCCTAGA	CAGAGCACTG	540
CTCTAATCCC	ATCCACTCGA	G				561

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEO ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145,

SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181. SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEO ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298,

SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307. SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEO ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEO ID NO:405, SEO ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451,

SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478. SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604,

SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757,

SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEO ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775. SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784, SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829, SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874, SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892, SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910,

SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937, SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973. SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEO ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID

NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEO ID NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEO ID NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEO ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEO ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID

NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID

NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ ID NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ ID NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID

NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, SEQ ID NO:1500, SEQ ID NO:1501, SEQ ID NO:1502, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID NO:1505, SEQ ID NO:1506, SEQ ID NO:1507, SEQ ID NO:1508, SEQ ID NO:1513, SEQ ID NO:1514, SEQ ID NO:1515, SEQ ID NO:1516, SEQ ID NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;

or a complement of said sequence.

## 2. An isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ

ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100. SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEO ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEO ID NO:234, SEO ID NO:235,

SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388,

SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEO ID NO:451. SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEO ID NO:455, SEO ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541,

SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604. SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEO ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694,

SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739. SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEO ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766. SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775, SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784, SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829, SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEO ID NO:846, SEQ ID NO:847,

SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874, SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892, SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEO ID NO:920, SEO ID NO:921, SEO ID NO:922, SEO ID NO:923, SEO ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937, SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEO ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000,

SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID

NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID

NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEO ID NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEO ID NO:1300, SEO ID NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID

```
NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEO ID
NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID
NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEO ID
NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEO ID
NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID
NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEO ID
NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEO ID
NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID
NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID
NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID
NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID
NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID
NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID
NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID
NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID
NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID
NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID
NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID
NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID
NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID
NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID
NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID
NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, SEQ ID NO:1500, SEQ ID
NO:1501, SEQ ID NO:1502, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID
NO:1505, SEQ ID NO:1506, SEQ ID NO:1507, SEQ ID NO:1508, SEQ ID
NO:1509, SEQ ID NO:1510, SEQ ID NO:1511, SEQ ID NO:1512, SEQ ID
NO:1513, SEQ ID NO:1514, SEQ ID NO:1515, SEQ ID NO:1516, SEQ ID
NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;
```

or a complement of said sequence.

3. An isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:1

NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEO ID NO:126, SEO ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,

SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244. SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325,

SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEO ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEO ID NO:361. SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEO ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEO ID NO:432, SEO ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478,

SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541. SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEO ID NO:549, SEO ID NO:550. SEQ ID NO:551, SEQ ID NO:552, SEO ID NO:553, SEO ID NO:554, SEO ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631,

SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775, SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784,

SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820. SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829. SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874, SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892, SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937,

SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEO ID NO:999, SEO ID NO:1000. SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEO ID NO:1048, SEQ ID NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID

NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEO ID NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID

NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID

NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ ID NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ ID NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID

NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, SEQ ID NO:1500, SEQ ID NO:1501, SEQ ID NO:1502, SEQ ID NO:1503, SEQ ID NO:1504, SEQ ID NO:1505, SEQ ID NO:1506, SEQ ID NO:1507, SEQ ID NO:1508, SEQ ID NO:1509, SEQ ID NO:1510, SEQ ID NO:1511, SEQ ID NO:1512, SEQ ID NO:1513, SEQ ID NO:1514, SEQ ID NO:1515, SEQ ID NO:1516, SEQ ID NO:1517, SEQ ID NO:1518, and SEQ ID NO:1519;

or a complement of said sequence.

4. An isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109,

SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145. SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEO ID NO:175, SEO ID NO:176, SEO ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262,

SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEO ID NO:315, SEQ ID NO:316. SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415,

SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424. SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451. SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568,

SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEO ID NO:704, SEQ ID NO:705, SEO ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721,

SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775, SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784, SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829, SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEO ID NO:866, SEO ID NO:867, SEO ID NO:868, SEO ID NO:869, SEQ ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874,

SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEO ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883. SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892. SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901. SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937, SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEO ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID

NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID

NO:1161, SEQ ID NO:1162, SEO ID NO:1163, SEQ ID NO:1164, SEO ID NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID

NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ ID